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AROA VIBPA STANDARD;
Q87QX9;
10-OCT-2003 (Rel. 42, Created)
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drosophila
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P10941
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                      141681 segs, 52070155 residues
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REV SIVCZ
UMEI YEAST
MDLB BUCBP
YK47 YEAST
MSRA VIBPA
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TYNK_BOVIN
CARB_STAAM
CARB_STAAM
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee.ebb.sib.ch).
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Lancet 361.743-749(2003).
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10-OCT-2003 (Rel. 42, Last annotation update)
3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-
3-phosphoshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS).
AROA OR VP1020.
Vibrio parahaemolyticus.
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HAMAP, MF 00210; 1.
InterPro; IPR001986; EPSP synth.
Pfam; PF00275; EPSP synthase; 1.
PROSITE; PS00104; EPSP SYNTHASE 1; 1.
PROSITE; PS00104; EPSP SYNTHASE 2; 1.
Aromatic amino acid blosynthesis; Transferase; Complete proteome. SEQUENCE 426 AA; 46094 MM; 373D39CC5BA1F70F CRC64;
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P40848
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P44677
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Pred. No. 5.6;
1; Mismatches 3; Indels
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-i- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-i- SIMILARITY: Belongs to the RPSP synthase family.
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   THIK SALTY
SISI YARIJ
YALIS YARIJ
YILS VIBBA
DHPI SCHPO
PERA CABEL
PDRB YEAST
A10A HUMAN
POLG PEWWN
ILLIA BOVIN
ILLIA CAPHI
ILLIA SHEEP
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STRAIN-RIMD 2210633 / Serotype 03:K6;
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Misc-difference
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                                                                                                          3, 2004, 11:31:01 ; Search time 45.9333 Seconds (without alignments) 67.664 Million cell updates/sec
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Compugen Ltd.
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GenCore version
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ALIGNMENTS

/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7" The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the virus Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5. 'note= "N-terminal acetyl" /note= "C-terminal amide" 'note= "D-form residue" Location/Qualifiers Brunck TK; ABB80525 standard; peptide; 11 AA Claim 17; Page 64; 69pp; English. 21-JUL-2000; 2000US-0220101P. 19-JUL-2001; 2001WO-US023169 (first entry) Lim-Wilby M, Levy OE, (CORV-) CORVAS INT INC WPI; 2002-361643/39.

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Gaps

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Indels

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Mismatches

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11; Conservative

Matches

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invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                    'note= "Valy1 carbony1 forming keto-amide linkage with
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-amide linkage with residue 7"
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                                                                                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46.
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                  ABB80566 standard; peptide; 11 AA.
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                                   Brunck TK;
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                                    Lim-Wilby M, Levy OE,
            (CORV-) CORVAS INT INC
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                                                                                                                                                                Levy OE,
                                                                                                                                       (CORV-) CORVAS INT INC
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11 AA;
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Matches 11;
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ABB80567 RESULT

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hopatitis C virus
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ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #39.
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ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus, HCV, serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #6.
                                                      Claim 17; Page 65; 69pp; English
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                                                                                                                                                                                                                                          1 EEVVPXGMSYS 11
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                                                                                                                                                                       Sequence 11 AA;
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Modified-site
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                                 protease
         Novel
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standard; peptide; 11 AA.

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EEVVPXGMSYS

(first entry

'note= "Norvaly1 carbony1 forming keto-amide linkage with

residue 7"

/note= "C-terminal amide" note= "D-form residue" note= "D-form residue"

Brunck TK;

Claim 17; Page 64; 69pp; English.

note= "N-terminal acetyl"

Location/Qualifiers

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        The sequence represents a peptide compound of the invention having the hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Leucyl carbonyl forming keto-amide linkage with
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #44
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                                                                                                                                                                96.2%; Score 50; DB 5; Length 11; 100.0%; Pred. No. 0.002; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             residue 7"
                                                                                                                                                                   Query Match 96.2
Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                     Sequence 11 AA;
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activity usefu
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                                                                                                                                                                                                                                                                                                                                                                              ABB80564;
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Gaps

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96.2%; Score 50; DB 5; Length 11; 100.0%; Pred. No. 0.002; ive 0; Mismatches 0; Indels

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ABB80561 standard; peptide; 11 AA.
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                    Misc-difference
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                                                                                                                                       Key
Modified-site
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                             ABB80561;
                                                                                                  virucide
                                                                                                                                                                                                                                                                                                                                                                                                                               protease
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                                                                                                                                                                                                                                                               /note= "Alpha-propynyl-glycinyl-carbonyl residue forming
a keto-amide linkage with residue 7"
11
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                     Gaps
                                                                                                                                                                                Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #48
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100.0%; Pred. No. 0.002;
iive 0; Mismatches 0; Indels
DB 5; Length 11;
0.002;
thes 0; Indels
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Pred. No. 0.00
0; Mismatches
                                                                                                                                                                                                                                                           'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                            /note= "C-terminal amide"
                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                           ABB80568 standard; peptide; 11 AA.
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   96.22,
100.0%; Pre-
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  96.2%;
                                                                                                                                                   (first entry)
                     11; Conservative
                                                       EEVVPXGMSYS 11
                                        1 EEVVPXGMSYS 11
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           Local Similarity
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   Query Match
            Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
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                                                                                                                                                                                                                                                                                  'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Oxymethionine"
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(first entry)
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11; Conservative

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1 EEVVPXGMSYS 11

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EEVVPXGMSYS

Fri

(first entry)

08-OCT-2002

/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"

/note= "C-terminal amide" 'note= "D-form residue"

'note= "N-terminal acetyl"

Location/Qualifiers

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                   Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
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Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4
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Best Local Similarity
The Total Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Norvaly1 carbony1 forming keto-amide linkage with
                                                        "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                  ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8
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Pred. No. 0.013;
); Mismatches 1; Indels
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                                  note= "N-terminal acetyl"
                                                                                                                                                "C-terminal amide"
                                                                                                 note= "D-form residue"
                                                                                                                        'note= "D-form residue"
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             Location/Qualifiers
                                                                                                                                                                                                                                                                                                   Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB80528 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                          2001WO-US023169
                                                                                                                                                                                                                                                  21-JUL-2000; 2000US-0220101P
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Matches 10; Conservative
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                                                             /note=
                                                                                                                                                                                                                                                                             (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                     Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EEVVPXGMDYS
                                                                                                                                                                                                                                                                                                                             WPI; 2002-361643/39.
                                                                                     Misc-difference
                                                                                                             Misc-difference
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Modified-site
             Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                     Novel peptide
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                                              Modified-site
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                                                                                                                                                                                                   31-JAN-2002
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Gaps

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Score 46; DB 5; Length 11; Pred. No. 0.013; 0; Mismatches 1; Indels

88.5%; 90.9%;

Conservative EEVVPXGMSYS 11

11

EEVVPXGMDYS

Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.

Synthetic

(first entry)

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
                                                             ___/note= "C-terminal amide"
                                  /note= "D-form residue"
                                                                                                                                                                                                                                            Lim-Wilby M, Levy OE, Brunck TK;
                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 64; 69pp; English.
                                                                                                                                                    19-JUL-2001; 2001WO-US023169.
                                                                                                                                                                                   21-JUL-2000; 2000US-0220101P
residue 7"
Misc-difference B
                                                                                                                                                                                                               (CORV-) CORVAS INT INC.
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                                                                                             WO200208251-A2
                                                 Modified-site
                                                                                                                          31-JAN-2002.
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Gaps 0;

Score 46; DB 5; Length 11; Pred. No. 0.013; 0; Mismatches 1; Indels

Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative

Sequence 11 AA;

Search completed: June 3, 2004, 11:48:22 Job time: 45.9333 secs

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Sequence Sequence Sequence

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DS-09-134-UOC-3738, Application US/09134000C

Sequence 3738, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:
APPLICANT: LYDIN DOUGETEE-Stamm et al APPLICANT: LYDIN DOUGETEE-Stamm et al APPLICANT: LYDIN DOUGETEE-STAMM ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTERACCECUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: DATE: 1998-08-13

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SEQ ID NO 3738

LIBRICH 332
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09408020
| Sequence 4, Application US/09408020
| Sequence 4, Application US/09408020
| Sequence 4, Application Galaxian
| Sequence 6.632310
| Sequence 6.632310
| APPLICANT: Swanson, Ronald V. APPLICANT: Feldman, Robert A. APPLICANT: Feldman, NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM TITLE REFERENCE: DCORP.002A | TILE REFERENCE: DCORP.002A | TILE REPERSINGE: 1999-09-29 | CURRENT FILING DATE: 1998-09-29 | PRIOR APPLICATION NUMBER: 60/102,294 | PRIOR PLING DATE: 1998-09-29 | NUMBER OF SEQ ID NOS: 123 | SOFTWARE: PASESEQ for Windows Version 3.0 | SEQ ID NO 4 | LENGTH: 13472 | LENGTH: 13472 | LENGTH: 13472 | LENGTH: 19472 | LENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 4; Length 3472;
Pred. No. 1.1e+02;
4; Mismatches 1; Indels
                          US-08-464 517-6
US-08-264-377-6
US-08-264-377-6
US-08-263-5000-6
US-08-264-517-23
US-08-246-361A-6
US-08-464-361A-23
US-08-465-361A-23
US-08-465-361A-23
US-08-46-361A-23
US-08-46-361A-23
US-08-46-361A-120-8
US-08-46-517-129
US-08-46-517-129
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US-08-46-517-129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ; ORGANISM: Cenarchaeum symbiosum US-09-408-020-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Enterococcus faecalis
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54.58;
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US-09-134-000C-3738
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Query Match
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Matches
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Sequence 73, Appl
Sequence 73, Appl
Sequence 2902, Ap
Sequence 7885, Appl
Sequence 2, Appli
Sequence 236, Appl
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                                                                                                          June 3, 2004, 11:36:47; Search time 11.7333 Seconds (without alignments) 48.399 Million cell updates/sec
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
                GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-134-000C-3738
US-09-228-986-7378
US-09-540-236-2902
US-09-328-352-7885
US-09-760-946-2
US-09-760-946-3
US-08-637-759B-236
US-08-637-759B-236
US-08-201-355A-236
US-08-201-945-236
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US-08-580-988A-23
US-08-460-694-4
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US-08-463-772-21
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US-08-464-517-22
US-08-246-361A-22
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US-07-667-711B-4
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Maximum Match 100%
Listing first 45 summaries
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                                                                                protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length DB
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Gaps

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Patent No. 6562958
GENERAL INFORMATION
APPLICANT; GAYY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUVANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICANION NUMBER: US/09/328,352
CURRENT APPLICANION NUMBER: US/09/328,352
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7885
LENGTH: 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cameron, Dale R.
APPLICANT: Cameron, Dale R.
APPLICANT: Gancon, Dale R.
APPLICANT: Ghicher, Anne-Marie
APPLICANT: Ghicher, Nathalie
APPLICANT: Ghicher, Nathalie
APPLICANT: Ghicher, Nathalie
APPLICANT: Halmos, Teddy
APPLICANT: Lilias-Brunds Facity Betties Active Against the Hepatitis C Virus
FILE REFERENCE: 13/076-1-C1
CURRENT PAPLICANTON NUMBER: US 09/760,946
CURRENT FILING DATE: 2001-08-23
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
; OTHER INFORMATION: Substrate for recombinant HCV NS3 protease radiometric assay
US-09-760-946-2
                                                                                                                                                                                                                                                                                                                                                                   65.4%; Score 34; DB 4; Length 1407; 66.7%; Pred. No. 2.5e+02; Live 2; Mismatches 1; Indels
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Sequence 7885, Application US/09328352
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Patent No. 6608027
GENERAL INPORMATION:
APPLICANT: Teantrizos, Youla S.
APPLICANT: Cameron, Dale R.
APPLICANT: Faucher, Anne-Marie
APPLICANT: Ghiro, Elise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09760946
Patent No. 6660802.
GENERAL INFORMATION:
APPLICANT: Fsantrizes, Youla S.
                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7885
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Best Local Similarity 45.5%;
Matches 5; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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US-09-760-946-2
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US-09-760-946-3
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Batent No. 6673910.
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: PCP DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PCP DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 2902
LENGTH: 1191
                                                                                                                                                                                                                                                                                                                                                                             Sequence 73, Application US/09228986

Patent No. 635198

Patent No. 635198

Patent No. 635198

APPLICANT: Strabala, Timothy

APPLICANT: Strabala, Timothy

APPLICANT: Nieuwenhuizen, Niels

TITLE OF INVENTION: Compositions Isolated from Plant Cells

TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling

FILE REFERENCE: 11000/1020

CURRENT PAPLICATION NUMBER: US/09/228,986

CURRENT FILING DATE: 1999-01-12

NUMBER OF SEQ ID NOS: 130

SEQ ID NO 73

LENGTH: 947
            ; NAME/KEY: MISC FEATURE
; LOCATION: (3277.. (328)
; OTHER INFORMATION: Amino acids 327 & 328 are Xaa wherein Xaa = any amino acid.
US-09-134-000C-3738
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                                                                                                                                       Query Match 69.2%; Score 36; DB 4; Length 382; Best Local Similarity 66.7%; Pred. No. 22; Matches 1; Indels Matches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.4%; Score 34; DB 4; Length 947; 66.7%; Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                               332 LIPEGMSYS 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-228-986-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: M.catarrhalis
US-09-540-236-2902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       686 VMPSGISYS 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               783 ÉILÞVĠMAY 791
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Best Local Similarity
'...hes 5; Conserve
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US-09-540-236-2902
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US-09-328-352-7885
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US-09-228-986-73
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63.5%;
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                       LENGTH: 45 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHERICAL: NO
US-08-637-759B-236
         SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acide
                                                                                                                                                                                                                                                    6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                  1 EEVVPXGMSY 10
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EEISPLGWSY 10
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Best Local Similarity
Matches 6; Conserva
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APPLICANT: Goudreau, Nathalie
APPLICANT: Halmos, Tredy
APPLICANT: Llinas-Brunet, Montse
TITLE OF INVENTION: Macrocyclic Peptides Active Against the Hepatitis C Virus
FILE REFERENCE: 13/0761-C1
CURRENT APPLICATION NUMBER: US/09/760,946
CURRENT PILING DATE: 2001-08-23
PRIOR PRIOR APPLICATION NUMBER: US 69/542,675
PRIOR APPLICATION NUMBER: US 60/128,011
PRIOR APPLICATION NUMBER: US 60/128,011
PRIOR APPLICATION NUMBER: US 60/128,011
NUMBER OF SEQ ID MOS: 5
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 63.5%; Score 33; DB 4; Length 12; Best Local Similarity 45.5%; Pred. No. 1.7; Matches 5; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 236, Application US/08637759B
Sequence 236, Application US/08637759B
Patent No. S87631
GENERAL INFORMATION:
GENERAL INFORMATION:
IGNERAL INFORMATION:
ITELEPROWN:
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INFORMATION FOR SEQ ID NO: 236:
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                                                                                                                                                                                                                                                                                                                                                                                        FEATURE: OTHER INFORMATION: Tracer for NS3 protease assay NAME/XEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DDIVPCSMSYT 11
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                                                                                                                                                                                                                                                                                               SEQ ID NO 3
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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Score 33; DB 2; Length 45; Pred. No. 7.8; 1; Mismatches 3; Indels
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Pred. No. 7.8;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IMP PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/871,355A

FILING DATE: 09-JUN-1997

CLASSIFICATION: 435

PRIOR APPLICATION: 435

ATPLING DATE: 11-DEC-1995

CLASSIFICATION: 435

ATPLING DATE: 11-DEC-1995

CLASSIFICATION: 435

ATPLING DATE: 11-DEC-1995

CLASSIFICATION: 435

ATPLING DATE: 11-DEC-1995

TELERRENCE/DOCKET NUMBER: RPMS 101 CON

TELECOMMUNICATION INFORMATION:

TELERRENCE (404) 873-8794

TELERRENCE (404) 873-8795

INFORMATION FOR SEQ ID NO: 236:

SEQUENCE CHRARACTERISTICS:

LEAGTH: 45 aniho acids
                                                                                                                                                                                                                                                                                                 Parent No. 6015669
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                          US-08-871-355A-236
; Sequence 236, Application US/08871355A
; Patent No. 6015669
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Sequence 66, Application US/09357952

Patent No. 6248904

GERERAL INFORMATION:
GERERAL INFORMATION:
APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
APPLICANT: Drewe, John A.
TITLE OF INVENTION: No. 6248904e1 Fluorescence Dyes and Their Applications for Whole-
ITTLE OF INVENTION: Pluorescence Screening Assays for Caspases, Peptidases, Proteases
ITTLE OF INVENTION: Other Enzymes and the Use Thereof
FILE REPERENCE: 1735.003001
CURRENT APPLICATION NUMBER: US/09/357,952
CURRENT PAPLICATION NUMBER: US 60/093,642
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5171197-30

FRACET NO. 5177197

APPLICANT: KANRAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;

MENNSTEDT, CARISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH,

JENN; HELDIN, CARL-HERNIEN;

TILE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING

HUMBER OF SEQUENCES: 53

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/487,343

FILING DATE: 27-FEB-1990
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                                                                                                                                                          RESULT 12
5177197
APPLICANT: KANZAKI, TETSUTO;OLOFSSON, ANDERS;MOREN, ANITA;
MENSTEDT, CHRISTER;HELLMAN, ULF;MIYAZONO, KOHEI;CLAESSON-WELSH,
JENN,HELDIN, CARL-HENRIK
TITLE OF INVERTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
CURRENT APPLICATION DATA:
APPLICATION NUBBR: US/07/487,343
FILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.5%; Score 33; DB 6; Length 1394; 45.5%; Pred. No. 3.9e+02; 1ve 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 6; Length 410;
Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
  3; Mismatches
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Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 45.5
Matches 5; Conservative
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399 KEICPGGMGYT 409
  5; Conservative
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                                                 1 EEVVPXGMSYS 11
                                                                         :|: | || |:
52 KEICPGGMGYT 62
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    Matches
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STATUS 11

SPACENT NO. 5177197

PALEANT: KANZAKI, TETSUTO;OLOFSSON, ANDERS;MOREN, ANITA;

APPLICANT: KANZAKI, TETSUTO;OLOFSSON, ANDERS;MOREN, ANITA;

SWENSTEDT, CHRISTER;HELLMAN, ULF;MIYAZONO, KOHEI;CLAESSON-WELSH;

LENA;HELDIN, CARL-HENRIK

HUMA;HELDIN, CARL-HENRIK

HUMAN TRANSPORMING GROWTH FACTOR-BETAL-BINDING PROTEIN

NUMBER OF SEQUENCES: 53

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/487,343

FILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 65;
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US-09-201-945-236

Sequence 236, Application US/09201945

Patent No. 6342215

GRNERAL INFORMATION:

APPLICANT: David William Holden

TITLE OF INVENTION: Identification of Genes

NUMBER OF SEQUENCES: 501

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrea L. Pabat

STREET: 2800 One Atlantic Center

STREET: 2800 One Atlantic Center

CITY: Atlanta

STATE: Georgia

COUNTRY: USA

COUNTRY: USA

ZIP: 30309-3450

COMPUTER: READABLE FORM:

MEDIUM TYEE: Ploppy disk

COUNTRY: PREDBALE FORM:

MEDIUM TYEE: Ploppy disk

COUNTRY: USA

ZIP: 30309-3450

COMPUTER: IN PC COMPATION

MEDIUM TYPE: Ploppy disk

COUNTRY: PREDBALE FORM:

MEDIUM TYPE: Ploppy disk

COUNTRY: USA

ZIP: 30309-3450

COMPUTER: IN PC COMPATION

MEDIUM TYPE: Ploppy disk

COUNTRY: PRION NUMBER: US/09/201,945

FILING DATE:

CLASSIFICATION NUMBER: 08/637,759

FILING DATE:

CLASSIFICATION NUMBER: 08/637,759
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Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Paber, Patrea 1.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 1284
TELECHNONICATION INFORMATION:
TELEPHONE: (404) 873-8734
TELEPHONE: (404) 873-8736
INFORMATION FOR SEQ ID NO: 236: SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EEVVPXGMSY 10
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Best Local Similarity
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Matches 6; Conserv
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; LENGTH: 65
5177197-51
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                             US-09-201-945-236
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us-09-909-164-5.rai

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Sequence 66, Application US/09521650
Sequence 66, Application US/09521650
Patent No. 6335429
GENERAL INFORMATION:
APPLICANT: While William A.
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cana, John F.W.
APPLICANT: Drew, John F.W.
APPLICANT: Drems, Han-Zhong
TITLE OF INVENTION: No. 6335429e1 Fluorogenic or Fluorescence
TITLE OF INVENTION: Use Thereof
TITLE OF INVENTION UNMER: US/09/521,650
CURRENT FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 09/168,888
EARLIER APPLICATION NUMBER: US 09/061,582
EARLIER APPLICATION NUMBER: US 09/061,582
EARLIER PILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 66
LENGTH: 10
THENGTH: 10
THENGTH: 10
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                                                                                                                                 TYPE: PRT
ORGANIEM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Synthetic
OTHER INFORMATION: Peptide
'S-09-357-952-66
                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Synthetic
OTHER INFORMATION: Peptide
IS-09-521-650-66
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Best Local Similarity 50.0%; Pred. No. 2.3;
Matches 5; Conservative 3; Mismatches 2; Indels
EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
SOFTWARE: PALENTIN VEY. 2.0
SEQ ID NO 66
LENGTH: 10
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!earch completed: June 3, 2004, 12:03:06
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June 3, 2004, 11:57:42; Search time 33.7333 Seconds (without alignments) 91.741 Million cell updates/sec
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/ cgnz 6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
/ cgnz 6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
/ cgnz 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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/ cgnz 6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Aaximum DB seq length: 200000000
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1 EEVVPXGMSYS 11
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Appli Appli

	Sequence 20, Appl	23,	24,	28,	200	ų e		37,		14,	22,	26,	27,	61,	62,	21,	25,	37,	32,	35,		47		46,		34,			Sequence 42, Appl
US-09-909-164-19	-60-SD	-60-SD	US-09-909-164-	-60-SD	US-09-909-16	-60-SD	2 US-09-909-164-36	-60-SD	3 US-09-909-164-43	-60-SD	-60-SD		-60-SD	US-09-909-16	-60-SN	US-09-909-164-	US-09-909-164	US-09-909-164-3	-60-SD	-60-SD	2 US-09-909-164-40	-60- S N	2 US-09-909-164-45	2 US-09-909-164-46	US-09-909-164-	-60-SN	-60-SN	2 US-09-909-164-39	2 US-09-909-164-42
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16	17	18	19	20	21	22	23	24	25	26	27				31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

OUT 1 09-909-164-5 09-90-164-5 APPLICATION WO. US20020068702A1 BEREAL INFORMATION: 10-07-908-10-10-10-10-10-10-10-10-10-10-10-10-10-	
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Sec 1	50
UUT 1 09-909-164-5 GREAL INFORMATION: US20020069702A1 EMERAL INFORMATION: US20020069702A1 APPLICANT: Corves International, Inc. APPLICANT: Lin-Wilby, Marguerita APPLICANT: Lin-Wilby APPLICANT: DOUGHOUS BERTILE REFRENCE: INOUISE: 003-03-05 CURRENT FILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 62 ENGTHAR INFORMATION: Marguerice FRATURE: PRF FRATURE: NOT RES INCATION: (1)(1) COTHER INFORMATION: 11-mer synthesized ac FEATURE: NOTHER INFORMATION: NOTHER INFORMATION: NOTHER INFORMATION: NOTHER INFORMATION: MADPATION FRATURE: NAME/KEY: MOD RES LOCATION: (11)(1) OTHER INFORMATION: MAIDATION OFHER INFORMATION: AMIDATION OFHER INFORMATION: AMIDATION OFHER INFORMATION: AMIDATION OFFICE OFF	Score 50;
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35/09 37/09 37/09 38:05/05/09 37/09/09/09/09/09/09/09/09/09/09/09/09/09/	96.2%;
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actic No.0220020 No.022001 No.022001 No.0320	
pplication US/099 io. US20020068702A MATION: Corvea Internation Lim.Wilby, Margue Levy, Odile E Brunck, Terence K ENTION: NOVEL DEP CE: IND1192-US COO-07-21 CA ID NOS: 62 LentIn Version 3. Lificial sequenc MATION: 11-mer sy COD_RES 1)(1) MATION: ACETYLATI INSC_FEATURE (6)(6) WATION: ACETYLATI COO RES (11)(1)	
A APP	ď
SULT 1 -09-909-164-5 Suganence 5: Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION: APPLICANT: Corvas International, I APPLICANT: Liew, Odile E APPLICANT: Liew, Odile E APPLICANT: Brunck, Terence K TITLE REFERENCE: INO1192-US CURRENT FILING DATE: 2003-03-05 FILE REFERENCE: LOOPERS: 06/20/1 CURRENT FILING DATE: 2000-07-21 NUMBER: OF SEQ ID NOS: 62 SOGTWARE: PARTICATION NUMBER: 60/220, 1 NUMBER: OF SEQ ID NOS: 62 SOGTWARE: PARTICATION NUMBER: 60/220, 1 NUMBER: OF SEQ ID NOS: 62 SOGTWARE: Ratentin version 3.1 SEQ ID NO 5 LENGTH: 11 CREATURE: NATICITICAL SEQUENCE FEATURE: NOD RES COCHTER INFORMATION: 11-mer synthes FEATURE: NOD RES LOCATION: (4). (1) OTHER INFORMATION: norvaline-(CO) FEATURE: NOD RES LOCATION: (6). (6) OTHER INFORMATION: norvaline-(CO) THER INFORMATION: NOTABLING FEATURE: NAME/KEY: MOD RES LOCATION: (11). (11) OTHER INFORMATION: AMIDATION FEATURE: NAME/KEY: MOD RES LOCATION: (11). (11)	Query Match
19-909-16 3-909-16 3-909-16 3-909-16 3-91-201 NERAL INI PPLICANT PREATURE: NAME/KEY NAME/KEY LOCATION OTHER INI PERATURE: NAME/KEY LOCATION OTHER INI PRATURE: NAME/KEY LOCATION OTHER INI OTHER INI PRATURE: NAME/KEY LOCATION OTHER INI OTHER INI OTHER INI PRATURE: NAME/KEY LOCATION OTHER INI	, L
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NES-09-909-164-10
| Sequence 10, Application US/09909164
| Sequence 10, Application US/09909164
| Sequence 10, Application No. US20020068702A1
| Public No. US20020068702A1
| APPLICANT: Lin-Wilby, Marguerita
| TILE REFERENCE: 1001192-US
| CURRENT APPLICATION NUMBER: US/09/909,164
| CURRENT FILING DATE: 2003-03-25
| PRIOR FILING DATE: 2003-03-21
| NUMBER OF SEQ ID NOS: 62
| SOFTWARE: Patentin version 3.1
| ENGTHE: Lin-Wilby DATE: Lin
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LOCATION: (6)...(6)
THER INFORMATION: norvaline-(CO)
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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COTHER INFORMATION: D-amino acid
US-09-909-164-9
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NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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NAME/KRY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
PEATURE:
                  NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
                                                                                                                                                                                          TYPE: PRT ORGANISM: artificial sequence
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THER INFORMATION: AMIDATION
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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NAME/KEY: MOD_RES
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Sequence 6, Application US/09909164

Sequence 6, Application US/09909164

Sequence 6, Application No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby

APPLICANT: Lim-Wilby

FILE REFERENCE: INOL192-US

CURRENT PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQ ID NO 6

LENGTH: Limited DATE: Limited DA
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Sequence 9, Application US/09909164
Schication No. US20020068702A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim.Wallby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Forence K
TILE ON INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR FILING DATE: 2000-07-21
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OTHER INFORMATION: 11-mer synthesized according to example 1
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                           Pred. No. 0.0014; i Mismatches 0; Indels
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LOCATION: (1) .. (1)
COTHER INFORMATION: ACETYLATION
FRATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6) .. (6)
COTHER INFORMATION: norvaline-(CO)
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (9) .. (9)
OTHER INFORMATION: D-amino acid
100.08; FI
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ORGANISM: artificial sequence
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, LOCATION: (11) ... (11)
, OTHER INPRMATION: AMIDATION
US-09-909-164-6
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Matches 11; Conserv
                      Best Local Similarity
Matches 11; Conserv
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Sequence 49, Application US/09909164
; Sequence 49, Application US/09909164
; Publication No. US202020068702A1
; Publication No. US202020068702A1
; GENERAL INFORMATION:
; APPLICANT: Corvas International, Inc.
; APPLICANT: Lim-Wilby, Marguerita
; TITLE OF INVENTION: NOVEL PEFTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEDATITIS C
; FILE REPERRICE: 1001-92-US
; CURRENT APPLICATION NUMBER: 60/220,101
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
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96.2%; Score 50; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                      FEATURE: OTHER INFORMATION: 11-mer synthesized according to example FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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100.0%; Pred. No. 0.0014;
tive 0; Mismatches 0;
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NAME/KEY: MISC_PEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norleacine-(CO)
                                                                                                                                                                                                                            NAME/KEY: MOD_RES
LOCATION: (1)...(1)
COTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
US-09-909-164-48
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OTHER INFORMATION: ACETYLATION
FRATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 48
                                                                                                       TYPE: PRT ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: artificial sequence
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Matches 11; Conservative
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NAME/KEY: MOD_RES
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Publication No. US20020068702A1

GENERAL INTORMATION:
GENERAL INTORMATION:
APPLICANT: Levy, Odile E
CURRENT APPLICANTON: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IND1192-US
CURRENT APPLICATION NUMBER: US(09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN Version 3.1
LENGTH: 11
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Sequence 48, Application US/09909164

Sequence 48, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lin-wilby, Marguerita
APPLICANT: Levy, Oddle E
APPLICANT: Levy, Oddle E
APPLICANT: Lin-wilby, Marguerita
APPLICANT: Levy, Oddle E
TITLE OF INVENTOR: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
FILE REPERENCE: US/09/09)164

CURRENT FILING DATE: 2003-03-25

PRIOR PILING DATE: 2000-07-21
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                                                                           Query Match 96.2%; Score 50; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 11; Conservative 0; Mismatches 0; Indels
  OTHER INFORMATION: D-amino acids JS-09-909-164-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
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| OTHER INFORMATION: valine-(CO)
| JS-09-909-164-47
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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NAME/KEY: MISC_FEATURE
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NAME/KEY: MOD_RES
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Sequence 52, Application US/09909164

| Sequence 52, Application No. US20020068702A1
| Publication No. US20020068702A1
| Publication No. US20020068702A1
| APPLICANT: Lim-Wilby, Marguerita
| CURRENT FILING DATE: 1001192-US
| PRIOR FILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SEQ ID NO 52
| LENGTH: Lim-Wilby, Marguerita
| LENGTH: Lim-Wilby, 
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96.2%; Score 50; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels
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LOCATION: (6)...(6)
; OTHER INFORMATION: (8,8)-allothreonine-(CO)
US-09-909-164-51
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; OTHER INFORMATION: propynyl glycine-(CO)
US-09-909-164-52
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FRATURE:
NAME/KEY: MOD_RES
                                                                                        LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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                                                                                                                                                                                FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
COTHER INFORMATION: AMIDATION
FEATURE:
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OTHER INFORMATION: AMIDATION
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US-09-909-164-8
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                                                                                                                               US-09-909-164-50

Sequence 50, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:
APPLICANT: Cin-wilby, Marguerita
APPLICANT: Lin-wilby, Marguerita
APPLICANT: Lin-wilby, Marguerita
APPLICANT: Brunck, Terence K
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TILE REFERENCE: IN01123-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR PRILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 50
LENGTH: 11
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| Sequence 5.7, Application US/09009164
| Sequence 5.7, Application No. US2002068702A1
| GENERAL INFORMATION:
| APPLICANT: Corvas International, Inc. APPLICANT: Lim-Wilby, Marguerita
| FILE REFERENCE: INOLI92-US
| CURRENT FILING DATE: 2000-07-21
| VINNERO F SEQ ID NOS: 62
| SOFTWARE: Patentin Version 3.1
| LENGTH: Lim-Wilby DATE: Lim
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ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
FEATURE:
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ORGANISM: artificial sequence
FEATURE:
1 EEVVPXGMSYS 11
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APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: INO1192-US
CURRENT APPLICATION NUMBER: US/09/909,164
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTION OF 52
SOFTWARE: PATENTION OF 52
SOFTWARE: PATENTION OF 52
SOFTWARE: ATENTION OF 53
LENGTH: 11
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OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11) ... (11)
OTHER INFORMATION: AMIDATION
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                                                                                                                                                                                                                                                                                                                                 Query Match

88.5%; Score 46; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 1; Indels
                                                                                     FEATURE:

NAME/KEY: MISC_FEATURE

LOCATION: (6)...(6)

OTHER INFORMATION: norvaline-(CO)

FEATURE:

NAME/KEY: MISC_FEATURE

LOCATION: (8)...(8)

OTHER INFORMATION: D-amino acid
US-09-909-164-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
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NAME/KEY: MISC_FEATURE
LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
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FEATURE:
NAME/KEY: MOD RES
NCATION: (11). (11)
OTHER INFORMATION: AMIDATION
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Best Local Similarity
Matches 10; Conserva
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US-09-909-164-13
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Sequence 12, Application US/09909164

Publication No. US20020068702A1

Sequence 12, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Lim-Wilby, Marguerita

CURRENT APPLICANTION NUMBER: 60/220,101

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQ ID NO 12

EBNOTH: LIM-WILDS

LENOTH: 11

TENOTH: 11

TENOTH: 11
                    APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile B
APPLICANT: Levy, Odile B
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION: NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 11
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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LOCATION: (9). (9)
OTHER INFORMATION: D-amino acid
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NOAME/KEY: MOD_RES
LOCATION: (1) - (1)
OTHER INFORMATION: ACETYLATION
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OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: artificial sequence
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Best Local Similarity 90.9%;
Matches 10; Conservative
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LCCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
IS-09-909-106-164-8
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  SENERAL INFORMATION:
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LOCATION: (1)...(1)
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Score 45; DB 12; Length 11;
Pred. No. 0.015;
0; Mismatches 1; Indels
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OTHER INFORMATION: norvaline-(CO)
FEATURE:
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1. LOCATION: (8) ...(8)

CTHER INFORMATION: D-amino acid

US-09-909-164-11
                                                                        LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
PEATURE:
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Best Local Similarity 90.9%;
Matches 10; Conservative
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LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
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| Sequence 11, Application US/09909164
| Publication No. US20020068702A1
| GENERAL INFORMATION:
| APPLICANT: Corvas International, Inc. APPLICANT: Lawy, Odile E
| APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
| TILLE REPERENCE: 100192-105
| TILLE REPERENCE: 100192-03-03-05
| FILLING DATE: 2003-03-25
| PRIOR PILLING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SOFTWARE: Patentin version 3.1
| LENGTH: 11
                                                                                                                                                                              APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Lim.Wilby, Marguerita
APPLICANT: Lim.Wilby, Marguerita
APPLICANT: Levy, Odile B
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: 08/99/99,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
SUMPRER: PATENT OF NOS: 62
SUFTWARE: PATENT OF NOS: 62
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ORGANTSM: artificial sequence
PERATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
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ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
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Pred. No. 0.015;
0; Mismatches 1; Indels
                                                                                Sequence 7, Application US/09909164
Publication No. US20020068702A1
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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NAME/KEY: MISC FEATURE
LOCATION: (9) ... (9)
OTHER INFORMATION: D-amino acid
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
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Best Local Similarity 90.9%;
Matches 10; Conservative (
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CCATION: (11)...(11)
COTHER INFORMATION: AMIDATION
US-09-909-164-7
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117.567 Million cell updates/sec
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                                                                                                                    June 3, 2004, 11:35:47 ; Search time 9 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                 'otal number of hits satisfying chosen parameters:
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1 EEVVPXGMSYS 11
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probable sulfate permease - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T39116
C;Accession: T39116
B;Hunt, C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
A;Accession: T39116
A;Accession:
                                                                                                                                                                                                                          K.Y.; Swanson, R.V.
hypothetical 367K protein - Cenarchaeum symbiosum C;Species: Caracchaeum symbiosum C;Species: Caracchaeum symbiosum C;Species: Caracchaeum symbiosum C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000 C;Accession: T31308
R;Schleper, C.; DeLong, E.F.; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, J. Bacteriol. 180, 5003-5009, 1998 chromosomal variation in natural populations A;Reference number: 220994; MUID:94422450; PMID:9748430
A;Recession: T31308
A;Accession: T31308
A;Coss-references: EMBL:AF083072; NID:93599993; PID:93599394; PIDN:AAC62699.1
C;Superfamily: Cenarchaeum symbiosum hypothetical 367K protein
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Local Similarity 54.5%; Pred. No. 60;
les 6; Conservative 4; Mismatches 1; Indels
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Pred. No. 21;
1; Mismatches 1; Indels
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77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
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A;Gross-references: EMBL:Z81109; PIDN:CAB03241.1; GSPDB:GN00023; CESP:R10D12.10
A;Experimental source: clone R10D12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Lycopersicon esculentum (tomato)
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
C;Accession: S57808
A;Ritle: Nature and regulation of pistil-expressed genes in tomato.
A;Reference number: S57808; MUID:95375233; PMID:7647301
A;Reference number: S57808
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Pattus norvegicus (Norway rat)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Sep-1999
C;Accession: S22-293; I786-65
R;Mitchalmore, C.; Traboni, C.; Cortese, R.
Nucleic Acids Res. 19, 141-147, 1991
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Cyspecies: Gaenorhabditis elegans
Cybate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
CyAccession: T24111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Status: preliminary, nucleic acid sequence not shown
A,Molecule type: mRNA
A,Residues: 1-25 AML>
A,Gross-references: EMBL:U20592, NID:g924625, PIDN:AAA80497.1; PID:g924626
C,Superfamily: plant Kunitz-type proteinase inhibitor
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2; Length 1498;
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Pred. No. 13;
3; Mismatches 2; Indels
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                                                                                                   2; Indels
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A;Molecule type: DNA
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A;Reference number: 219842
     Score 36; DB pred. No. 63; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
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A,Introns: 23/3; 56/3; 113/3; 257/2
     69.2%;
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illarity 54.5%;
Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                   Conservative
                                                                                                                                                                                                                                                                                               1276 EQKIPMGMSY 1285
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les 6; Conserv
     Query Match
Best Local Similarity
Matches 6; Conserv
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R; Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
R; Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
R; Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
A; Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yelld
A; Reference number: A42452, MUD: 92188538; PMID:1546458
A; Accession: A42452
A; Accession: A42452
A; Accession: A42452
A; Accession: A42452
A; Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
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                                                                                                                                                                                                                                                                                          C,Accession: T40413

E,E,Dane, M.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.

Submitted to the EMBL Data Library, August 1998

A,Reference number: 221926

A,Recference number: 221926

A,Recference number: DNA

A,Residuas: preliminary; translated from GB/EMBL/DDBJ

A,Residuae: 1-877 < LYNA

A,Residuae: 1-877 < LYNA

A,Residuae: 1-877 < LYNA

A,Residuae: 1-877 < LYNA

A,Residuae: 1-87 < LYNA

A,Residuae: 1-8
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A;Molecule type: DNA
A;Residues: 1-1498 «KUR»
A;Cross-references: GB:AB001437; PIDN:AAK81629.1; PID:g15026814; GSPDB:GN00168
A;Cross-references: Clostridium acetobutylicum ATCC824
C;Genetics: A;Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VI protein - tobacco yellow dwarf virus (strain Australia)
C;Species: tobacco yellow dwarf virus
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
                                                                                                                                             sulfate permease - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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Score 36; DB 2; Pred. No. 3.5; 3; Mismatches

Similarity 60.0%; 6; Conservative 3

Query Match Best Local Similarity Matches 6; Conserv

Query Match
Best Local Similarity 77.8
Matches 7; Conservative

C,Genetics: A,Gene: SPDB:SPBC3H7.02 A,Map position: 2

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A;Cross-references: SGD:S0005539
A;Map position: 15R
C;Superfamily: hypothetical protein YOR013w
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Best Local Similarity 66.7%;
Matches 6; Conservative
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2405 WPAGLTYS 2413
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.Title: Isolation of two cDNAs encoding zinc finger proteins which bind to the alpha 1-; Reference number: 158280; MUID:91187610; PMID:1901405
.Accession: 822293
.Accession: 822293
.Molecule type: mRNA
.Residues: 1-670 cMTP
.Residues: 1-670 cMTP
.Residues: 1-670 cMTP
.Residues: 2-670 c
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bubmitted to GenBank, June 2000

Authors: Ferreira, V.C.A.; Ferro, J.A.; Franca, S.C.; Franca, S.C.; Franco, M.C.; Frohm, J. J., Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuremae, E.E.; Laigh hado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.G.; Nunes, L.R.; Oliveira, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Goliveira, R.C.; Palmieri, D.A odrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Sancelli, R.V.; Sawasak, Authors: da Silva, A.C.R.; da Silva, A.M.; Verioveki-Almeida, S.; Vettore, A.L.; Z.; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Xylella fastidiosa, Dempired, Agricultured, Verland, Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 #text_changes or IS-157, 2000 #text_changes or IS-157, 2000 #text_changes of the plant pathogen Xylella fastidiosa.

*Reference number: Ag2515; MUID:20365717; PMID:10910347
*Note: for a complete list of authors see reference number A59328 below
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;Molecule type: DNA
sesidues: 1.749 <SIM>
;Cross-references: GB:AE003967; GB:AE003849; NID:g9106347; PIDN:AAF84162.1; GSPDB:GN001
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48;
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Pred. No. 48;
0; Mismatches
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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A; Reference number: A34203; MUID:90169514; PMID:2106471
A; Reference number: A34203; MUID:90169514; PMID:2106471
A; Accession: A34203
A; Status: preliminary
A; Molecule type: mRNA
A; Redidues: L-2717 < RAN>
A; Reladdues: L-2717 < RAN>
A; Cross-references: EMBL:X51435; NID:938017; PIDN:CAA35798.1; PID:938018
B; Baldwin Jr., A.S.; LeClair, K.P.; Singh, H.; Sharp, P.A.
Mol. Cell. Biol. 10, 1406-1414, 199
A; Reference number: A34779; MUID:90205817; PMID:2108316
A; Recession: A34779; MUID:90205817; PMID:2108316
A; Reterence number: A34779
A; Reterence number: A34779
A; Reterence number: A34779
A; Reterence number: Biol. 1072, N/, 1074-1168, YK', 1170-1225, VV', 1227-1434, N/, 1436-1607, I', 1609-16'
A; Cross-references: GB:M32019
C; Superfamily: HIV-EP2 enhancer-binding protein
C; Keywords: DNA binding; transcription; zinc finger
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rell division inhibitor (minD-2) homolog - Archaeoglobus fulgidus

cell division inhibitor (minD-2) homolog - Archaeoglobus fulgidus

C;Species: Archaeoglobus fulgidus

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 26-Aug-1999

C;Accession: K69491

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, G.G.; Gill, S.; Kirkness, E.F., Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
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Pred. No. 14;
1; Mismatches
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A.Autnors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A.Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeq A.Reference number: A62250; MUID:98049343; PMID:9389475
A.Recession: H69491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable ABC substrate-binding protein, iron UU359 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Species: B8-Aug-2000 #text_change 02-Sep-2000 C;Dacession: B8-2000 #text_change 02-Sep-2000 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, B.Y.; Cassell, G.H. submitted to GenBank, February 2000 A;Decession: The complete sequence of Ureaplasma urealyticum: Alternate views of a min A;Reference number: A82870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein 1 - Campylobacter jejuni (fragment)
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Species: 16-Aug-1996 #text_change 08-Oct-1999
C;Accession: 140758; 847317
R;Hani, E.K.; Chan, V.L.
J. Bacteriol. 177, 2396-2402, 1995
A;Title: Expression and characterization of Campylobacter jejuni benzoylglycine amidohyd A;Reference number: 140758; MUID:952473; PMID:7730270
                                                                                                                                                                                                                                               A;Residues: 1-252 «KUE»
A;Cross-references: GB:AE000970; GB:AE000782; NID:g2689293; FIDN:AAB89318.1; PID:g264860
C;Superfamily: cell division inhibitor minD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: GB:AE002133; GB:AF222894; NID:g6899339; PIDN:AAF30768.1; GSPDB:GN001; Experimental source: serovar 3; biovar 1
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                                                                                                                                                                                     Status: preliminary; nucleic acid sequence not shown; translation not shown Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                               65.4%; Score 34; DB 2; Length 252; 75.0%; Pred. No. 24; vative 1; Mismatches 1; Indels
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A;Molecule type: DNA
A;Residues: 1-94 <RES>
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Best Local Similarity 75.0
Matches 6; Conservative
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81 EVIPAGMS 88
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Best Local Similarity
Matches 7; Conserv
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A,Gene: ABCsbp-5; UU359
A,Genetic code: SGC3
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Molecule type: DNA
Residues: 1-544 <GLA>
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C;Accession: B90544
F;Chanbaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I., Nichald, C.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I., Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pult A;Recence number: A99512; MUID:21267165; PMID:11353084
A;Accession: B90544
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                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AL445566; PID:g14089674; PIDN:CAC13434.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
508 ribosomal protein L20 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
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Pred. No. 17;
0; Mismatches 2; Indels
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AjGenetic code: SGC3
CjSuperfamily: Escherichia coli ribosomal protein L20
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Best Local Similarity 77.8%;
Matches 7; Conservative
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A; Residues: 1-116 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=ATCC 25586;

MEDINES-1886394; PubMed=11889109;

Maptines-1886394; PubMed=11889109;

Maptines-1898394; PubMed=11889109;

Maptines-1898394; PubMed=189894;

Maptines-1898394; PubMed=189894;

Maptines-1898394; PubMed=189894;

Maptines-1898394; PubMed=189894;

Maptines-1898394; Maptines-189896;

Maptines-1898394; PubMed=189896;

Maptines-1898394; PubMed=189896;

Maptines-1898394; PubMed=189896;

Maptines-1898394; PubMed=189896;

Maptines-1898396; PubMed=18986;

Maptines-1898396; PubM
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escherichia
escherichia
                     homo sapien
homo sapien
                                                    crithidia f
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                                                                                                                             rattus norv
tomato aspe
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamcyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamcyl-phosphate synthetase ammonia chain).
CARB OR FN0422.
944677 P 944677 P 944677 P 944677 P 999616 P 999518 P 952384 P 952384 P 952384 P 952384 P 956911 P 956918 P 96918 P 916918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
Fusobacterium.
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                                                                                                                                                                                                                                                        AL I GNMENTS
                   ENP3_HUMAN
S216_HUMAN
GSP_CRIFA
PRTP_HSV6U
PRTP_HSV6Z
SCT1_YEAST
EDD_RAT
                                                                                                                                          VIA_TAV
RHSA_ECOLI
RHSC_ECOLI
RHSB_ECOLI
   FOLB HABIN
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INTEPRO; IPR006475; CarA L glu.

INTEPRO; IPR006491; CPase L.

INTEPRO; IPR005499; CPase L. D2.

INTEPRO; IPR005480; CPase L. D3.

INTEPRO; IPR005481; CPase L. N.

INTEPRO; IPR004362; MGS IIRe.

Pfam; PF00289; CPSase L. Chain; 2.

Pfam; PF00289; CPSase L. Chain; 2.
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PF02787; CPSase_L_D3; 1.
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726
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 CARB FUSNN
QBRGB6;
 CARB FUSNIN
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                                                                                                                                            (without alignments)
117.693 Million cell updates/sec
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                                                                                                                           time 4.86667 Seconds
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Q04351
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Q28330
Q045489
Q097xb0
Q097xb0
P6696
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P30279
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                             otal number of hits satisfying chosen parameters:
                                                                                                                             June 3, 2004, 11:32:06; Search
                                                                                                                                                                                                                                                                                                                                141681 segs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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CY14_NEUCR
A10A_HUMAN
RL20_MYCPU
YJ49_ARCFU
Y990_CAMJE
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Maximum Match 1008
Listing first 45 summaries
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MOUSE
RAT
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MOUSE
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GSR2
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52
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Result No.

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"The genome sequence of Schizosaccharomyces pombe.";
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AC P316T9
DT 01-JUL
DT 01-JUL
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DE WY1.
OS TOBACC
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Matches
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=972;

Nod V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Rajandream M.A., Lyne M., Lyne R., Stewart A., Radouco U., Peat N., Hayles U., Bakes S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Radouco S., Hornby T., Howarth S., Huckle E.U., Hunt S., Jagele K., Genles K., Tones L., Jones M., Leather S., McDonald S., McLean J., Honger K., O'Neil S., Mungall K., Murphy L., Nibbett D., Odell C., Annes K., O'Neil S., Mangall K., Murphy L., Nibbett D., Odell C., Attherford K., Rutter S., Saunderes D., Seeger K., Sharp S., Relton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Welton J., Volnckart G., Aert R., Schaefer M., Maeller-Auer S., Rebell C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Rabbin C., Puchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Rabbin C., Puchs M., Reiner S., Gloux S., Lelaure V., Mottier S., Glet D., Sanches S., Kannapez S., Moestl D., Hilbert H., Rainbert H., Mandutt R., Purnelle B., Goffeau A., Cadieu E., Dimenaz J., Sanchez M., Garzon A., Thode G., Dagar R.R., Cruzado L., Jimenez J., Sanchez M., dal Rey F., Benito J., Ander M., Gallardin C., Pallada V.A., Garzon A., Howeller J., Moreno S., Annapez M., Rochet M., Gallardin C., Pallada V.A., Garzon A., Revuelta J.L., Moreno S., Annapez M., Rochet M., Gallardin C., Pallada V.A., Garzon A., Revuelta J.L., Moreno S., Annapez M., Rochet M., Gallardin C., Pallada V.A., Revuelta J.L., Moreno S., Annapez M., Rochet M., Gallardin C., Pallada V.A., Revuelta J.L., Moreno S., Annapez M., Rochet M., Gallardin C., Pallada V.A., Revuelta J.L., Moreno S., Annapez M., Rochet M., Callada V., Nares P.; Shpakovski G.V., Ussery D., B
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                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Pfam; PF02142; MGS; 1.

TIGREAMS; TIGRO1369; CPSASE.

TIGREAMS; TIGRO1369; CPSASE 1; 2.

PROSITE; PS00866; CPSASE 1; 2.

PROSITE; PS00867; CPSASE 2; 2.

PROSITE; PS00867; CPSASE 2; 2.

PROSITE; PS00867; CPSASE 2; 2.

DOMAIN 401 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.

T 401 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.

DOMAIN 547 929 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

DOMAIN 920 GARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

TEPERAT 1 546

REPERAT 1 546
                                                                                                                                                                                                           ATP (POTENTIAL).
ATP (POTENTIAL).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                     Score 38; DB 1; Length 1058; Pred. No. 7; 3; Mismatches 1; Indels
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
Probable Sulfate permease C3H7.02.
                                                                                                                                                                                                                                                                                                                                                          73.1%;
60.0%;
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Best Local Similarity 60...
Best Conservative
Conservative
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190 EIVPNGLNYS 199
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302
302
284
298
300
820
820
1058 AA;
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NCBI_TaxID=4896;
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                                                                                                                                                                                            REPEAT
NP_BIND
NP_BIND
METAL
                                                                                                                                                                                                                                                                                                                             SEQUENCE
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074377;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                   SIMILARLIY.
-- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-- SIMILARITY: Belongs to the SLC26A/SulP transporter (TC 2.A.53)
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Nature 415:871-880(2002).
-I- FUNCTION: HIGH AFFINITY UPTAKE OF SULFATE INTO THE CELL (BY SIMILARITY).
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Viruses, ssDNA viruses; Geminiviridae; Mastrevirus.
NCBI_TaxID=31599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
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                                                                                                                                                                                                                         family.
-!- SIMILARITY: Contains 1 STAS domain.
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PIR, T40413; T40413.
T40413; T40413.
T40413; T40413.
TA0413; T40413.
InterPro; IPR001902.
FROUNDE, SUBP.
FROUNDE, FRO
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TRANSMEM 133 153
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P31619;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sauer U., Duerre P.;
"Sequence and molecular characterization of a DNA region encoding a
"Sequence and molecular characterization of a DNA region encoding a
small heat shock protein of Clostridium acetobutylicum.";
J. Bacteriol. 175:3394-3400(1993).
-!- SIMILARITY: Contains 2 FtsK domains.
-!- CAUTION: Ref.2 sequence differs from that shown due to frameshifts
in positions 76 and 106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
                                                                                                                                                                                                                                                   Gabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                    69.2%; Score 36; DB 1; Length 102; 60.0%; Pred. No. 1.6; tive 3; Mismatches 1; Indels
                                                                                                                                                                              01-FEB-1994 (Rel. 28, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein CAC3709.
                                                                                                                                                                                                                                                                                                                                                                         PRT; 1498 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-108 FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=93273706; Pubmed=8501044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AE007866; AAK81629.1; -.
EMBL, X65276; CAA46379.1; ALT_FRAME.
PIR; B97355; B97355.
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                                                                                                                                           InterPro, IPR002621; Gemini mov. Pfam; PF01708; Gemini mov; I. Hypothetical protein. SEQUENCE 102 AA; 11178 MW: D4
                                                                                                                      EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                 Local Similarity 60.0 les 6; Conservative
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7 QVVPSGINYS 16
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01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel. 42, Last sequence update)
10-CCT-2003 (Rel. 42, Last amnotation update)
Zinc finger protein 40 (Human immunodeficiency virus type I enhancer-binding protein 1) (HIV-BP1) (Major histocompatibility complex binding protein 1) (MBP-1) (Positive regulatory domain II binding factor 1)
(PRDII-BF1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fan C.M., Maniatis T.; "A DNA-binding protein containing two widely separated zinc finger motifs that recognize the same DNA sequence."; Genes Dev. 4:29-42(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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MEDLINE=92232664; PubMed=1567844;
Omichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E.,
Gronenborn A.M.;
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-i- DOMAIN: CONTAINS TWO SETS OF 2 ZINO-FINGERS, WHICH ARE WID SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A ZINO-FINGER IN-BETWEEN.
-i- SIMILARITY: STRONG, TO HIVEP2.
Pfam; PF01580; FtsK SpoiliE; 2.
PROSITE; PS50901; FTSK; 2.
Hypothetical protein; ATP-binding; Complete proteome; Repeat.
DOMAIN 655 857 FTSK 1.
DOMAIN 1001 1188 FTSK 2.
NP_BIND 675 682 ATP (POTENTIAL).
                                                                                                                                                                                                                         69.2%; Score 36; DB 1; Length 1498; 60.0%; Pred. No. 27; 2; Indels ive 2; Mismatches 2; Indels
                                                                                                                                        675 682 ATP (POTENTIAL).
1498 AA; 168968 MW; FF42037A335A9649 CRC64;
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MEDLINE=91064333; PubMed=2248949;
Omichinski J.G., Clore G.M., Appella E., Sakaguchi K.,
Omichinski M.;
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MEDLINE=90169514; PubMed=2106471;
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ses 6; Conservative
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ID ZEP1 HU
AC P15822;
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Conservative
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les 6; Conserv
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SEQUENCE FROM N.A.
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDIINE-3418925. PubMed-8140616;
Sandal N.W., Marcker K.A.;
"Similarities between a soybean nodulin, Neurospora crassa sulphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=91129256; PubMed=1825178;
MEDLINE=91129256; Fubwad=1825178;
Ketter J.S., Jaral G., Fu Y.-H., Marzluf G.A.;
"Nucleotide sequence, messenger RNA stability, and DNA recognition "Nucleotide sequence, messenger RNA stability, and DNA recognition elements of cys-14, the structural gene for sulfate permease II in
                                                                                                                                                  CO., GO.0005634; C:nucleus; TAS.

GO; GO:0003677; F:DNA binding; TAS.

GO; GO:0003677; F:DNA binding; TAS.

FinterPro.; IRRODORS; Zif CZH2.

FAM: PF00036; Zf-CZH2; 4.

SMART; SM00355; ZnP CZH2; 4.

PROSITE; PS00028; ZiNC FINGER CZH2_1; 4.

PROSITE; PS00157; ZINC_FINGER_CZH2_2; 4.

Transcription regulation; Zinc-finger; Metal-binding; DNA-binding; Norlear protein; Repeat; 3D-structure.
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Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBL_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35; DB 1; Length 2717;
Pred. No. 80;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           297217 MW; D45D3CA951FEA561 CRC64;
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C2HC-TYPE (POTENTIAL).
C2HC-TYPE (POTENTIAL).
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1991 (Rel. 20, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Sulfate permease II.
                                                        EMBL; X51435; CAA35798.1; -.
PIR; A34203; A34203.
PDB; 3ZNF; 15-JAN-92.
PDB; 4ZNF; 15-JAN-92.
PDB; 1BBO; 31-OCT-93.
TRANSPAC; T00497; -.
Genew; HGNC, 4920; HIVEP1.
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2127 213
2717 AA;
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Best Local Similarity
Matches 6; Conserv
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Neurospora crassa.
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P23622;
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ZN_FING
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DOMAIN
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CY14_NEUCR
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permease II and a putative human tumour suppressor.";

Trends Blochem. Sci. 19:19-19(1994).
-!- FUNCTION: UPTARE OF SULFATE INTO THE CELL.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- INDUCTION: Highly expressed, but only in cells subject to sulfur limitation, and it is turned on by the positive-acting Cys-3 sulfur regulatory protein.
-!- MISCELLANEOUS: SULFATE PERMEASE II IS MAINLY FOUND IN MYCELIA.
-!- SIMILARITY: Belongs to the SLC26A/SulP transporter (TC 2.A.53)
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28-MAY-2000 (Rel. 39, Created)
10-0CT-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Potential phospholipid-transporting ATPase VA (EC 3.6.3.1) (ATPVA)
ATP10A OR ATP10C OR ATPVC OR KIAA0566.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Buteria; Primates; Catarrhini; Hominidae; Homo.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Pfam; PF00916; Sulfate transp; 1.
TGRAMH; TIGR00815; SulP; 1.
PROSITE; PS01130; SLC26A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M59167; AAA33615.1; ALT_SEQ.
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MEDLINE=21313119; PubMed=11353404;

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TESUB-Brain;

X MEDLINE-Brain;

NEDLINE-Brain;

NEDLINE-BRAIN;

NEDLINE-BRAIN;

Nomura N., Ohara O.;

Preddiction of the coding sequences of unidentified human genes. IX.

The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

L DNA Res. 5:31-391999;

C -!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.

SUBCELDIAR LOCATION: Integral membrane protein (By similarity).

I TISSUB SPECIFICITY: Widely expressed, with highest levels in Kidney, followed by lung, brain, prostate, testis, ovary and small intestine.

I TISSUB SPECIFICITY: Widely expressed, with highest levels in Kidney, followed by lung, brain, prostate, testis, ovary and small intestine.

I TISSUB SPECIFICITY: Midely expressed, with highest levels in Kidney, followed by lung, brain, prostate, testis, ovary and small intestine.

I TISSUB SPECIFICITY: Midely expressed, with highest levels in Kidney, followed by lung, brain, prostate, testis, ovary and small intestine.

I TISSUB SPECIFICITY: Midely expressed, with highest levels in ASIS (MINI-105830) also known as "happy puppet syndrome'. As is characterized by features of severe motor and intellectual retardation, microcephaly, ataxia, frequent jerky limb movements and flapping of the arms and hands, hypotonial hypotomentation, seizures, absence of speech, frequent smiling and episodes of paroxysmal laughter, and an unusual facies characterized by macrostomia, a large mandible and open-mouthed expression, a great propensity for protruding the tongue ('tongue thrusting'), and an occipilatel groove.

-I SIMILARITY: Belongs to the cation transport ATPases family (P-type and a Progensity for protruding the tongue ('tongue and an occipilatel groove.)
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                                                                                                                                                                                                                                                                                                           TISSUE=Skin,

WEDLINE=22388257; PubMed=12477932;

WEDLINE=22388257; PubMed=12477932;

REDLINE=22388257; PubMed=12477932;

REDLINE=22388257; PubMed=12477932;

REDLINE=22388257; PubMed=12477932;

RIAUGHER R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zoederg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Did Chenko L., Marusina K., Farana A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Poraldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Rapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,

Brownstein M.J., McKwan P.J., McKernan K.J., Malek J.B., Gunarane P.H.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodersten B.M., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rachersely R.W., Trouchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz M.N.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

"Generation and initial analysis of more than 15,000 full-length

Human and mouse cDNA sequences",

"Generation and initial analysis of more than 15,000 full-length

Funnan and mouse cDNA sequences",
Herzing L.B.K., Kim S.-J., Cook E.H. Jr., Ledbetter D.H.;
"The human aminophospholipid-transporting Arbase gene ArploC maps adjacent to UBE3A and exhibits similar imprinted expression.";
Am. J. Hum. Genet. 68:1501-1505 (2001).
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DR EMBL; AY029495; AAK33100.1; JOINED.

DR EMBL; AY029495; AAK33100.1; JOINED.

DR EMBL; AY029497; AAK33100.1; JOINED.

DR EMBL; AY029499; AAK33100.1; JOINED.

DR EMBL; AY029499; AAK33100.1; JOINED.

DR EMBL; AY029500; AAK33100.1; JOINED.

DR EMBL; AY029502; AAK33100.1; JOINED.

DR EMBL; AY029503; AAK33100.1; JOINED.

DR EMBL; AR001139; C: Integral to membrane; NAS.

DR GO; GO:0000360; F: regulation of cell shape; NAS.

DR THCEPTO; IPRO0539; Flippade.

DR THCEPTO; IPRO0539; Flippade.

DR FAUN; PRO0119; CATATPASE.

DR FIGRAMS; TIGRO1494; ATPASE E1.E2.

DR FRINTS; PRO0119; CATATPASE.

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THYLOGARS; TORNEMSE ST.

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PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
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1499 AA; 167687 MW; D4996A4D0635A6BD CRC64;
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ses 8; Conservative
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ID RL20 MYCPU
AC Q98QY0;
DT 28-FEB-2003 (FDT 28-FEB-2003 (FDT)
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J. Bacteriol. 177:2396-2402(1995).
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TIGR; AF1949; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 EESIPDGASY
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                                                                                                                                                                                                                                                                                                    Mycoplasma pulmonis.",
Nucleic Acids Res. 29:2145-2153(2001).
Nucleic Acids Res. 29:2145-2153(2001).
Nucleic Acids Res. 29:2145-2153(2001).

-!- FUNCTION: This protein binds directly to 23s ribosomal necessary for the in vitro assembly process of the 50s ribosomal subunit. It is not involved in the protein synthesizing functions of that subunit (By similarity).
-!- SIMILANITY: Belongs to the L20P family of ribosomal proteins.
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                                                                                                                                                                  STRAIN=UAB CTIP;
MEDLINE=21267165; PubMed=11353084;
Ambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
Blanchard A.;
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STRANT-VC-16 / DSM 4304 / ATCC 49558;
MEDLINE-98049343; PubMed-9388475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kalavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
                                                                                                                                                                                                                                                                                  "The complete genome sequence of the murine respiratory pathogen
508 ribosomal protein L20.
RPLT OR MYPU_2610.
Mycoplasma pulmonis.
Bacteria, Firmicutes, Mollicutes, Mycoplasmataceae, Mycoplasma.
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C59C748901B18F14 CRC64;
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Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae, Archaeoglobus.
NCBI_TaxID=2234;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
4-Fppchetical protein AF1949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AL445533, CAC13434.1; -.
PIR, E90544, E90544.
Mypulist; MYD 2610; -.
HAMAP, F 00382; -i.
InterPro; IPR005813; Ribosomal L20.
InterPro; IPR005812; Ribosomal L20.
FRIM: PR00453; Ribosomal L20, Tropom; PR00662; RIBOSOMALL20.
ProDom; PD002389; L20; 1.
TIGRFAMS; TICR01033; PD1T bact; 1.
PROSINE, TOR01033; RIBOSOMALL20;
Ribosomal protein; RRNA-binding; Complete SEQUENCE 116 AA; 13565 MW; C59C74890
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                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                 NCBI_TaxID=2107;
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Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McMeil L.K., Badger J.H., Glodek A., Zhou L., Coverbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Wencen J.C., Clen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campylobacter jejuni.
Bacteria; Proteobacteria; Bpsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
                                                                                                                                                                                                                                                                            "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 160-253 FROM N.A.
STRAIN=ATCC 43431 / TGH 9011;
MEDLINE=55247673; PubMed=7730270;
MEDLINE=55247673; PubMed=7730270;
"Expression and varacterization of Campylobacter jejuni benzoylglycine amidohydrolase (Hippuricase) gene in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 7 27 POTENTIAL.
TRANSMEM 141 161 POTENTIAL.
SEQUENCE 165 AA; 17588 MW; BEC17054810ADBF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y990 CAMJE STANDARD; PRT; 253 AA. P45489; Q9RNVO; 101-NOV-1995 (Rel. 32, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
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Vibrio cholerae.
                                                                                                                                                                                                                                                Name=1;
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CONFLICT
CONFLICT
SEQUENCE
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AROA VIBCH
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Matches
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MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Haibh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCPI_TaxID=10090;
                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                        63.5%; Score 33; DB 1; Length 253; 55.6%; Pred. No. 18; 2; Indels iive 2; Mismatches 2; Indels
                                                                                                                                                                                  Hypothetical protein; Complete proteome.
SEQUENCE 253 AA; 29783 MW; F96D3FF3265F8A6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            CTX3_MOUSE STANDARD; PRT; 280 AA. 291387; 09CXQ4; Created) 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) c20ORF103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                          EMBL, AL139076; CAB73246.1; -. EMBL, 236940; CAA85392.1; -. PIR, CB1374; CB1374.
                                                                                                                                                                                                                                        Query Match 63.5
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                       185 DIFPSGMSY 193
                                                                                                                                                                                                                                                                                                                  2 EVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
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CTX3_MOUSE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMRL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=09D387-2; Sequence=VSP 003820;
-!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts
in positions 174 and 239.
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Ascad. Sci. U.S.A. 99:16899-16903(2002).
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
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PROPERTIAL.
PROPERTIAL.
PROPERTIAL.
CYTOPLASHIC (POTENTIAL).
N.LINKED (GLCNAC. .) (POTENTIAL).
MISSING (GLCNAC. .) (POTENTIAL).
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
29-FEB-2005 (Rel. 41, Last annotation update)
29-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)
anolpyruvylshikimate-3-phosphate synthase) (RPSP synthase)
ARCA OR VC1732.
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Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.5%; Score 33; DB 1; Length 280; 75.0%; Pred. No. 20; rive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event = Alternative splicing; Named isoforms = 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9D387-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AK014127; BAB29169.1; -- EMBL; AK018222; BAB31124.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1920368; 3110035N03Rik.
MGD; MGI:1923411; 6330527006Rik.
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230 2
238 2
280 AA;
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-El TOT N16961 / Serotype O1;

MEDLINE-20406833; PubMed=10952301;

Heidelberg J.F., Bisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Hsp90 co-chaperone Cdc37 (Hsp90 chaperone protein kinase-targeting subunit) (Cell division control protein 37).
CDC37 OR SPBC9B6.10.
Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 406:477-483(2000)
-1- CATANTUC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyviny1)-3-phosphoshikimate.
-1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; ME_0210; -; 1.

HINGETPO: IPRO001264; Arch.

INTERPRO: IPRO01966; ESPE SYNth.

PFONOM: PPOUNDES; ESPE SYNthase; 1.

PROD175; PROSP SYNTHASE; 1.

PROSITE; PS00186; ESPE SYNTHASE_1; 1.

PROSITE; PS00886; ESPE SYNTHASE_1; 1.

AROMATIC ANION ACIDATION A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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Pred. No. 31;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Westwood D.A.; Westwood D.K.; Preston N.C., Fantes P.A.; "Schizosaccharcomyces pombe cdc37 gene."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: Cycoplasmic (Probable).
-1- SUBCELLULAR LOCATION: Cycoplasmic (Probable).
-1- SIMILARITY: Belongs to the BPSP synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        466 AA
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TIGR, VC1732; -.
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094740;
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CC37_SCHPO
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STRAIN=CPN50;
MEDLINE=88336297; PubMed=2901768;
                                                                                                                    EMBL; AF182076; AAF62873.1; -. EMBL; BC004229; AAH04229.1; -. EMBL; BC001311; AAH06311.1; -. EMBL; BC010095; AAH10095.1; -.
                                                                                                                                                                                                              AF296124; AAG30413.1; -. AL359335; CAB94786.1; -. AL359336; CAB94787.1; -.
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                                                                                                                                                                                                                                                                                 EMBL; AL122063; CABS9242.
SWISS-2DPAGE; Q9NZMS; HUM
Genew; HGNC:4333; GLTSCR2
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EMBL; AL359335; C
EMBL; AL359336; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., McDwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Ryilalon D.K., Madan A., Nodergren E.J., Lu X., Gibbs R.A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Generation and mouse cDNA sequences.",

Human and mouse cDNA sequences.",

Human and mouse cDNA sequences.",

Human and mouse cDNA sequences.",
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-!- SUBGNIT: Interacts with HSV-1 early proteins ICP22 and ICP0.
-!- SUBCELLUIAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: Expressed at high levels in heart and pancreas, moderate levels in placenta, liver, skeletal muscle, and kidney, and low levels in brain and lung.
-!- SIMILARITY: Belongs to the GITSCR2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 9-478 FROM N.A., AND SUBCELLULAR LOCATION.
MEDLINE=99214318; PubMed=10196275;
Bruni R., Fineschi B., Ogle W.O., Roizman B.;
"A novel cellular protein, p60, interacting with both herpes simplex virus 1 regulatory proteins ICP22 and ICP0 is modified in a cell-type-specific manner and is recruited to the nucleus after
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=20175430; PubMed=10708517;
Smith J.S., Tachibana I., Poll U., Lee H.K., Thanarajasingam U.,
Portier B.P., Ucki K., Billings K., Ramaswamy S., Mohrenweiser H.W.,
Scheithauer B.W., Louis D.N., Jenkins R.B.;
"A transcript map of the chromosome 19q-Arm glioma tumor suppressor
                                                                                                                                                                                                 Eukarycta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                      GSR2_HUMAN STANDARD; PRT; 478 AA.
Q9NZM5; Q9BTC6; Q9HAX6; Q9NPP1; Q9NPR4; Q9UF12;
16-OCT-2001 [Rel. 40, Created)
16-OCT-2001 [Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glioma tumor suppressor candidate region gene 2 protein (p60).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Andreu N., Estivill X., Escarceller M., Sumoy L., Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
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J. Virol. 73:3810-3817(1999).
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE - Q.

| FTIG=VAR 011486.
| GGS -> HEG (IN REF. 2; AAH04229).
| GG -> R (IN REF. 3).
| RRKEQLWBKLAKQGELPREVRRAQARLIANESATRAKPGPQD TVERF. -> SGRSSYGRSWPSRASSPGGAQGPSPVAQPFCN KGPNZAFGHRIAA (IN REF. 3).
| SDNPLDRPLVGQDEFFLE -> LNNPDKPVVWFGCLFPG (IN REF. 3).
| CHN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A -> S (IN REF. 2; AAH04229).
D -> H (IN REF. 3).
PEGNILLADRFKSFQRRNMISHERAKFKRYKVKLVEKRAF
REIQ -> VITVSGRGAPCPVMTPELLIPVPPRGYGRHHGCP
WAGFVGPMPRG (IN REF. 5).
SGILLADRFKSFGRRNMISPRERAKFKRYKVKLVEKRAFR
EIQL -> RGCHSFBTGSRAFRGGI (IN REF. 3).
7F18923E348CB52B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CRNSO;
MEDLLINE=87055/020; PubMed=2877971;
Garnier I., Cole S.T.;
"Characterization of a bacteriocinogenic plasmid from Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid pIP404.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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Pred. No. 35;
1; Mismatches 3; Indels
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01-JAN-1988 (Rel. 06, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
Bacteriocin BCN5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005622; C:intracellular; NAS.
Nuclear protein; Polymorphism.
VARIANT 389
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                                                                                                 STRAIN=CPNF0;
MEDLINE=89039249; PubMed=2460717;
MEDLINE=89039249; PubMed=2460717;
MEDLINE=89039249; PubMed=2460717;
MEDLINE=80039249; PubMed=2460717;
Studies of UV-inducible promoters from Clostridium perfringens in vivo and in vitro.";
vivo and in vitro.";
vivo and in vitro.";
-1- FUNCTION: MAY FUNCTION AS AN IONOPHORE.
-1- INDUCTION: By UV irradiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, M14481, AAA98248.1; -.
EMBL, M32882, AAA98249.1; -.
EMBL, M32882, AAA98249.1; -.
EMBL, M30881, AAA98249.1; -.
InterPro; IPR000834; Peptidase M14.
InterPro; IPR000834; SH3 bac.
InterPro; IRR00286; SH3b, 3.
SWART; SM00287; SH3b, 3.
Antibictic; Bacteriocin; Plasmid.
Antibictic; Bacteriocin; Plasmid.
BACKERN 815
BEQUENCE 890 AA; 96699 MW; P4ESE8971C31C6C6 CRC64;
perfringens and molecular genetic analysis of the bacteriocin-encoding gene."; J. Bacteriol. 168:1189-1196 (1986).
                                                                                 SEQUENCE OF 1-14 FROM N.A.
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Query Match 63.5%; Score 33; DB 1; Length 890; Best Local Similarity 66.7%; Pred. No. 67; Matches 6; Conservative 1; Mismatches 2; Indels

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Search completed: June 3, 2004, 11:49:50 Job time: 6.86667 secs

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Pfam; PF00873; ACR
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Q40129 lycopersico
Q7v6g4 prochloroco
Q9xvk4 caenorhabdi
Q8c1d7 mus musculu
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116.206 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Q98FX1
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sp_mammal:*
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sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_organelle:*
sp_bhage:*
sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       £
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_archea:*
sp_bacteria:*
sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seg length: 0 Maximum DB seg length: 20000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                   1 EEVVPXGMSYS 11
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Match Length DB
                                                                                                                                                                                                                                                                                                                                             US-09-909-164-5
52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_human:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPTREMBL 25:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pitle:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                   seguence:
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212010101 4201 9 22 9294	Q8ktg4 candidatus Q8re56 fusobacteri Q7sy67 xenopus lae Q7u552 synechococc
07000 000 0 77 0001	. Q8KTQ4 .6 Q8RE56 .3 Q7SY67 .6 Q7USS2
	22008
	63.5 63.5 63.5
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ALIGNMENTS

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PERJULT 1

OBDIHO

PRELIMINARY; PRT; 1044 AA.

OBDIHO;

OBDIHO;

OBDIHO;

OBDIHO;

OLWAR-2003 (TrEWBLrel. 23, Created)

OLWAR-2003 (TrEWBLrel. 24, Last sequence update)

OLWAR-2003 (TrEWBLrel. 24, Last annotation update)

Multidrug efflux transporter.

Multidrug efflux transporter.

Multidrug efflux transporter.

NOREL TAXID=32046;

NOREL TAXID
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Gaps

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Q815A7 Q815A7;

ACCOOR READER TO THE SECOND THE SECOND SECON

RESULT 2 Q815A7

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"Genomic analysis reveals chromosomal variation in natural populations of the uncultured psychrophilic archaeon Cenarchaeum symbiosum."; of the uncultured psychrophilic archaeon Cenarchaeum symbiosum."; of the uncultured psychrophilic archaeon Cenarchaeum symbiosum."; nn EmBL; AF083072; AAC66699.1; of COOOC6810; Paransporter activity; IEA.

PIR; T31308; T31308; C:membrane; IEA.

GO; GO:0006215; F:transporter activity; IEA.

RO; GO:0006810; F:transport; IEA.

InterPro; IPR001681; P:transport; IEA.

RO; GO:0006810; P:transport; IEA.

WHYDORIE; PS00402; BPD_TRANSP_INN_MEMBR; 1.

WHYDORHEtical protein.

WHYDORHEtical protein.

SEQUENCE 3472 AA; 367058 MW; 37F80707030F9355 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical procedin.
Cenarchaeum symbiosum.
Archaea; Crenarchaeota; Thermoprotei; Cenarchaeales; Cenarchaeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hunt C., Aves S., McDougall R.C., Rajandream M.A., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=B;
MEDLINE=98422450; PubMed=9748430;
Schleper C., DeLong E.F., Preston C.M., Feldman R.A., Wu K.Y.,
Swanson R.V.;
                                                                                                                       73.1%; Score 38; DB 16; Length 387; 60.0%; Pred. No. 15; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 1; Length 3472;
Pred. No. 1.7e+02;
4; Mismatches 1; Indels
Pfam, PF01546, Peptidase M20, 1.
Hydrolase, Complete proteome.
SEQUENCE 387 AA, 41180 MW, 131BFF8E64306829 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe (Pission yeast).
Eukaryota; Pungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
Probable sulfate permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 3472 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
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2294 EDVIPRGISFS 2304
                                                                                                                           Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                    367 DEAIPHGMSY 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 REVVPXGMSYS 11
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NCBI_TaxID=4896;
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SEQUENCE FROM N.A.
STRAIN±972h-;
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074056
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MEDLINE=21082930; PubMed=11214968;
Rancko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Matanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Mateumoto M., Mateuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
Mcomplete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22608415; PubMed=12721630; Ivanova N., Candelon B., Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Kaparral V., Bhatracharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walumas T., Grechkin Y., Pusch G., Haselkorn R., Ponstein M., Ehrlich S.D., Overbeek R., Kyrpides N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of Bacillus cereus and comparative analysis with Bacillus anthracis.";
Nature 423:87-91(2003).
EMBL; AE017015; AAP12123.1;
InterPro; IRR00437; Prok lipoprot S.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhizobium loti (Mesorhizobium loti).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Phyllobacteriaceae, Mesorhizobium.
"NCBL_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                            BC5259.
Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria; Firmicutes; Bacillales; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344 AA; 38539 MW; C55268ACB7225995 CRC64;
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EMBL, AP003002; BABSO445.1; -.

EO, GO:0016787; F:Npdrolage activity; IEA.

GO; GO:0008237; F:metallopeptidase activity; IEA.

GO; GO:0008237; F:metallopeptidase activity; IEA.

GO; GO:0006508; P:proteolygis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter substrate-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         387 AA
                                                                                                                                                                                                                                 344 AA
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                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q98FX1
Q98FX1;
01-0CT-2001 (TEMBLEEL: 18,
01-0CT-2001 (TEMBLEEL: 18,
01-JUN-2003 (TEMBLEEL: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 73.1
Best Local Similarity 60.0
Matches 6; Conservative
                                          843 EEVLPNGIGYS 853
                                                                                                                                                                                                                                 PRELIMINARY;
   1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 EEIAPLGLSY 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=226900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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SEQUENCE 344 AA
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RESULT 3

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SEQUENCE FROM N.A.
STRAIN-NOD; TISSUE-Thymus;
MEDINNE-22354683; PubMed=12466851;
The FANTOM COnsortium.
the RANTOM Consortium.
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08VD18 PRELIMINARY, PRT; 484 AA.
08VD18; CTEMBLE-1 20, Created)
01-MAR-2002 (TEMBLE-1 20, Last sequence update)
01-MAR-2003 (TEMBLE-1 23, Last annotation update)
81milar to glioma tumor suppressor candidate region gene 2.
GLTSCR2 OR AM53641.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia. Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                    69.2%; Score 36; DB 11; Length 471; 60.0%; Pred. No. 51; 2; Indels ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to glioma tumor suppressor CANDIDATE region gene
                                                                                Strausberg R.; Strausberg R.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC055810, AAH58810.1; MGD; MGI:2154441; Gltscr2. Hypothetical protein. NOW TER SEQUENCE 471 AA, 54506 MW; E0DA685C374A9760 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.; Submitted (MOV-2001) to the EMBL/GenBank/DDBJ databases Submitted (MOV-2001) to the EMBL; BEC017637; AAH17637.1; SEMBL; BEC017637; AAH17637.1; SEQUENCE 48441; G15835 MW; BBB45F3B4BE02A36 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
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                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         226 EVIPAGASYN 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||:| | ||:
239 EVIPAGASYN 248
                                                                                                                                                                                                                                                                                                                                         2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=Salivary gland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EVVPXGMSYS 11
                                          SEQUENCE FROM N.A.
    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxiD=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
Q8BTX4
                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
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    STARBERS
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O1-JUN-2002 (TTEMBLrel. 21, Last sequence update)

O1-JUN-2003 (TTEMBLrel. 21, Last annotation update)

O1-OCT-2003 (TTEMBLrel. 25, Last annotation update)

Hypothetical protein (Fragment).

Hypothetical (Mouse).

Mus musculus (Mouse).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinse; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycoplasma penetrans.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=28227;
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A Saaaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furn Yayanino C., Horino A., Shiba T., Sasaki T., Hattori M.;
The complete genomic sequence of Wycoplasma penetrans, an intracellular bacterial pathogen in humans.";
I Woleic Acids Res. 30:5233-5300(2002).
EMBL; APO04171; BAC44062.1;
RIMERPRO; IPR009985; ConA.like.lec.gl.
RIMERPRO; IPR009985; ConA.like.lec.gl.
RIMERPRO; IPR00900; Lipoprotein.17.
R PGAMO; Lipoprotein.17.
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 16; Length 1123; Pred. No. 81;
                                                                                                                                                                                                                                                                                                               Query Match
Pest Local Similarity 77.8%; Pred. No. 59;
Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL132779; CAB60015.1; -.
PIR; T39116; T39116.
                                                                                                                                                                                                                                                                           93517 MW; ED4833E162B69077 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
MYPE 2560 paralog, 57%.
                                                     Genebal Spombe; SPAC869.05c; -. Genebal Spombe; SPAC869.05c; -. Genebal Spombe; SPAC869.05c; -. GO; GO:0008271; F:sulfate porter activity; IEA. GO; GO:0008272; F:sulfate porter activity; IEA. GO; GO:0008272; F:sulfate transport; IEA. InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulph_transpt. Pfam; PF00916; Sulfate_transp; 1. Pfam; PF00916; Sulfate_transp; 1. PROSITES : SULP; 1. PROSITES : G40 AA; 93517 MM; ED48332162B69077 CFSEQUENCE  640 AA; 93517 MM; ED48332162B69077 CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1123 AA
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70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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08R126

RESULT 7

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QBEWD4

RESULT 6

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Gape

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08BK35 Q8BK35

ACCOCC OCT REPRETED THE SET TH

RESULT 10 Q8BK35

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STRAIN=DC3000;
Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
White O., Fraser C., Collmer A.,
"Complete sequence of Pseudomonas syringae.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
TIGR: PSPT00620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R TIGR; EXETUTOLEUS; IEA.

R GO; GO:0003677; F:DNA binding; IEA.

CO; GO:0003677; F:DNA binding; IEA.

R GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.

R GO; GO:00063809; F:DNA-directed RNA pollymerase activity; IEA.

R GO; GO:00063809; F:DNA-directed RNA poll Ra.

R INTERPRO; IPR007080; RNA poll Ra.

R INTERPRO; IPR007080; RNA poll Ra.

R INTERPRO; IPR007081; RNA poll Ra.

R Ffam; PP04997; RNA poll Ra.

R Ffam; PP04993; RNA poll Ra.

R Ffam; PP04993; RNA poll Ra.

R Ffam; PP04998; RNA poll Ra.

R Ffam; PP0
  "Role of mobile DNA in the evolution of vancomycin-resistant
                                                                                                                                                                                                                                                                                                                                                                               69.2%; Score 36; DB 16; Length 559; 66.7%; Pred. No. 62; Live 2; Mismatches 1; Indels
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66.7%; Pred. No. 1.7e+02;
tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                559 AA; 61476 MW; CC15418D33D53DE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-07N-2003 (TrEMBLrel. 24, Created)
01-07N-2003 (TrEMBLrel. 24, Last sequence update)
01-07T-2003 (TrEMBLrel. 25, Last annotation update)
DNA-directed RNA polymerase, beta' subunit.
RPOC OR PSPTO0620.
                 Enterococcus facealis.";
Science 299:2071-2074(2003).
EMBL, ARD16947; AA079943.1;
TIGR, EFFO063;
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000943; Prob Lipoprot_S.
InterPro; IPR000943; PRO Lipoprot_S.
Pfam; PF00496; SBP bac_5; 1.
PROSITE; PS004013; PROKĀR_LIPOPROTEIN; 1.
Complete protecome.
SEQUENCE 559 AA; 61476 MW; CC15418D33D53DB7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1399 AA
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nes 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 LIPEGMSYS 359
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Matches
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Q889X7
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MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
The RANTOM Consortium,
The RANTOM Consortium,
The RANTOM Consortium,
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Mature 420:553-573 (2002).
MSTURE 420:553-573 (2002).
MGD; MGI:2154441; BAC36760.1; -.
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STRAIN=V583 / ATCC 700802;
STRAIN=V583 / ATCC 700802;
MEDLINE=22550857; PubMed=12663927;
Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R.,
Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Tettelinh H., Dodson M.T., Umayam L., Brinkac L., Beanan M.,
Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
                                                                                                                                                                                                                         Gaps
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Bacteria; Firmicutes; Lactobacillales, Enterococcaceae; Enterococcus.
NCBL_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).

Bukarwaculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

MCBI_TaxID=10090;
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Pred. No. 53;
2; Mismatches 2; Indels
                                                                                                                                                              69.2%; Score 36; DB 11; Length 484; 60.0%; Pred. No. 53; vative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MIN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to glioma tumor suppressor CANDIDATE region gene
        60,70 tut. 20163-573 (2002).
MATURE 420.563-573 (2002).
EMBL; AK088461; BAC40367.1; -.
MOD; MGI:2154441; G1t8cr2.
GENTENCE 484 AA; 55806 MW; B3056425B5EBCAD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             484 AA; 55792 MW; EB67949BCBE92D44 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pheromone binding protein, putative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             559 AA.
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60,770 full-length cDNAs.";
                                                                                                                                    Query Match
Best Local Similarity 60.0-
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Best Local Similarity 60.0.
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                                                                                                                                                                                                                                                                                                                             239 EVIPAGASYN 248
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Q839T9;
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Length 1399;

RESULT 11
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0839T4
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Indels

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Pred. No. 41; 2; Mismatches

60.08;

2 EVVPXGMSYS 11

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Best Local Similarity 60.0
Matches 6; Conservative
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Q9XVK4
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Srreptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Phospholipid and glycerol acyltransferase (From 'motifs_6.msf').
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 67.3%; Score 35; DB 10; Length 225; Best Local Similarity 54.5%; Pred. No. 37; Matches 6; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 225 UNKOVMN.
225 AA; 25188 MW; 1074C261D20CFDAD CRC64;
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EMBL; BX572098; CAEZ1267.1; -.
ACyltransferage; Transferage; Complete proteome.
SEQUENCE 245 AA; 26907 MW; 106F7C4CBE2C6427 CRC64;
                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein precursor.
Lycopersicon esculentum (Tomato).
                                                                                                                                                 225 AA
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                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-VP36; TISSUE-Pistil;
MEDLINE-95375233; PubMed-7647301;
Milligan S.B., Gasser C.S.;
                                                                                                                                            PRELIMINARY;
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NCBI_TaxID=74547;
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67.3%; Score 35; DB 16; Length 245;

Query Match

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                                              01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
010-OCT-2003 (TrEMBLrel. 25, Last annotation update)
010-OCT-2003 (TrEMBLrel. 25, Last annotation update)
02enorhabditis elegans.
02enorhabditis elegans.
02enorhabditidae; Peloderinae; Caenorhabditis.
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GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004672; F:protein Kinase activity; IEA.

GO; GO:0010640; F:transferase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IER000719; Prot_Kinase.
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50.0%; Pred. No. 75;
ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                              Percy C.M.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding; Transferase. SEQUENCE 425 AA; 49410 MW; 5D96E29B08C8E9D6 CRC64;
  425 AA
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ProDom, PD000001, Prot kinase, 1.
PROSITE, PS50011; PROTEIN KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: June 3, 2004, 11:57:30 Job time : 30.8667 sec8
  PRT;
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                investigating biology.";
Science 282:2012-2018(1998).
EMBL, 281109; CAB03241.1; --
PIR; T24111, T24111.
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nes 5, Conservative
PRELIMINARY;
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                                                                                                                                                                                                                                                                      NCBI_TaxID=6239;
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  Q9XVK4
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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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          Abb86553 Rbb86652 Abb86652 Abb86652 Abb86653 Abb866543 Abb866543 Abb866543 Abb86654 Abb86655 Abb86655 Abb86655 Abb866551 Abb86651 Abb866651 Abb866651 Abb866651 Abb8666651 Abb866667 Abb866667 Abb866667 Abb866667 Abb866
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ABB60543
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ABB60548
ABB60547
ABB60557
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Misc-difference
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Abb80525 Hepatitis
Abb80521 Hepatitis
Abb80526 Hepatitis
Abb80566 Hepatitis
Abb80566 Hepatitis
Abb80565 Hepatitis
Abb80565 Hepatitis
Abb80567 Hepatitis
Abb80567 Hepatitis
Abb80561 Hepatitis
                                                                                       3, 2004, 11:31:01 ; Search time 45.9333 Seconds (without alignments) 67.664 Million cell updates/sec
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         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                                                                                                                               otal number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1 EEVVPXGMSYS 11
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invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                               Score 50; DB 5; Length 1.,
Pred. No. 0.002;
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                                                                                     Sequence 11 AA;
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residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                     Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                                                                                                                                           note= "N-terminal acetyl"
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                                                                                       ABB80522 standard; peptide; 11 AA.
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RESULT 4

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Matches 11
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                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46.
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                                                                                                                                                                                                             'note= "Niterminal acetyl"
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/note= "C-terminal amide"
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           ABB80566 standard; peptide; 11 AA.
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                               /note= "Valyl carbonyl forming keto-amide linkage with residue 7"
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                                                              'note= "N-terminal acetyl"
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Location/Qualifiers
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protease.
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                                                                                                                                               Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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11
/note= "C-terminal amide"
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Best Local Similarity 100.0%; Pi
Matches 11; Conservative 0;
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                                                                                                               Levy OE,
                                                                                             (CORV-) CORVAS INT INC
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Modified-site
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                                                                                                                                                                  protease
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ABB80567
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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(CORV-) CORVAS INT INC.
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residue 7"
                  peptide compound having hepatitis C virus protease inhibitory ity useful for treating disorders associated with hepatitis C virus
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ABB80526
ID ABB80526 standard; peptide; 11 AA.
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                                                                                                   Claim 17;
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                  Novel pep
activity
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Claim 17; Page 64; 69pp; English.

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         The sequence represents a peptide compound of the invention having the peptides of the invepatites C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcommide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Leucyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                             Score 50; DB 5; Length 11; Pred. No. 0.002; 0; Indels
                                                                                                                                                   96.2%; Scc...
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                             Query Match
Best Local Similarity
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'note= "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
                                                                                                                                                                                 'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                               /note= "C-terminal amide"
                                                                                                                                                                                                                                                        'note= "D-form residue"
                                                                                                                                                                                                                                    'note= "Oxymethionine"
                                                                                                                                                          Location/Qualifiers
                    ABB80561 standard; peptide; 11 AA.
                                                                                                                                                                                                                 residue 7°
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activity
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                                                                                                                                                                                                                                                                                                             note= "Alpha-propynyl-glycinyl-carbonyl residue forming a keto-amide linkage with residue 7"
                                 Gaps
                                                                                                                                                                                                            Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #48.
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Pred. No. 0.002;
0, Mismatches 0; Indels
Score 50; DB 5; Length 11;
Pred. No. 0.002;
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llarity 100.0%; Pr
Conservative 0;
         ch 96.2%; Scc
| Similarity 100.0%; Pr
| 11; Conservative 0;
                                                                                                                             ABB80568 standard; peptide; 11
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                                                                  1 EEVVPXGMSYS 11
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Best Local Similarity
Matches 11; Conserv
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ity useful for treating disorders associated with hepatitis C virus
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Pred. No. 0.013;
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19-JUL-2001; 2001WO-US023169.
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                                                                                                  (CORV-) CORVAS INT INC
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"Norvalyl carbonyl forming keto-amide linkage with
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Pred. No. 0.013;
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                                                'note= "N-terminal acetyl"
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                                                                                                                                                                                                                      'note= "Norvaly1 carbony1 forming keto-amide linkage with
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                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4
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Pred. No. 0.013;
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90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORV-) CORVAS INT INC
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Best Local Similarity
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08-OCT-2002
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protease.

Novel

Synthetic

ABB80529;

RESULT 14 \$BB80529

Matches

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of the

/note= "C-terminal amide" /note= "D-form residue"

residue 7"

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Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                              Claim 17; Page 64; 69pp; English.
                                                                       19-JUL-2001; 2001WO-US023169.
                                                                                     21-JUL-2000; 2000US-0220101P.
                                                                                                                   Lim-Wilby M, Levy OE,
                                                                                                   (CORV-) CORVAS INT INC.
                                                                                                                                 WPI; 2002-361643/39.
      Misc-difference
                                          WO200208251-A2
                   Modified-site
                                                        31-JAN-2002.
                                                                                                                                                                protease.
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Brunck TK;

The sequence represents a peptide compound of the invention having the peptides of the invention are alpha ketoanide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus 0; Gaps Score 46, DB 5, Length 11; Pred. No. 0.013; 0, Mismatches 1; Indels Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative 0 Sequence 11 AA;

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Search completed: June 3, 2004, 11:48:22 Job time: 45.9333 secs

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ORGANISM: Enterococcus faecalis
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Sequence 73, Appli
Sequence 2902, Appli
Sequence 2902, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 256, Appli
Sequence 256, Appli
Sequence 236, Appli
Sequence 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                 June 3, 2004, 11:36:47; Search time 11.7333 Seconds (without alignments) 48.399 Million cell updates/sec
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(cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/2/iaa/RECTUS_COMB.pep:*

(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-328-152-7885
US-09-760-946-2
US-09-637-759B-236
US-08-637-759B-236
US-09-201-945-236
US-09-201-945-236
S177197-1
S177197-51
S177197-51
S177197-30
US-09-357-952-66
US-09-357-952-66
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US-08-460-744-4
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US-08-460-742-2
US-08-461-517-22
US-08-461-517-22
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-09-228-986-73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   389414 seqs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 EEVVPXGMSYS 11
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Perfect score:
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28 32 61.5 236 3 US-08-463-772-22 Sequence 22, Appl 30 32 61.5 236 5 PCT-US99-05000-22 Sequence 22, Appl 31 32 61.5 280 2 US-08-464-517-6 Sequence 6, Appl 32 61.5 280 2 US-08-464-36.4 Sequence 6, Appl 33 32 61.5 289 2 US-08-246-36.4 Sequence 6, Appl 33 32 61.5 289 5 PCT-US99-05000-6 Sequence 6, Appl 33 32 61.5 289 5 PCT-US99-05000-6 Sequence 6, Appl 32 61.5 292 2 US-08-464-517-23 Sequence 6, Appl 32 61.5 292 2 US-08-246-36.4 Sequence 23, Appl 32 61.5 292 2 US-08-246-36.4 Sequence 23, Appl 32 61.5 292 2 US-08-246-36.4 Sequence 23, Appl 32 61.5 292 2 US-08-464-517-29 Sequence 23, Appl 32 61.5 292 2 US-08-464-517-29 Sequence 23, Appl 40 32 61.5 295 1 US-08-494-120-8 Sequence 23, Appl 41 32 61.5 295 2 US-08-464-517-19 Sequence 2, Appl 43 61.5 295 2 US-08-464-517-19 Sequence 2, Appl 44 32 61.5 295 2 US-08-464-517-19 Sequence 2, Appl 44 32 61.5 295 2 US-08-464-517-19 Sequence 2, Appl 44 32 61.5 295 2 US-08-464-517-19 Sequence 2, Appl 44 32 61.5 295 2 US-08-464-517-29 Sequence 2, Appl 44 32 61.5 295 2 US-08-464-517-29 Sequence 2, Appl 45 32 61.5 295 2 US-08-464-517-29 Sequence 2, Appl 45 32 61.5 295 2 US-08-464-517-29 Sequence 2, Appl 45 32 61.5 295 2 US-08-464-517-29 Sequence 2, Appl 45 32 61.5 295 2 US-08-464-517-29 Sequence 2, Appl 45 32 61.5 295 2 US-08-464-517-29 Sequence 2, Appl 45 32 61.5 295 2 US-08-464-517-29 Sequence 2, Appl 45 32 61.5 295 2 US-08-464-517-29 Sequence 19, Appl 45 32 61.5 295 2 US-08-464-517-29 Sequence 19, Appl 45 32 61.5 295 2 US-08-464-517-29 Sequence 19, Appl 45 32 61.5 295 2 US-08-464-517-29 Sequence 19, Appl 45 32 61.5 295 2 US-08-464-517-29 Sequence 19, Appl 45 32 61.5 295 2 US-08-464-517-29 Sequence 19, Appl 45 32 61.5 295 2 US-08-464-517-29 Sequence 19, Appl 45 32 61.5 295 2 US-08-464-517-29 Sequence 19, Appl 45 32 61.5 295 2 US-08-464-517-29 Sequence 19, Appl 45 32 61.5 295 2 US-08-464-517-29 Sequence 19, Appl 45 32 61.5 295 2 US-08-464-517-29 Sequence 19, Appl 45 32 61.5 295 2 US-08-464-517-29 Sequence 19, Appl 45 32 61.5 295 2 US-08-464-517-29 Sequence 19, Appl 45 20.50 00.50 00.50	RESULT 1 US-09-408-020-4 US-09-408-020-4 Sequence 4, Application US/09408020 Patent No. 6632937 GENERAL INFORMATION: APPLICANT: Swanson Ronald V. APPLICANT: Feldman, Robert A. APPLICANT: Feldman, Robert A. APPLICANT: Feldman, Robert A. APPLICANT: Feldman, Robert A. APPLICANT: Peldman, Robert A. APPLICANT: Peldman, Robert A. CURRENT PAPLICANTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM FILE REFERENCE: DCORP.002A CURRENT PLING DATE: 1998-09-29 CURRENT PLING DATE: 1998-09-29 NUMBER OF SEQ ID NOS: 123 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4 LENGTH: 3472 TYPE: PRT CURRENT: PRT CORGANISM: Cenarchaeum symbiosum US-09-408-020-4	<pre>puery Match</pre>	RESULT 2 US-09-134-000C-1738 Sequence 3738, Application US/09134000C Sequence 3738, Application US/09134000C Sequence 3738, Application US/09134000C GENERAL INFORMATION: APPLICANT: Lynn Doucette-Stamm et al APPLICANTON: NUCENTICA ADIO NUCENTICA AND THERAPEUTICS CURRENT APPLICATION NUMBER: US 60/055,778 PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR PILING DATE: 1998-08-15 SOUTWARE: PatentIn version 3.1 SEQ ID NO 3738 TYPE: PATE TYP
0 0 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-09-408- Sequence Patent N GENERAL APPLICA APPLICA APPLICA TILE RE CURRENT CURRENT CURRENT PRIOR P NUMBER SEQ ID N IENGTH SEQ ID N IENGTH IENGTH SEQ ID N IENGTH CURRENT CONTWARE CON	Query Ma Best Loc Matches Qy Db 2	RESULT 2 US-09-134- Sequence Sequence PACENT N PACENT N TITLE O TITLE O TITLE O TITLE O FILE RE CURRENT PRIOR A PRIOR

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Parent No. 6562958
GENERAL INPORMATION
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-01PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Teatherizes, Youla S.
APPLICANT: Teatherizes, Youla S.
APPLICANT: Teatherizes, Youla S.
APPLICANT: Teatherizes, Anne-Marie
APPLICANT: Faucher, Anne-Marie
APPLICANT: Gonderau, Nachalie
APPLICANT: Halmos Tedderau, Nachalie
APPLICANT: Halmos Tedderau, Montse
TITLE OF INVENTION: Macrocyclic Peptides Active Against the Hepatitis C Virus
FILE REFERENCE: 13/076-1-C1
CURRENT FILING DATE: 2000-08-23
CURRENT FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Version 3.1
SEQ ID NO 2
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Substrate for recombinant HCV NS3 protease radiometric assay
US-09-760-946-2
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                                                                                                                                                                                                                                                                                                                                                     Length 1407;
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45.5%; Pred. No. 1.7;
tive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                     Query Match 65.4%; Score 34; DB 4; 3
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 1
      Application US/09328352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09760946
Patent No. 6608027
GENERAL INFORMATION:
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Patent No. 6608027
GENERAL INFORMATION:
APPLICANT: Tsancrizos, Youla S.
APPLICANT: Cameron, Dale R.
APPLICANT: Faucher, Anne-Marie
APPLICANT: Ghiro, Elise
                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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Best Local Similarity 45.5
Matches 5; Conservative
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      Seguence 7885,
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Fatent No. 6673910
GENERAL INFORMATION:
APPLICAT: Gary L. Breton et al.
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPBUTICS
FILE REPERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2902
LENGTH: 1191
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION WUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 73
LENGTH: 947
; FEATURE:
NAME/KEY: MISC FEATURE
; LOCATION: (327)...(328)
; COCATION: (327)...(328)
; OTHER INFORMATION: Amino acids 327 & 328 are Xaa wherein Xaa = any amino acid.
US-09-134-000C-3738
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Pred. No. 2e+02;
                                                                                                                                 69.2%; Score 36; DB 4; Length 382; 66.7%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 947;
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Pred. No. 1.6e+02;
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Sequence 73, Application US/09228986
Patent No. 6359198
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55.6%;
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                             Conservative
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Matches 5; Conservative
                                                                                                                                                                                                                                             332 LIPEGMSYS 340
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US-09-228-986-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: M.catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    686 VMPSGISYS 694
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783 EILPVGMAY 791
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Matches 6; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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US-09-540-236-2902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-540-236-2902
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US-09-328-352-7885
                                                                                                                                   Query Match
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SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 6; Conserva
                                                                                                                                        linear
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                        TOPOLOGY: lin

MOLECULE TYPE:

HYPOTHETICAL: N

US-08-637-759B-236
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US-08-871-355A-236
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APPLICANT: Goudreau, Nathalie
APPLICANT: Halmos, Teddy
APPLICANT: Llinas-Brunct, Montse
TITLE OF INVENTION: Macrocyclic Peptides Active Against the Hepatitis C Virus
FILE REPERENCE: 13/076-1-01
CURRENT APPLICATION NUMBER: US/09/760,946
CURRENT PILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US 69/542,675
PRIOR APPLICATION NUMBER: US 60/128,011
PRIOR APPLICATION NUMBER: US 60/128,011
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (10); ; OTHER INFORMATION: Tyr at position 10 is iodinated with I-125 US-09-760-946-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 63.5%; Score 33; DB 4; Length 12; Best Local Similarity 45.5%; Pred. No. 1.7; Matches 5; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-637-759B-236

Sequence 236, Application US/08637759B

Patent No. 5876931

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Identification of Genes
NUMBER OF SEQUENCES:
ADDRESSEE:
ADDRESSEE:
ADDRESSEE:
ADDRESSEE:
ADDRESSEE:
ADDRESSEE:
AT laint a
STREET:
1201 West Peachtree Street
CITY: Atlanta
STREET:
1201 West Peachtree
STREET
STPE:
COUNTRY:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
PILING DATE:
APPLICATION NUMBER:
PILING DATE:
APPLICATION NUMBER:
PILING DATE:
APPLICATION NUMBER:
PILING DATE:
APPLICATION NUMBER:
ATLANSIFICATION:
ASSIFICATION:
ASSIFICATION:
ASSIFICATION:
ASSIFICATION NUMBER:
ATCANSIFICATION NUMBER:
ATCANSIFICATION NUMBER:
ATTANDER PEACH
ATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1) OTHER INFORMATION: Asp at position 1 is biotinylated NAME/KEY: MOD RES LOCATION: (10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION: Tracer for NS3 protease assay
NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 BEVVPXGMSYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 3
LENGTH: 12
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Pred. No. 7.8;
1; Mismatches 3; Indels
                                                                                 Score 33; DB 2; Length 45;
Pred. No. 7.8;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1201 West Peachtree Street
CITY: Atlanta
STREET: 2001 West Peachtree Street
CITY: Atlanta
COUNTRY: Georgia
COUNTRY: Georgia
COMPUTER: Georgia
COMPUTER: Table FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ORBEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/71,355A
FILING DATE: 09-UIN-1997
CLASSIFICATION: 435
PRIOR APPLICATION 435
PRIOR APPLICATION WEBER: PCT/GB95/02875
FILING DATE: 11-DBC-1995
CLASSIFICATION NUMBER: 13,284
REFERENCE/DOCKET NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
TELEPHONE: (404) 873-8795
INFORMATION POR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE AMINO acids
WUNDER: Amino acids
                                                                                                                                                                                                                                                                                                      Sequence 236, Application US/08871355A
FREENT NO. 6015669
GENERAL INFORMATION:
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSE: Patrea L. Paber
STREET: 2800 One Allantic Center
STREET: 1201 West Peachtree Street
                                                                                   63.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.5%;
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Best Local Similarity 60.0
Matches 6; Conservative
protein
NO
                                                                                                                             6; Conservative
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EEISPLGWSY 10
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Gaps

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Indels

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3; Mismatches

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5; Conservative
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US-09-357-952-66
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KANZAKI, TETSUTO, OLOFSSON, ANDERS, MOREN, ANITA;
HERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH,
LENA, HELDIN, CARL-HENLMAN, TEAL-HENLMAN, TEAL-HENLMAN, TEAL-HENLMAN, TEAL-BENNERSENG
HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
HUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 4; Length 45; Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3, Indels
                                                                                                                                                                                                                                                  Sequence 236, Application US/09201945
Fatent No. 6342215
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTON: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
STREET: 2800 One Atlantic Center
STREET: 2800 One Atlantic Center
STREET: 1201 West peachtree Street
CITY: Atlanta
STATE: Georgia
SCOUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/487,343
FILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPMS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
TELEPANE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EEISPLGWSY 10
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;Patent No. 5177197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LENGTH: 65
5177197-51
                  JS-09-201-945-236
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DB 6; Length 65; 12;

Score 33; Pred. No. 1

63.5%; 45.5%;

Query Match Best Local Similarity

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APPLICANT: Zhang, Han-Zhong
APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Drawe, John A.
TITLE OF INVENTION: No. 6248904e1 Fluorescence Dyes and Their Applications for Whole TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease FILE REFERENCE: 1735.003001
CURRENT APPLICATION NUMBER: US/09/357,952
CURRENT FILING DATE: 1999-07-21
EARLIER APPLICATION NUMBER: US 60/093,642
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                                                                                                                                       FACTOR NO. 5177197

FACTOR NO. 5177197

FAPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;

MENASTEDT, CHRISTER; HELLMAN, ULF, MIYAZONO, KOHEI; CLAESSON-WELSH,

LENA; HELDIT, CARL-HENRIK

TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING

HUMAN TRANSFORMING GROWHF FACTOR-BETAL-BINDING PROTEIN

NUMBER OF SEQUENCES: 53

CURRENT APPLICATION DATA;

APPLICATION NUMBER: US/07/487,343

FILING DATE: 27-FEB-1990
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5177197-30
FALOR NO. 5177197
**PATON NO. CARL-HENLAN, ULF, MIYAZONO, KOHEI; CLAESSON-WELSH, ILENA; HEDLIN, CARL-HENIRK
**ITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
**HUMAN TRANSPORMING GROWTH FACTOR-BETA1-BINDING PROTEIN
**CURRENT APPLICATION DATA:
**APPLICATION NUMBER: US/07/487,343
**FILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.5%; Score 33; DB 6; Length 1394;
45.5%; Pred. No. 3.9e+02;
ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 6; Length 410;
Pred. No. 97;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 66, Application US/09357952
Patent No. 6248904
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 45.5
Matches 5; Conservative
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Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         399 KEICPGGMGYT 409
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                                 :|: | || |:
52 KBICPGGMGYT 62
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1 EEVVPXGMSYS 11
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LENGTH: 1394
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GENERAL INFORMATION;
APPLICANT: Cai, Sui Xiong
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: 1735.029002
CURRENT FLLING DATE: 12998-10-0
EARLIER APPLICATION NUMBER: US 60/061,582
EARLIER FILING DATE: 1998-10-10
EARLIER FILING DATE: 1998-10-10
EARLIER FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 142
SCOFTWARE: Patentin Ver. 2.0
SEQ ID NO 66
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Synthetic
OTHER INFORMATION: Peptide
JS-09-357-952-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 61.5%; Score 32; DB 4; Length 10; Best Local Similarity 50.0%; Pred. No. 2.3; Matches 5; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                  Query Match 61.5%; Score 32; DB 3; Length 10; Best Local Similarity 50.0%; Pred. No. 2.3; Matches 5; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
TS-09-521-650-66
Patent No. 6335429
EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 66
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EEVVPXGMSY 10
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Gaps

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Search completed: June 3, 2004, 12:03:06 Job time: 11.8 secs

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Score 50;
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16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Appl
                                                                                                          June 3, 2004, 11:57:42; Search time 33.7333 Seconds (without alignments) 91.741 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, A Sequence 10, Sequence 10, Sequence 48, Sequence 49, Sequence 51, Sequence 51, Sequence 12, Sequence 12, Sequence 12, Sequence 7, M Sequence 17, M Sequence 17, M Sequence 11, M Sequence 11, M Sequence 11, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US010_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US010_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US010_NEW_PUB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US010_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US00_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US00_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US00_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                       1155919
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-909-164-6
US-09-909-164-10
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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16 45 86.5 11 12 US- 18 45 86.5 11 12 US- 19 45 86.5 11 12 US- 20 44 84.6 11 12 US- 21 44 84.6 11 12 US- 22 44 84.6 11 12 US- 23 44 84.6 11 12 US- 24 48 84.6 11 12 US- 25 44 84.6 11 12 US- 26 42 80.8 11 12 US- 27 41 78.8 11 12 US- 28 41 78.8 11 12 US- 29 41 78.8 11 12 US- 31 40 76.9 11 12 US- 31 40 76.9 11 12 US- 32 40 76.9 11 12 US- 33 40 76.9 11 12 US- 34 40 76.9 11 12 US- 35 40 76.9 11 12 US- 36 40 76.9 11 12 US- 37 40 76.9 11 12 US- 38 40 76.9 11 12 US- 39 75.0 11 12 US- 44 39 75.0 11 12 US- 45 39 75.0 11 12 US- 46 39 75.0 11 12 US- 47 39 75.0 11 12 US- 48 44 39 75.0 11 12 US- 49 APPLICANT: Lewy, Odile E 40 76.9 11 12 US- 41 39 75.0 11 12 US- 42 39 75.0 11 12 US- 44 39 75.0 11 12 US- 45 APPLICANT: Lewy, Odile E 45 APPLICANT: Lewy, Odile E 46 DINCANTION: NUMBER: 60/220, 1 45 BRIOR APPLICATION NUMBER: 60/220, 1 45 BRIOR APPLICATION NUMBER: 60/220, 1 45 BRIOR APPLICATION NUMBER: 60/220, 1 45 BRIOR APPLICATION: (1).1(1) OTHER INFORMATION: (1).1(1) OTHER INFORMATION: NUMBER: NAME/KEY: MOD_RES 45 UCCATION: (6)(6) 60 THER INFORMATION: NUMBER: NAME/KEY: MOD_RES 60 UD MS ES 60 U	S-09-909- Query Ma

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APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
URRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 10
LENGTH: 11
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3, 0.0014;
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96.2%; Score 50; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 11; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MISC FEATURE LOCATION: (6). (6) OTHER INFORMATION: norvaline-(CO)
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// LOCATION: (8)...(8)

// OTHER INFORMATION: D-amino acid

US-09-909-164-9
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NAME/KREY: MOD_RES
LOCATION: (1)...(1)
CTHER INFORMATION: ACETYLATION
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OTHER INFORMATION: ACETYLATION
PEATURE:
NUMBER OF SEQ ID NOS: 62
SOFWRARE: Patentin version 3.1
SEQ ID NO L
LENGTH: 11
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
FEATURE:
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NAME/KEY: MOD RES
LOCATION: (11). (11)
OTHER INFORMATION: AMIDATION
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NAME/KEY: MISC_FEATURE
LOCATION: (8)..(9)
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Publication No. US20020068702A1
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim.Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TILLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT PILING DATE: 2003-03-03
PRIOR FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                          APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile B
APPLICANT: Levy, Odile B
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PPPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR PPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
LENGTHARE: Patentin version 3.1
LENGTH: 11
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ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
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     Pred. No. 0.0014;
; Mismatches 0; Indels
                                                                                                                                                                                                                                   Sequence 6, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
     Best Local Similarity 100.0%; P
Matches 11; Conservative 0;
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OTHER INFORMATION: D-amino acid
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NAME/KEY: MOD_RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
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LOCATION: (11)...(11)
CYHER INFORMATION: AMIDATION
US-09-909-164-6
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Best Local Similarity
Matches 11; Conserv
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APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: NoveE, Partine APPLICANTON NUMBER: US/09/909,164
CURRENT APPLICANTON NUMBER: US/020,101
PRIOR APPLICANTON NUMBER: 00/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 49
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ORGANISM: artificial sequence
PERATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
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OTHER INFORMATION: 11-mer synthesized according to example
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NAME/KEY: MOD RES

LOCATION: (11)

OTHER INFORMATION: AMIDATION
FRATURE:

NAME/KEY: MACC FEATURE

LOCATION: (6)...(6)

OTHER INFORMATION: norleucine-(CO)
US-09-909-164-49
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LOCATION: (6)...(6)
CTHER INFORMATION: leucine-(CO)
US-09-909-164-48
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NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
NUMBER OF SEQ ID NOS: 62
SOFWARE: Patentin version 3.1
SEQ ID NO 48
LENGTH: 11
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ORGANISM: artificial sequence
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NAME/KEY: MOD RES
LOCATION: (11)...(11)
FEATURE:
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APPLICANT: Corvas International, Inc.
APPLICANT: Lim-wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPRENCE: INUIN192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOPTHARE: Patentin version 3.1
LENGTH: 11
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Sequence 48, Application US/0909164
Sequence 8. Application US/0909164
Publication No. US20020068702A1
GENERAL INPORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lin-wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
PILE REPERENCE: IN01.92-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PLING DATE: 2000-07-21
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                                                                                                                    0; Indels
                                                                      DB 12;
. 0.0014;
                                                                Query Match 96.2%; Score 50; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 11; Conservative 0; Mismatches
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Publication No. US20020068702A1
GENERAL INFORMATION:
OTHER INFORMATION: D-amino acids JS-09-909-164-10
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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LOCATION: (6)._(6)
OTHER INFORMATION: valine-(CO)
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NAME/KEY: MOD RES
LOCATION: (11)..(1
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US-09-909-164-52

i Sequence 52, Application US/09909164

i Sequence 52, Application US/09909164

i Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Wilby, Marguerita

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQ ID NO 52

Lumber: Lim-Wilby, Marguerita

NUMBER: Marguerita

SEQ ID NO 52

Lumber: Lim-Wilby, Marguerita

Marguerita

Marguerita

SEQ ID NO 52
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96.2%; Score 50; DB 12;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0;
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j OTHER INFORMATION: (8,8)-allothreonine-(CO)

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) LOCATION: (6)..(6)
; OTHER INFORMATION: propynyl glycine-(CO)
US-09-909-164-52
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US-06-909-164-8
Aguence 8, Application US/09909164
; Publication No. US20020068702A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAATURE:
NAME/KRY: MOD RES
LOCATION: (1) _ (1)
OTHER INFORMATION: ACETYLATION
ENTURE:
NAME/KRY: MOD RES
LOCATION: (11) _ (11)
OTHER INFORMATION: AMIDATION
FEATURE:
NAME/FEST: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: artificial sequence
                                                                                            FRATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 REVVPXGMSYS 11
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                                                                                                         MESUL: 8

Sequence 50, Application US/09909164

Sequence 50, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Lidwilby, Marguerita

APPLICANT: Lidwilby, Marguerita

APPLICANT: Lidwy, Odie E

APPLICANT: Lidwy, Odie E

APPLICANT: Lidwy, Odie E

TILE REFERENCE: IN01192-US

CURRENT APPLICANTON NUMBER: US/09/909,164

CURRENT APPLICANTON NUMBER: 60/220,101

PRIOR FILING DATE: 2003-03-25

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTHARE: PatentIn version 3.1

SEQ ID NO 50

LENGTH: 11
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Publication No. US20020068702A1
GENERAL INFORMATION

BEDELICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-1-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT PILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.1
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LOCATION: (1)..(1)
PEATURE: INFORMATION: ACETYLATION
FEATURE: INFORMATION: ACETYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MISC_PEATURE
| LOCATION: (6)...(6)
| 10CATION: (5)...(6)
| US-09-909-164-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: artificial sequence
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LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
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Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EEVVPXGMSYS 11
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US-09-909-164-51
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LENGTH: 11
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US-09-909-164-13
US-09-909-164-13

INS-09-909-164-13

Sequence 13, Application US/09909164

Publication No. US20020068702A1

Sequence 13, Application US/09909164

Publication No. US20020068702A1

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFRENCE: IN01192-08

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

LENGTH: 11

TYPE: PRT
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                                                                                                                                                                                                                                                                                                               88.5%; Score 46; DB 12; Length 11; 90.9%; Pred. No. 0.0091; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.5%; Score 46; DB 12; Length 11; 90.9%; Pred. No. 0.0091; tive 0; Mismatches 1; Indels
                                                                                              NAME/KEX: MISC FEATURE
COCATION: (6)...(6)
COCATION: (6)...(6)
PEATURE: INFORMATION: norvaline-(CO)
PEATURE: NAME/KEY: MISC_FEATURE
LOCATION: (8)...(6)
COTHER INFORMATION: D-amino acid
US-09-909-164-12
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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J.OCATION: (8)..(9)
OTHER INFORMATION: D-amino acids
US-09-909-164-13
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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         NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
FRATURE:
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NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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Matches 10; Conservative
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Matches 10; Conservative
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APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Oddle E
APPLICANT: Levy, Oddle E
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: INDIA 192-08
CURRENT APPLICATION NUMBER: US/09/909,164
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PELING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTHARE: PATCHIN VERSION 3.1
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APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPRENCE: IND.132-02
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SSOTHWARE: Patentin version 3.1
LENGTH: 11
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NAME/KEY: MOD_RES
LOCATION: (1)...(1)
PEATURE:
PEATURE:
PEATURE:
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Pred. No. 0.0091;
0; Mismatches 1;
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Publication No. US20020068702A1
GENERAL INFORMATION:
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OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (9)...(9)
OTHER INFORMATION: D-amino acid
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LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: artificial sequence
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ORGANISM: artificial sequence
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Best Local Similarity 90.9%;
Matches 10; Conservative
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LOCATION: (11)...(11)
COTHER INFORMATION: AMIDATION
1S-09-909-164-8
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NAME/KEY: MISC_FEATURE
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IS-09-909-164-12
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LENGTH: 11
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Query Match 86.5%; Score 45; DB 12; Length 11; Best Local Similarity 90.9%; Pred. No. 0.015; Matches 10; Conservative 0; Mismatches 1; Indels
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Job time : 34.7333 secs
                                                                                                                                                             FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                       ; NAME/KEY: MISC_FEATURE
; LOCATION: (8)...(8)
; OTHER INFORMATION: D-amino acid
US-09-909-164-11
                  LOCATION: (1) ...(1)
OTHER INFORMATION: ACETYLATION
                                                                                    NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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AME/KEY: MOD_RES
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  Sequence 7, Application US/09909164

Sequence 7, Application US/09909164

Publication No. US20020068702A1

SEQUENCE 1 INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lord, Odile E

APPLICANT: Brunck, Terence K

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: IN0192-US

CURRENT APPLICATION NUMBER: 05/09/909,164

CURRENT FILING DATE: 2003-03-25

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PATENT NO THE OF SEQ ID NOS: 62

SEQ ID NO 7

LENGTH: 11
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APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
ITILE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IND.192-08
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTHARE: Patentin version 3.1
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OTHER INFORMATION: 11-mer synthesized according to example 1
FRATURE:
NAME/KEY: MOD RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
FRATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6) ... (6)
OTHER INFORMATION: norvaline-(CO)
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Pred. No. 0.01
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (9). . . (9)
OTHER INFORMATION: D-amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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NAME/KEY: MISC FEATURE
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US-09-909-164-11
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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)M protein - protein search, using sw model

June 3, 2004, 11:35:47; Search time 9 Seconds (without alignments) 117.567 Million cell updates/sec tun on:

US-09-909-164-6 52 1 EEVVPXGMSYS 11 litle: sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 scoring table:

283366 seqs, 96191526 residues searched:

283366 otal number of hits satisfying chosen parameters:

finimum DB seq length: 0 faximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*

Jatabase

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	17	probable sulfate p	permease	V1 protein - tobac	DNA segregation AT	hypothetical prote	hypothetical prote	zinc finger protei	topoisomerase IV s	DNA-binding protei	hypothetical prote	cell division inhi	probable ABC subst	hypothetical prote	밁		_	_	hypothetical prote	ጄ	hypothetical prote	3-phosphoshikimate	cdc37 protein - fi	iron(III) ABC tran	bacteriocin BCN5 -	ATP-dependent DNA		transforming growt	
SUMMARIES	ΩĦ	T31308			A42452		_	_	S22293	H82691	A34203	S54619	H69491	C82900	140758	E90544	D69493	C81374	T34536	S75817	T47670	F72281	D82163	T43653	D82352	A30481	328	D87046	562	233
	DB	7	(1	~	7	N	N	α	~	~	7	~	7	7	N	7	N	0	N	7	~	7	~	(7)	N	N	~	N	N	0
	Length	3472	840	877	102	1498	225	425	670	749	2717	156	252	544	94	116	165	253	259	284	298	368	426	466	653	890	1028	1152	1394	1401
dю	Query	3.	Η.	Η.	ď	φ.	۲.	ζ.	۲.	۲.	۲.	'n.	'n.	'n.	w.	63.5		ω.	m.	ë.	w.	m.	'n.	'n.	'n.	۳.	'n.	'n.	'n.	•
	Score	m	37	37	36	36	35	35	35	33	35	34	34	34	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33
	tesult No.	! !	(1	т	4	ហ	9	1	80	σ	10	11	12	13	14	15	16	17	18	13	70	21	22	23	24	25	26	27	28	53

hypothetical prote	masking protein pr	hypothetical prote	transport protein	rho protein GDP-di	hypothetical prote	cyclin D2 - rat	cyclin D2 - rat	cyclin D2 - mouse	cyclin D2 - human	cyclin D1 - Africa	cyclin D2 - Africa	cyclin D2 - chicke	cyclin D1 - zebra	cyclin D3 - human	cyclin D1 - human
T04456	A38261	E97333	PQ0616	T01457	B72481	JC4011	158372	A41984	A42822	S57922	S57925	JC4579	S62730	B42822	A38977
~1	N	N	N	N	~	N	7	~	7	~	~	7	~	N	7
1548	1712	84	175	223	279	288	288	289	289	291	291	291	291	292	295
63.5	63.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5
33	33	32	32	32	32	32	32	32	32	32	32	32	32	32	32
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4.5

ALIGNMENTS

hypothetical 367K protein - Cenarchaeum symbiosum
C;Species: Cenarchaeum gymbiosum
C;Species: Cenarchaeum gymbiosum
C;Species: Cenarchaeum gymbiosum
C;Accession: T31308
R;Schleper, C; DeLong, E.F; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V.
Bacteriol. 180, 5003-5009, 1998
A;Fitle: Genomic analysis reveals chromosomal variation in natural populations of the un-A;Reference number: 220994; MUID:98422450; PMID:9748430
A;Accession: T31308
A;Accession: T31308
A;Accession: T31308
A;Residues preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3472 <SCH>
A;Residues: 1-3472 <SCH>
A;Cross-references: EMBL:AF083072; NID:93599393; PID:93599384; PIDN:AAC62699.1
C;Superfamily: Cenarchaeum symbiosum hypothetical 367K protein

ö Gaps .. Query Match 73.1%; Score 38; DB 2; Length 3472; Best Local Similarity 54.5%; Pred. No. 60; Matches 6; Conservative 4; Mismatches 1; Indels

1 EEVVPXGMSYS 11 ઠે

|:|:| |:|:| 2294 EDVIPRGISFS 2304 셤

RESULT 2

probable sulfate permease - fission yeast (Schizosaccharomyces pombe)
probable sulfate permease - fission yeast (Schizosaccharomyces pombe)
Cispecies: Schizosaccharomyces pombe
Cispecies: Schizosaccharomyces pombe
Cispecies: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change O3-Dec-1999
Ciscossion: T33116
Aibut. C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Aibut. C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Aibut. C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Aibut. C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
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Aibut. C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
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Aibut. C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Aibut. C.; Aibut. C.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Aibut. C.; Aibut. C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Aibut. C.; Aves, McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Aibut. C.; Aves, McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Aibut. C.; Aves, McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Aibut. C.; Aves, M.A.; Barrell, M.A.; Barrell, B.G.
Aibut. C.; Aves, M.A.; Barrell,

A; Map position: 1

71.2%; Score 37; DB 2; Length 840; llarity 77.8%; Pred. No. 21; Conservative 1; Mismatches 1; Indels Query Match Best Local Similarity Matches 7; Conserv

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Gaps

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135 VVPQGMSYA 143

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A;Experimental source: clone R10D12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Lycopersicon esculentum (tomato)
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
C;Accession: S57810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein R10D12.10 - Caenorhabditis elegans
C;bpecises Caenorhabditis elegans
C;bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24111
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Sep-1999
C;Accession: S22293; I78-Day (C;Accession: S22293; I78-Day)
R;Mitchelmore, C; Traboni, C; Cortese, R.
Nucleic Acids Res. 19, 141-147, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U20592; NID:9924625; PIDN:AAA80497.1; PID:9924626
C;Superfamily: plant Kunitz-type proteinase inhibitor
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Plant Mol. Biol. 28, 691-711, 1995
A,Title: Nature and regulation of pistil-expressed genes in tomato.
A,Reference number: S57808; MUID:95375233; PMID:7647301
A,Accession: S57810
A,Status: preliminary, nucleic acid sequence not shown
     2; Length 1498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.3%; Score 35; DB 2; Length 225; 54.5%; Pred. No. 13; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 425;
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A;Reference number: 219842
A;Accession: T24111
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-425 <WILL>
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Score 36; DB
Pred. No. 63;
2; Mismatches
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     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ypothetical protein precursor (clone TPP11)
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A;Introns: 23/3; 56/3; 113/3; 257/2
69.2%;
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Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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Matches 6; Conservative
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A,Residues: 1-225 <MI
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Best Local S
Matches 5
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C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Date: 1997355
R;Accession: B97355
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4873-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA segregation Arpase, Fiek/SpoiliE family, YUKA B. subtilis ortholog [imported] - Clos
C.Species: Clostridium acetobutylicum
C.Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DWA
A;Residues: 1-877 - LYNA
A;Residues: 1-877 - LYNA
A;Cross-references: EMBL:AL031261; PIDN:CAA20298.1; GSPDB:GN00067; SPDB:SPBC3H7.02
A;Experimental source: strain 972h-; cosmid c3H7
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A.Molecule type: DNA
A.Residues: 1-1498 «KUR»
A.Cressreferences: GB:AE001437; PIDN:AAK81629.1; PID:g15026814; GSPDB:GN00168
A.Experimental source: Clostridium acetobutylicum ATCC824
C.Genetics:
                                                                                                                                                                      C;Species: Schizosaccharome, journe, journe, journe, journe, journe, journe, journe, journe, journe, series, s
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Species: tobacco yellow dwarf virus
Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                - fission yeast (Schizosaccharomyces pombe)
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Score 36; DB 2, Pred. No. 3.5; 3; Mismatches

69.2%;

Query Match
Best Local Similarity 60..
Best Gonervative

2 EVVPXGMSYS 11 | | | | | :: | | | 16

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Genetics:

Query Match 71.2 Best Local Similarity 77.6 Matches 7; Conservative

A, Gene: SPDB:SPBC3H7.02 A; Map position: 2

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A,Title: A DNA-binding protein containing two widely separated zinc finger motifs that r
A,Reference number: A34203, MUID:90169514; PMID:2106471
A,Accession: A34203
A,Status: prediminary
A,Molecule type: mRNA
A,Residues: 1-2717 < PRAN>
A,Cross.references: BMBL:X51435, NID:g38017; PIDN:CAA35798.1; PID:g38018
R,Baldwin Jr., A.S.; LeClair, K.P.; Singh, H.; Sharp, P.A.
MOI. Cell. Biol. 10, 1406-1414, 1990
A,Title: A large protein containing zinc finger domains binds to related sequence elemen A;Reference number: A34779; MUID:90205817; PMID:2108316
A,Reference number: A34779; MUID:90205817; PMID:2108316
A,Reference number: Gall-107, No. 1074-1168, K.', 1170-1225, VV', 1227-1434, No. 1436-1607, 'I', 1609-16
A,Reducine type: mRNA
A,Reducine type
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hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
C.Species: Saccharomyces cerevisiae
C.Date: 08-Ual-1995 #sequence_revisiae
C.Date: 08-Ual-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C.Accession: S54619, S66879
R.de Haan, M.; Maarse, A.C.; Grivell, L.A.
submitted to the EMBL Data Library, May 1995
A.Reference number: S54617
A.Reference number: S54617
A.Reference number: S54617
A.Reference number: S6877
A.Reference number: S6877
A.Ression: S6887
A.Ression: S6887
A.Reference number: S6887
A.Ression: S6887
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A.Ression: S6887
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A.Ression: S6887
A.Residues: L.156 < DEW
A.Ression: S6887
A.Residues: L.156 < DEW
A.Residues: EMBL:X34920, NID:g1420109; PIDN:CAA99201.1; PID:g1420111; MIDS:YOR01
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C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 26-Aug-1999
C;Accession. #65491
R;Xlenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson .; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
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Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 1;
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A;Map position: 15R
C;Superfamily: hypothetical protein YOR013w
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2405 WPAGLTYS 2413
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H69491
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R;anconymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a Complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       **Simpson, A.J.G.; Reinach, P.C.; Arrida, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Pariones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Acencio, M.; Alvarenga, R.; Pariones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Carreira, A.J.G.; Reinach, C.B.; Docena, C.; Bl-Dorry, H.; Facincani, A.P.; Ferreira, A.J.G.; Docena, C.; Bl-Dorry, H.; Facincani, A.P.; Ferreira, A.J.G.; Submitted to GenBank, June 2000
**Juthores: Ferreira, V.C.A.; Ferro, J.A.; Frage, J.S.; Franca, S.C.; Franco, M.C.; Frohm, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitalima, J.P.; Krieger, J.B.; Kuramae, E.E.; Laigrina, J.D.; Junqueira, M.M.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.M.P.; Matsukuma, A.Y.; Marino, C.L.; Marques, M.V.; Martins, E.C.; Myaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Addiques, V.; Rosa, A.J. de M.; de Oliveira, M.C.; de Sa, R.G.; Santelli, R.V.; Sawasak, Hauthors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.M.; Silva, A.M.; da Silva, A.L.; Zawasak, A.D.; Taubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zawasak, A.D.; Danger, A.B.; Santelli, R.V.; Sawasak, A.D.; Danger, A.B.; Santelli, R.V.; Sawasak, A.B.; Santellia, R.V.; R.S., Santellia, R.V.; Sawasak, A.B.; Santellia, R.V.; Sawasak, R.S.; Santellia, R.V.; Sawasak, R.S.; Santellia, R.V.; Sawasak, R.S.; Santellia, R.V.; Sawasak, R.S.; Santellia, R.V.; Sawasak,
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A;Molecule type: DNA
A;Residues: 1-749 <SIM>
A;Cross-references: GB:AE003967; GB:AE003849; NID:g9106347; PIDN:AAF84162.1; GSPDB:GN001
     A,Title: Isolation of two cDNAs encoding zinc finger proteins which bind to the alpha A,Reference number: IS8280; MUID:91187610; PMID:1901405
A,Accession: S22293
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; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
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                                                                                                                                        A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1.670 < MIT>
A; Residues: 1.670 < MIT>
A; Cross-references: EMBL: X54250; NID: 957519; PIDN: CAA38151.1; PID: 957520
A; Note: the authors did not translate the codon for residue 1
2; Superfamily: HIV-EP2 enhancer-binding protein
2; Keywords: DNA binding; transcription regulation; zinc finger
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Pred. No. 48;
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Search completed: June 3, 2004, 11:59:58 Job time: 9 secs
                                                                                                                                 A;Status: preliminary, nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Reddues: 1-22 <RLD. * A;Residues: 1-22 <RLD. * A;Residues: 1-22 <RLD. * A;Residues: 1-22 <RLD. * A;Cross-references: GB:AE000970; GB:AE000782; NID:g2689293; PIDN:AAB89318.1; PID:g264860 C;Superfamily: cell division inhibitor minD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: C82900
A;Status: preliminary
A;Molecule type: DNA
A;Resides: 1-544 GLAA
A;Resides: 1-546 GLAA
A;Experimental source: serovar 3; biovar 1
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C.Species: Campylobacter jejuni
C.Species: Gampylobacter jejuni
C.Species: 16-Aug-1996 #text_change 08-Oct-1999
C.Accession: 140788; 847317
R.Hani, E.K.; Chan, V.L.
R.Hani, E.K.; Chan, V.L.
A.Fittle: Expression and characterization of Campylobacter jejuni benzoylglycine amidohyd
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: H69491
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R.Glass, J.I., Lekkowitz, E.J., Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, Pebruary 2000
A.Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a 1
A.Reference number: A82870
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Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
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14;
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55;
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A;Molecule type: DNA
A;Residues: 1-94 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 2
Pred. No. 14;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 2
Pred. No. 55;
1; Mismatches
                                                                                                                                                                                                                                                                                  Query Match 65.4%; Score 34; DB Best Local Similarity 75.0%; Pred. No. 24; Matches 6; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.4%;
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Best Local Similarity 55.6%;
Matches 5; Conservative
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Best Local Similarity 70.0.
Best Local 7; Conservative
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26 DIFPSGMSY 34
                                                                                                                                                                                                                                                                                                                                                                                                                                   81 EVIPAGMS 88
                                                                                                                                                                                                                                                                                                                                                                                    2 EVVPXGMS 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: ABCsbp-5; UU359
A;Genetic code: SGC3
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508 ribosomal protein L20 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Accession: E90544
R;Chambaud, I.; Heilig; R.; Farris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.
R;Chambaud, I.; Heilig; R.; Farris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.
R;Chambard, I.; Heilig; R.; Farris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmor: A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;References: G90544
A;References: G9054
A;References: G90544
A;
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my on:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN=ATCC 25586;

MEDINE=21886394; PubMed=11889109;

MEDINE=21886394; PubMed=11889109;

MEDINE=21886394; PubMed=11889109;

Mapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,

Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,

N. Masleva O., Chu L., Kogan Y., Chaga O., Goltsman B., Bernal A.,

N. Masleva O., Chu L., Kogan Y., Chaga O., Goltsman B., Bernal A.,

N. Josova M., Walumas T., Pusch G., Haselkorn R.,

Larsen M., Kyrpides N., Overbeek R.;

Ronstein M., Kyrpides N., Overbeek R.;

Tomoreatum strain ATCC 25586.",

U. Bacteriol. 184:2005-2018(2002).

U. DATMITT CACTITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + 1-Grantmanet + carbamoyl phosphate.

C. - CATALYAT ATCHITY: A ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + 1-glutamate + carbamoyl phosphate.

C. - PATHWAY: Pyrimidine biosynthesis; first step.

C. - PATHWAY: Pyrimidine biosynthesis; the small (or glutamine) chain

D. SUBUNIT: Composed of two chains; the small (or glutamine) the sused by the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).

STANDARD CONTRACTOR CON
             homo sapien
homo sapien
crithidia f
human herpe
human herpe
                                                                                                                           escherichia
escherichia
escherichia
                                                                                     saccharomyc
                                                                                                 rattus norv
tomato aspe
                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
26-FEB-2003 (Rel. 41, Last annotation update)
phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
944677 P 944677 P 944677 P 944677 P 95555 P 955284 P 952544 P 952784 P 952784 P 958931 P 958931 P 956918 P 96918
                                                                                                                                                                                                                                                                                                                                                                                        Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                        PRT; 1058 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the carB family.
                                                                                                                                                                                                   AL IGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB010554; AA194625.1; ALT_INIT.
HAWAP; MF 01210; -; 1.
HREPERO; IPR006275; CarA Lglu.
INCEPPO; IPR005493; CPase L. D2.
INCEPPO; IPR005499; CPase L. D2.
INCEPPO; IPR005491; CPase L. D3.
INCEPPO; IPR005491; CPase L. N.
INCEPPO; IPR005401; CPase L. N.
INCEPPO; IPR004362; MGS IIke.
Fram; PF00289; CPSase L. Chain; 2.
Pfam; PF02787; CPSase L. Chain; 2.
Pfam; PF02787; CPSase L. D3; 1.
             ENP3_HUMAN
$216_HUMAN
GSP_CRIFA
PRTF_HSV6U
PRTF_HSV6Z
PRTF_TSV6Z
SCTI_YEAST
EDD_RAT
                                                                                                                        RHSA ECOLI
RHSC ECOLI
RHSB ECOLI
   TOLB
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   6017666176661
61766617666176661
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QBRG86;
   RESULT 1
CARB_FUSNN
   xenopus lae
gallus gall
homo sapien
homo sapien
mus musculu
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clostridium
homo sapien
neurospora
homo sapien
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vibrio chol
schizosacch
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clostridium
mus musculu
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vibrio chol
homo sapien
rattus norv
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homo sapien
mus musculu
brachydanio
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campylobact
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                                                                                                 June 3, 2004, 11:32:06; Search time 4.86667 Seconds (without alignments) 117.693 Million cell updates/sec
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P31619
Q04351
P15822
P23622
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098qv0
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Q8cg19
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P50755
P49706
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                      Sotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                          141681 seqs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A10A HUMAN
RL20 MYCFU
YJ49 ARCFU
Y990 CAMJE
CTX3 MOUSE
AROA VIBCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
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Y1A9 CLOAB
ZEP1 HUMAN
CY14 NEUCR
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CLOPE
MOUSE
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Maximum Match 100%
Listing first 45 summaries
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                                                                       M protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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52
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Perfect score:
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MOGU V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Sgouros J., Peat N., Hayles J., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Gentles S., Goble A., Hamlin N., Harris D., Hidalyo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones M., Leather S., McDonald S., McLean J.,
Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
Oliver K., O'Neil S., Pearson D., Quall M.A., Rabbinowitsch E.,
Rutherford K., Rutter S., Sanders D., Seeger K., Sharp S.,
Rutherford K., Taylor R.G., Trivey A., Walsh S.V., Warren T., Whitehead S.,
Woodward J., Volckaert G., Aert R., Schoefer M., Mulbert H.,
Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mulbert H.,
A Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Ber P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Porsburg S.L.,
Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
                                                                                                                                                                                                                                                                                                                                                                           ö
PFam; PF02142; MGS; 1.

R PRINTS; PR00098; CPSASE.

DR TIGREDAMs; TIGR01369; CPSASE11 Lrg; 1.

DR PROSITE; PS00866; CPSASE 1; 2.

DR PROSITE; PS00867; CPSASE 2; 2.

KW Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

CARBOX/PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                            ATP (POTENTIAL).

352 ATP (POTENTIAL).

284 MANGANESE I (BY SIMILARITY).

300 MANGANESE I AND 2 (BY SIMILARITY).

820 MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

821 MANGANESE 3 (BY SIMILARITY).

822 MANGANESE 3 (BY SIMILARITY).

823 MANGANESE 3 (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                           Score 38; DB 1; Length 1058;
Pred. No. 7;
3; Mismatches 1; Indels
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Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Probable sulfate permease C3H7.02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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Best Local Similarity
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074377;
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DOMAIN
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BEPEAT
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SULH SCHPO
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                                                                                           -1- FUNCTION: HIGH AFFINITY UPTAKE OF SULFATE INTO THE CELL (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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enome sequence of Schizosaccharomyces pombe.";
415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tobacco yellow dwarf virus (strain Australia) (TYDN
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-071-1993 (Rel. 26, Created)
01-071-1993 (Rel. 26, Last sequence update)
01-071-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 102 AA
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POTENTIAL.
POTENTIAL.
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POTENTIAL.
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POTENTIAL.
                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Contains 1 STAS domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMEL; AL031261; CAA20298.1; -...
PIR; T40413; T40413.
GeneDB Sponde, SPEC17.0; -...
InterPro; IPR0012045; STAS.
InterPro; IPR001902; Sulph_transpt.
Pfam; PF01740; STAS.
IGRFAMS; TIGR00815; S11fate transp; 1...
Pfam; PR00916; Sulfate transp; 1...
PROSITE; PS01130; SLC26A; 1...
PROSITE; PS01130; SLC26A; 1...
Transport; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96373 MW;
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es 7; Conserv
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TRANSMEM 1
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Y11K_TYDVA
D Y11K_TYDVA
AC P31619;
DT 01-JUL-1993
DT 01-J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         small heat shock protein of Closridium acetobutylicum.";
J. Bacteriol. 175:3394-3400(1993).
-!- SIMILARITY: Contains 2 PtsK domains.
-!- CAUTION: Ref. 2 sequence differs from that shown due to frameshifts in positions 76 and 106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moelling J. Breto, m. Moelling J. Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tathagov R.L., Sabathe F., Douecte-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin B.V., Smith D.R.; "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acerobutylicum.", J. Bacteriol. 183:4823-4838(2001).

[2]
SEQUENCE OF 1-108 FROM N.A.
SEQUENCE OF 1-108 FROM N.A.
MEDLINE=93273706; PubMed=8501044;
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sauer U., Duerre P.;
"Sequence and molecular characterization of a DNA region encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
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                                                                                                                                                                                                                                                                                           Score 36; DB 1; Length 102;
Pred. No. 1.6;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                             102 AA; 11178 MW; A40ECF1E0AF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein CAC3709.
CAC3709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1498 AA
                                                                                                                             or send an email to license@isb-sib.ch).
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MEDLINE-21359325; PubMed-11466286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE007866; AAK81629.1; -.
EMBL; X65276; CAA46379.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                InterPro; IPR002621; Gemini mov. Pfam; PF01708; Gemini mov; 1. Hypothetical protein.
                                                                                                                                                                 EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                                                 69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium acetobutylicum.
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                         7 QVVPSGINYS 16
                                                                                                                                                                                                                                                                                                                                                                       2 EVVPXGMSYS 11
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                                                                                                                                                                                                                                                             SEQUENCE
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PIR; B97355; B97355. InterPro; IPR002543; FtsK_SpoIIIB.

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01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
2inc finger protein 40 (Human immunodeficiency virus type I enhancer-
binding protein 1) (HIV-EP1) (Major histocompatibility complex binding
protein 1) (MBP-1) (Positive regulatory domain II binding factor 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "High-resolution solution structure of the double Cys2His2 zinc finger from the human enhancer binding protein MBP-1."; Biochemistry 31:3907-3917(1992).

Biochemistry 31:3907-3917(1992).

FUNCTION: THIS PROTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE 5'-GGGACTTTCG-3' WHICH IS FOUND IN THE ENHANCER ELEMENTS OF NUMEROUS VIRAL PROMOTERS SUCH AS THOSE OF SY40, CWY, OR HIVI. IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I MIC. INTERBERKINIA SEGEPTOR, AND INTERFERON-BETA GENES: IT MAY ACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NMR OF 2113-2142.
MEDITME-SUCK4333; PubMed=2248949;
MEDITME-SUCK4333; PubMed=2248949;
Omichinski J.G., Clore G.M., Appella E., Sakaguchi K.,
Gronenborn A.M.;
"High-resolution three-dimensional structure of a single zinc finger
"High-resolution three-dimensional protein in solution.";
Biochemistry 29:9324-9334(1990).
                                                                                                                                                                                                                                                                                                                                   Gaps
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SUBCELLULAR LOCATION: Nuclear.
INDUCTIVE BY MILOGENS AND Phorbol ester.
DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY
SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=90169514; PubMed=2106471;
MEDLINE=90169514; PubMed=2106471;
MEDLINE=90169514; PubMed=2106471;
"A DNA-binding protein containing two widely separated zinc finger motifs that recognize the same DNA sequence.";
Genes Dev. 4:29-42(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92222684; PubMed=1567844;
Omichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E.,
Gronenborn A.M.;
                                                                                                                                                                                                                                                                                                                                   ö
Pfam, PF01580; FtsK_Spoilie; 2.
PROSTIE; PS50901; FTSK; 2.
DOWAIN 655 857 FTSK 1.
DOWAIN 1001 1188 FTSK 1.
DOWAIN 1001 1188 FTSK 1.
SPECTOR 1.
SPECTOR 2.
SPECTOR 2.
SPECTOR 3.

                                                                                                                                                                                                                                                          Score 36; DB 1; Length 1498;
Pred. No. 27;
2; Mismatches 2; Indels
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-!- SIMILARITY: STRONG, TO HIVEP2.
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                                                                                                                                                                                                                                                             69.2%;
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        |::| ||||
1276 EQKIPMGMSY 1285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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HIVEP1 OR ZNF40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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P15822;
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      STTTS
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[2]
SEQUENCE FROM N.A.
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TRANSMEM
TRANSMEM
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TRANSMEM
TRANSMEM
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TRANSMEM
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A10A_HO
A10A_HO
A10A_HO
DT 30-MAY
DT 28-FBB
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                          DR GO; GO: 0005674; C:nucleus; TAS.

DR GO; GO: 0005677; F:DNA binding; TAS.

BROJ: PF000967; Zaf.CH2.

DR Pfau; PF00096; Zaf.CH2.

DR PROSITE; PS00028; ZINC FINGER C2H2.

DR PROSITE; PS00028; ZINC FINGER C2H2.2; 4.

DR PROSITE; PS0157; ZINC FINGER C2H2.7; 4.

DR PROSITE; PS0167; ZINC FINGER C2H2.7; 4.

TAN FING 434 436 C2H3-TYPE.

FT ZN FING 958 981 C2HC-TYPE.

FT ZN FING 2109 C2H3-TYPE.

FT ZN FING 2109 C2H3-TYPE.

T ZN FING 2115 2139 C2H2-TYPE.

T STRAND 2088 2088 POLY-SER.
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SEQUENCE FROM N.A.
MEDLINE=91129256; PubMed=1825178;
Ketter J.S., Jarai G., Fu Y.-H., Marzluf G.A.;
Ketter J.S., Jarai G., Fu Y.-H., Marzluf G.A.;
"Nucleotide sequence, messenger RNA stability, and DNA recognition
"Nucleotide sequence, messenger INA stability, and DNA recognition
elements of cys-14, the structural gene for sulfate permease II in
elements of cys-14, .---/1091).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROBABLE REVISIONS.
MEDIINE-S4189205. Pubmed-8140616;
Sandal N.N., Marcker K.A.;
"Similarities between a soybean nodulin, Neurospora crassa sulphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neurospora crassa.
Bukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.3%; Score 35; DB 1; Length 2717; 66.7%; Pred. No. 80; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2717 AA; 297217 MW; D45D3CA951FEA561 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1991 (Rel. 20, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
110-CCT-2003 (Rel. 42, Last annotation update)
Sulfate permease II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                           EMBL; X51435; CAA35798.1; -.
PIR; A34203; A34203.
PDB; 3ZNF; 15-7AN-92.
PDB; 4ZNF; 15-7AN-92.
PDB; 1BBO; 31-0CT-93.
TRANSFAC; T00497; -.
Genew; HGNN:4920; HIVEP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
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2405 VVPAGLTYS 2413
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2109
2116
2124
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2139
806
2088
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Matches 6; Conserv
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2099
2099
21109
2115
2123
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P23622;
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STRAND
HELIX
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CY14 NEUCR
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permease II and a putative human tumour suppressor.";
Trends Biochem. Sci. 19:19-19[1994].
-!- FUNCTION: UPTAKE OF SULFATE INTO THE CELL.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- INDUCTION: Highly expressed, but only in cells subject to sulfur limitation, and it is turned on by the positive-acting Cys-3 sulfur regulatory protein.
-!- MISCELLANBOUS: SULFATE PERMEASE II IS MAINLY FOUND IN MYCELIA.
-!- SIMILARITY: Belongs to the SLC26A/SulP transporter (TC 2.A.53)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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SEQUENCE FROM N.A.

BEDLINE-1225279; PubMed=11326269;

Meguro M., Kashiwagi A., Mitsuya K., Nakao M., Kondo I., Saitoh S.,
Oshimura M.;

"A novel maternally expressed gene, ATP10C, encodes a putative
aminophospholipid translocase associated with Angelman syndrome.";
Nat. Genet. 2819-20(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           060312; 096914; Octobroll 139, Created)
28-FRB-2000 (Rel. 39, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
(Aninophospholipid-transporting Arpase VA (EC 3.6.3.1) (ATPVA)
ATP10A OR ATP10C OR ATPVC OR KIAA0566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . . .) (POTENTIAL).
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Bukaryota, Metazoa, Chordata; Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Pred. No. 36;
2; Mismatches 1; Indels
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4FC604B60798CE77 CRC64;
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Pfam, PRO0916, Sulfate transp, 1.

TIGRAMS, TIGROOBIS, BULP, 1.

PROSITE, PSO1130, SLC26A, 1.

Transport; Transmembrane; Glycoprotein.
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PIR; A37956; A37956.
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788 AA;
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                                                                                                                                                                                                                        MEDLINE=22388257; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alusaner R.D., Colling B., Buctow K.H., Schemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buctow K.H., Schemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buctow K.H., Schemen C.M., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci F., Prange C.,
Raha S.S., Loquallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Ginbaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakeelley R.W., Touchman J.W., Gfreen E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.R.;
Generation and initial analysis of more than 15,000 full-length
MEDLINE=21313119; PubMed=11353404;
Herzing L.B.K., Kim S.-J., Cook B.H. Ur., Ledbetter D.H.;
"The human aminophospholipid-transporting ATPase gene ATPIOC maps adjacent to UBE3A and exhibits similar imprinted expression.";
Am. J. Hum. Genet. 68:1501-1505(2001).
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L) AY029467; AAK33100.1; --
L) AY029469; AAK33100.1; JOINED.
L) AY029469; AAK33100.1; JOINED.
L) AY029499; AAK33100.1; JOINED.
L) AY029491; AAK33100.1; JOINED.
L: AY029492; AAK33100.1; JOINED.
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                                                                                                                   Am. J. Hum. Genet.
[3]
SEQUENCE FROM N.A.
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Gaps
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PRINTS, PR00119; CATATPASE.
TIGRRAMS, TIGR01652; ATPase-Pippid; 1.
TIGRRAMS, TIGR01494; ATPase P-type; 6.
PROSITE; PS001154; ATPASE E1 22; 1.
Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
                                                                                                                                                                                                                                                                                                                                     GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0004012; F:phospholipid-translocating ATPase activity; NAS.
GO; GO:00008360; P:regulation of cell shape; NAS.
InterPro; IPR001757; ATPase El-E2.
InterPro; IPR00539; Alippase.
InterPro; IPR005834; Hydrolase.
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PHOSPHOKYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
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Pred. No. 70;
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167687 MW; D4996A4D0635A6BD CRC64;
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
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EMBL; AY029493; AAX33100.1; JOINED. EMBL; AY029494; AAX33100.1; JOINED. EMBL; AY029494; AAX33100.1; JOINED. EMBL; AY029495; AAX33100.1; JOINED. EMBL; AY029497; AAX33100.1; JOINED. EMBL; AY029499; AAX33100.1; JOINED. EMBL; AY029500; AAX33100.1; JOINED. EMBL; AY029501; AAX33100.1; JOINED. EMBL; AY029503; AAX33100.1; JOINED. EMBL; AY029503; AAX33100.1; JOINED. EMBL; BY025503; AAX33100.1; JOINED. EMBL; AS011138; BAAS5492.1; FRBL; AS011138; FRBL; AS011138
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les 8; Conservative
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Multigene family
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1499
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Q98QV0;
28-FEB-2003 (
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Kirkness B.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McKell L.K., Badger J.H., Glodek A., Zhou L., Coverbeek R., Gocarn J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A., Wenson T.W., Olsen G.J., Fraser C.M., Smith H.O., Woose C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=NCTC 11168;
MEDIATHS=2015. PubMed=10688204;
MEDIATHS=2015.0912; PubMed=10688204;
MEDIATHS=2015.0912; PubMed=10688204;
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Ouail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
. Reveals hypervariable sequences.";
Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Campylobacter jejuni.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
                                                                                                                                                                           "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
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STRAIN=ATCC 43431 / TGH 9011;
MEDLINE=95247673; PubMed=7730270;
MEDLINE=95247673; PubMed=7730270;
"Expression and characterization of Campylobacter jejuni benzoylglycine amidohydrolase (Hippuricase) gene in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.5%; Score 33; DB 1; Length 165; 60.0%; Pred. No. 12; tive 1; Mismatches 3; Indels
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PIR; D65493; D69493.
TIGR: AF1949; -.
Hypotherical protein; Transmembrane; Complete proteome.
TRANSMEM 7 27 POTENTIAL.
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165 AA; 17588 MW; BBC17054810ADBF8 CRC64;
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                                                                                                                                                                                                                                                                                                                            Mycoplasma pulmonis.",
Nucleic Acids Res. 29:2145-2153(2001).
Nucleic Researy for the in vitro assembly process of the 50s ribosomal subunit. It is not involved in the protein synthesizing functions of that subunit (By similarity).
Is IMILARITY: Belongs to the L20P family of ribosomal proteins.
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                                                                                                                                                                         STRAIN=UAB CTIP;
MEDLINE=21267165; PubMed=11353084;
Chamband I., Heilig R., Ferris S., Barbe V., Samson D., Galisson Moszer I., Dybvig K., Wroblewski H., Vlari A., Rocha B.P.C.,
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
                                                                                                                                                                                                                                                                                                 "The complete genome sequence of the murine respiratory pathogen
50S ribosomal protein L20.
RPLT OR MYPU-2610.
Wyczplasma pulmonis.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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C59C748901B18F14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaeoglobus fulgidus.
Archaea, Euryarchaeota, Archaeoglobi, Archaeoglobales,
Archaeoglobaceae, Archaeoglobus.
NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.5%; Score 33; DB 1; 77.8%; Pred. No. 8.1; iive 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein AF1949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL445563; CAC13434.1; -.
PIR; E90544; E90544.
Mypulist; MYPU 2610; -.
HAMAP; MF 00382; -; 1.
InterPro; IRR05813; Ribosomal L20.
InterPro; IRR05813; Ribosomal L20.
Ffan; PP00453; Ribosomal L20; I.
Promi; PR00453; Ribosomal L20; I.
Promi; PR00453; Ribosomal L20; I.
Promi; PR00423; Ribosomal L20; I.
Promi; PR00423; Ribosomal L20; I.
Promi; PR00423; Ribosomal L20; I.
Ribosomal Protein; Ribosomal L20; I.
Ribosomal Protein; Ribosomal L20; I.
Ribosomal Protein; RAM, 13565; MM; C59C748901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 VVPXGMSYS 11
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                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                    NCBI_TaxID=2107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YJ49 ARCFU
ID YJ49 ARCFU
AC O28330;
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Gaps

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221
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Q9KRB0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=2
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CONFLICT
SEQUENCE
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AROA_VIBCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
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the Buropean Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ENGURNEE FROM N. (ISOPORMS 1 AND 2).

STRAIN=C57BL/6J; TISOFOEMS 1 AND 2).

STRAIN=C57BL/6J; TISOFOEMS 1 AND 2).

KRWAIJ J., Shinagawa A., Shibata K., Yoohino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Kondo H., Rachkawa T., Fukuda S., Alazawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Asito T., Gazaki Y., Gajobori T., Bono H., Kasukawa T., Saito R., Asdota K., Matsuda H., Rachtawa T., Saito R., Fleischmann W., Gazeterland T., Gissi C., King B., Kochiwa H., Fleischmann W., Gazeterland T., Gissi C., King B., Kochiwa H., Schriml L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno W., Aono H., Baldarelli R., Barsh G., Bulke J., Bult C., Fletcher C., Fulita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Mazzarelli J., Mombaerts P., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Lyons P., Ratch B., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Havsahizaki W., Kawaji H., Kohtsuki S., Havsahizaki S., Kawaji H., Kohtsuki S., Havsahizaki Y., Schotsuki S., Kawaji H., Kohtsuki S., Kayang K., Havsahizaki Y., Kantis S., Kayani H., Kohtsuki S., Havsahizaki S., Kakusuki 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=2238825; PubMed12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Stausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.R., Rubin G.M., Hong L., Tagneton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McZernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                             63.5%; Score 33; DB 1; Length 253; 55.6%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                      Hypothetical protein, Complete proteome.
SEQUENCE 253 AA; 29783 MW; F96D3FF3265F8A6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTX3 MOUSE STANDARD; PRT; 280 AA. Q9D387; Q9CXQ4; 28-FEB-2003 (Rel. 41, Created) 26-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Protein C20orf103 homolog precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                      EMBL; AL139076; CAB73246.1; -.
EMBL; 236940; CAA85392.1; -.
PIR; C81374; C81374; C81374
PIR; 140758; 140758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Mammary fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 55.6
les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: | ||||
185 DIFPSGMSY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 EVVPXGMSY 10
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TAX MOUSE

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Matches
      임임임임임임목독표표
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseesiab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=09D387-2; Sequence=VSP 003820;
-1- CAUTION: Ref.1 sequence differs from that shown due to frameshifts
in positions 174 and 239.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.

YOPOPLASHOE (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL)
N-LINKED (GLCNAC. ...) (POTENTIAL)
N-LINKED (GLCNAC. ...) (POTENTIAL)
N-LINKED (GLCNAC. ...) (POTENTIAL)
                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Vibrionaceae; Vibrio.
NCBL TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   b > V (IN REF. 1; BAB31124).
c -> P (IN REF. 1; BAB31124).
p -> A (IN REF. 1; BAB31124).
realID7BF9FD5CCEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN C200RF103 HOMOLOG. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Missing (in isoform 2). /FTId=VSP 003820.
                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fransmembrane; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 20;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q9D387-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AK014127; BAB29169.1; -.
EMBL; AK018222; BAB31124.1; ALT_FRAME.
EMBL; BC004791; AAH04791.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1920368; 3110035N03Rik.
MGD; MGI:1923411; 6330527006Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 230 Q
238 238 P
280 AA; 31721 MW;
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Similarity 75.0%;
6; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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Best Local Similarity
Matches 6; Conserv
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDIATAN-E1 Tor N16961 / Serotype 01;

MEDIATAN-E1 Tor N16961 / Serotype 01;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey B.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Eichardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;

"DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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28-FBB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
119-90CT-2003 (Rel. 42, Last annotation update)
119-90C co-chaperone Cdc37 (Hsp90 chaperone protein kinase-targeting subunit) (Cell division control protein 37).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 406:477-483 (2000).
-!- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate.
-!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway; sixth step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGN, VC172; ...
HAWAP, MF 00210; ...
InterPro; IPR001086; EPSP synth.
InterPro; IPR001986; EPSP synth.
Prodom, P001867; EPSP synthase; 1.
Prodom, P001867; EPSP synthase; 1.
Prodom; P00104; EPSP SYNTHASE; 1.
PROSTIE; P00104; EPSP SYNTHASE; 1; 1.
PROSTIE; P00104; EPSP SYNTHASE; 1; 1.
Aromatic anion acid biosynthesis; Transferase; Complete protecme. SEQUENCE 426 AA; 46101 MW; 38852D6483BFEIC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Westwood P.K., Preston N.C., Fantes P.A.;
"Schizosaccharomyces pombe cdc37 gene.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBMIT: Monomer (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-1- SIMILARITY: Belongs to the EPSP synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Fungi, Agoomycota, Schizogaccharomycetes,
Schizogaccharomycetales, Schizogaccharomycetaceae,
Schizogaccharomyces.
Schizogaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           466 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE004251; AAF94882.1; -.
PIR; D82163; D82163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 60.0
ses 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                           MEDITIRE-1848401; PubMed=185380; MEDITIRE-1848401; PubMed=1853360; MEDITIRE-1848401; PubMed=185360; Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chilingworth T., Churcher C.M., Cherry C. Churcher C.M., Cherry B., Connor R., Cronin M., Davis P., Feltwell T., Fraser A. Collins M., Connor R., Davis P., Feltwell T., Fraser A. Gollins M., Connor R., Davis P., Hochel E.J., Hunt S., Jagels K., Jones L., Jones M., Harris D., Hidalgo J., Hodgson G., Horlory S., Wooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Noney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., A. Skelton J., Stenton S., Stavens K., Starp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor R.G., Trvey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Woodward J., Volckaert G., Aert R., Robben J., Hilbert H., Malsh S.V., Marren T., Whitehead S., Relfens M., Ender M., Medler H., Reinhardt R., Pohl T.M., Ber P., Zimmernann W., Wedler H., Reinhardt R., Purnelle S., Lelaure V., Mottier S., Lucas M., Rochet M., Gailardt R., Moore K., Hurt S.M., Lucas M., Rochet M., Gallard V.A., Garzon A., Thode G., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., McCombie W.R., Pauleen I., Potashkin J., Shangkovski G.V., Useery D., Barrell B.G., Nurse P., Shakevski G.V., Usery D., Barrell B.G., Nurse P., Shakevski G.V., Usery D., Barrell B.G., Nurse P., Shakevski G.V., Usersy D., Barrell B.G., Nurse P., Shakevski G.V., Der Schlizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=2245455; PubMed=12861001;
Tatebe H., Shiozaki K.;
Tatebe H., Shiozaki K.;
Tatebe H., Shiozaki K.;
Tatebe H., Shiozaki K.;
Mol. Cell. Biol. 23:5132-5142(2003)
-! FUNCTION: Co-chaperone that binds to numerous kinases and promotes their interaction with the Hsp90 complex, resulting in stabilization and promotion of their activity.
-! SUBUNIT: Forms a complex with Hsp90. Interacts with styl.
-! SUBCELULAR LOCATION: Nuclear, and cytoplasmic. When in the nucleus associated with chromatin.
-! SIMILARITY: Belongs to the CDC37 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gарв
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EMBL; AJ132376; CAB38757.1; -.
EMBL; AJ132376; CAB38757.1; -.
EMBL; AJ132376; CAB38757.1; -.
EMBL; AAJ49769; CAB42371.2; -.
GENEDB SPOWDe; SPBC9B6.10; -.
InterPro; IPR004918; Cdc37.
Pfam, PF03234; Cdc37; Cdc37; Cdc37; Cdc37; Cdc37; Capperone; Cell duision; Cell cycle; Nuclear protein.
SEQUENCE 466 AA; 52554 MW; 647238B34CABB3C5 CRC64;
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Straubberg R.L., Feinmenter. School School School Straubberg R.L., Feinmenter. School 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S., Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBUNIT: Interacts with HSV-I early proteins ICP22 and ICP0.
-!- SUBCELLUIAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: Expressed at high levels in heart and pancreas, moderate levels in placenta, liver, skeletal muscle, and kidney, and low levels in brain and lung.
-!- SIMILARITY: Belongs to the GITSCR2 family.
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=20175430; PubMed=10708517;
Smith J.S., Tachibana I., Pohl U., Lee H.K., Thanarajasingam U.,
Portier B.P., Ucki K., Billings R. Ramaswamy S., Mohrenweiser H.W.,
Scheithauer B.W., Louis D.N., Jenkins R.B.;
"A transcript map of the chromosome 19q-Arm glioma tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 9-478 FROM N.A., AND SUBCELLULAR LOCATION.
MEDLINE=99214318; PubMed=10196275;
Bruni R., Fineschi B., Ogle W.O., Roizman B.;
"A novel cellular protein, p60, interacting with both herpes simplex virus 1 regulatory proteins ICP22 and ICP0 is modified in a cell-type-specific manner and is recruited to the nucleus after
                                                                                                                                                                                             Eukaryota, Metazoa, Chordata; Craniata; Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
GSR2_HUMAN STANDARD; PRT; 478 AA.
QSNZMS; QSBTC6; QSHAX6; QSNPP1; QSNRR4; QSUF12;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glicma tumor suppressor candidate region gene 2 protein (p60).
GLTSCR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 12-478 FROM N.A.
Andreu N., Estivill X., Escarceller M., Sumoy L.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                            Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                         R -> Q.

//FTId=VAR. 011486.

GGS -> HEG (IN REF. 2; AAH04229).

G -> R (IN REF. 3).

RRKEGLWEKTAKGGELPREVRRAGARLINDSATRAKPGPQD

RYERD -> SGRSSYGRSWPERASSPGGAGQFSPVAOPFCN

KGPNPAFGHIAA (IN REF. 3).

SDNPLDRPLVGQDEFFIE -> INNPDKPVVWPGCLFPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IN REF. 3).

- S (IN REF. 2; AAH04229).

D -> H (IN REF. 3).

PEGNILRDRFKSFORRNMIEPRERAKFKRYTKVKLVEKRAF

REIQ -> VLTVSCRRADACPVMTPBILLPVPPRGYGRHHGCP

WAGPVGPMERG (IN REF. 5).

EGNILRDRFKSFORRNMIEPRERAKFKRKYKVKLVEKRAFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CPN50;
MEDLINE-87055/020; PubMed=2877971;
Garrier I., Cole S.T.;
"Characterization of a bacteriocinogenic plasmid from Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIQL -> RGQHSFETGSRAFRGGI (IN REF. 7F18923E348CB52B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid pIP404.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 1; Length 478; Pred. No. 35; 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
Bacteriocin BCN5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       890 AA
                                                                                                                                                                                                                                                                                                    30; GO:0005622; C:intracellular; NAS.
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                                                                                       EMBL, AF182076, AAF62873.1, --
EMBL, BC004229; AAH04229.1; --
EMBL, BC0100951, AAH06311.1; --
EMBL, BC010095, AAH10095.1; --
EMBL, AF286124; AAG30413.1; --
EMBL, AL359335; CAB94786.1; --
EMBL, AL329335; CAB94786.1; --
EMBL, AL122063; CAB59242.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CPN50;
MEDLINE=88336297; PubMed=2901768;
                                                                                                                                                                                                                                                                                                                      Nuclear protein, Polymorphism.
VARIANT 389 389 R
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                                                                                                                                                                                                                                               Q9NZMS; HUMAN
                                                                                                                                                                                                                                                              Genew; HGNC:4333; GLTSCR2
MIM; 605691; -.
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Best Local Similarity 60.0
Matches 6; Conservative
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                                        63.5%; Score 33; DB 1; Length 890; 66.7%; Pred. No. 67; 2; Indels rative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN 815 869 HYDROPHOBIC.
SEQUENCE 890 AA, 96699 MW; F4E5E8971C3C6C6 CRC64;
perfringens and molecular genetic analysis of the bacteriocin-encoding gene."; J. Bacteriol. 168:1189-1196(1986).
                                                                                                                                                                                                                                                                                                                 EMBL; M14481; AAA98248.1; -.
EMBL; M32882; AAA98249.1; -.
                                                                                                                                                                                                                                                                                                                                                        PIR, A30481; A30481.
InterPro; PR000844; Peptidase_M14.
InterPro; IRR008846; SH3 bac.
Ffam; PF00246; Zn_carbopept; 1.
SMART; SM00287; SH3b; 3.
SMART; SM00287; SH3b; 3.
PARTIDIOLIC; Bacteriocin; Plasmid
DOMAIN
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Matches 6, Conservative
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MEDLINE-2225144; PubMed=12240834;
A MEDLINE-22255144; PubMed=12240834;
A Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., A Matanabe A., Iriguothi M., Kawashima K., Kimura T., Kishida Y., Kityokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
Tomoplete genome structure of the thermophilic cyanobacterium Enternosynechococcus elongatus BP-1.";
DNA Res. 9:123-130(2002)
EMBL; APPOS374; BAGO9170.1;
CGO; GO:0006215; F:transporter activity; IEA.
GO; GO:0006215; F:transporter activity; IEA.
R GO; GO:0006315; P:transporter activity; IEA.
R InterPro; IPR0014764; HALI.
R InterPro; IPR0014764; HALI.
R Pfam; PF00873; ACR_tran; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synechococcus elongatus (Thermosynechococcus elongatus)
Bacteria: Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1044 AA.
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                            Q81587
Q01487
Q8PMI6
Q8PAT2
Q9PDM6
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012479
097152
028342
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Q8RE56
Q7SY67
Q7U5S2
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Q8G4I5
Q8XT05
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Q9PQD2
Q7UWU7
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Q8TX62
Q8PPP5
Q8VUA8
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Q8IYM3
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TIGRFAMS; TIGR00915; 2A0602; 1.
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TLL1618.
                                                                                     75.0%;
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Matches 7; Conserv
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SEQUENCE 1044 AZ
01-MAR-2003
01-MAR-2003
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Q915a7 bacillus ce
Q98fx1 rhizobium 1
Q94C56 cenarchaeum
Q9ury8 schizosacch
Q8wd4 mycoplasma
Q8rd18 mus musculu
Q8btx4 mus musculu
Q8btx4 mus musculu
Q8btx9 enterocococu
Q839ty enterocococu
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Q40129 lycopersico
Q7v6q4 prochloroco
Q9xvk4 caenorhabdi
Q8c1d7 mus musculu
                                                                       June 3, 2004, 11:35:06.; Search time 29.8667 Seconds (without alignments) 116.206 Million cell updates/sec
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          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Q815A7
Q98FX1
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Q7V6Q4
Q9XVK4
Q8C1D7
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*Sp_organelle:*
*Sp_phage:*
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*Sp_vortus:*
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*Sp_archeap:*
*Sp_archeap:*
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Gapop 10.0 , Gapext 0.5
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pp archea:*
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sp_numan:*
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1 EEVVPXGMSYS 11
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Perfect score:
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SEQUENCE FROM N.A.
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Q9URY8
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MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Kanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-2268415; PubMed=12721630;
Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Raparral V., Bhatrecharya A., Reznik G., Mikhailova N., Lapidus A.,
Gub L., Maur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
Overbeek R., Kyrpides N.;
Genome sequence of Bacillus cereus and comparative analysis with
Bacillus anthracis.";
Nature 423:87-91(2003).
EMBL, AB012015; AAP12123.1; -.
EMBL, AB013015; AAP12123.1; -.
EnterPro; IPR000437; Prok Lipoprot_S.
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Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Phyllobacteriaceae, Mesorhizobium.
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                                                                                                                                                                                                                                                                                                                                                          Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=226900;
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EMBL, AP003002; BAB50445.1; -.

GO; GO:0016787; F:Mydrolase activity; IEA.

GO; GO:0008237; F:metallopeptidase activity; IEA.

GO; GO:0008237; F:metallopeptidase activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR002933; Peptidase_M20.
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Last annotation update)
                                                                                                                                                                                         344 AA
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01-JUN-2003 (TrEMBLrel. 24, Last sequence u
01-OCT-2003 (TrEMBLrel. 25, Last annotation
ABC transporter substrate-binding protein.
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01-0CT-2001 (TrEMBLrel. 18,
01-JUN-2003 (TrEMBLrel. 24,
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Matches 6; Conservative
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843 EEVLPNGIGYS 853
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1 EEVVPXGMSYS 11
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152 EEIAPLGLSY 161
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Q98FX1;
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Cenarchaeum.
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STRAIN=972h-;
Hunt C., Aves S., McDougall R.C., Rajandream M.A., Barrell B.G.;
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MEDINE=98422450; PubMed=9748430;
Schlepper C. DeLong E.F., Preston C.M., Feldman R.A., Wu K.Y.,
Swanson R.V.;
                                                                         / Match 73.1%; Score 38; DB 16; Length 387; Local Similarity 60.0%; Pred. No. 15; es 6; Conservative 2; Mismatches 2; Indels
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54.5%; Pred. No. 1.7e+02;
ive 4; Mismatches 1; Indels
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Hydrolase; Complete protecme.
SEQUENCE 387 AA; 41180 MW; 131BFF8E64306829 CRC64;
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Probable sulfate permease.
SPAC869.05C.
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Last annotation update)
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PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; 1.
                                                                                                                                                                                                                                                                                                                                                Created)
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01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1996 (TrEMBLrel. 08,
01-OCT-2003 (TrEMBLrel. 25,
Hypothetical protein.
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les 6; Conservative
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367 DEAIPHGMSY 376
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                                                                                                                                                                1 EEVVPXGMSY 10
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484 AA.
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2; Mismatches
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Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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Strausberg R.;
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                                                   SEQUENCE FROM N.A.
TISSUE=Liver;
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     NCBI_TaxID=10090;
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Q8BTX4
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Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
"The complete genomic sequence of Mycoplasma penetrans, an
intracellular bacterial pathogen in humans.";
Nucleic Acids Res. 30:5293-5300(2002).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma penetrans.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=28227;
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                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 71.2%; Score 37; DB 3; Length 840; Best Local Similarity 77.8%; Pred. No. 59; Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1123 AA; 123636 MW; A4D707330E3DB4AC CRC64;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL132779; CAB60015.1; -.
                                                                                                                                                                                                                                                                                                                                 93517 MW; ED4833E162B69077 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 21, Last sequence update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                           PIN, T39116, T39116.

GeneDB SPombe, SPAC66.05c; -
Go, GO:0016020, C:membrane, IEA.
GO; GO:0008272; F:sulfate porter activity; IEA.
GO; GO:0008272; F:sulfate borter activity; IEA.
GO; GO:0008272; F:sulfate transport; IEA.
InterPro; IPR0012645; STAS.
InterPro; IPR001902; Sulph_transpt.
Pfam; PF001916; Sulfate_transpt.
Pfam; PF00916; Sulfate_transpt.
TIGRFAMS; TIGR00815; Gulf; 1.
PROSITE; PSS0801; STAS; 1.
SEQUENCE 840 AA; 93517 MW; ED4833E162B69077 CR
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InterPro; IPR009895; Cona_Like_lec_gl.
InterPro; IPR00936; Lipoprotein_17
Pfam; PF04200; Lipoprotein_17; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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Best Local Similarity 70.0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 VVPQGMSYA 143
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SEQUENCE 1123 AJ
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)8EWD4
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STRAIN=NOD; TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851;
THE FANNE CONSOrtium,
The FANNE Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                           Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus.
MCBI_TaxID=10090;
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                                                                                                                                                                                                                                                   Score 36; DB 11; Length 471;
Pred. No. 51; 2; Indels
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
1-MAR-2003 (TrEMBLrel. 22, Last annotation update)
Similar to gliona tumor suppressor candidate region gene 2.
GLISCR2 OR AMS36441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to glioma tumor suppressor CANDIDATE region gene
Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025810; AAH25810.1; -.
MGD; MGI:2154441; G1tscr2.
Hypothetical protein.
NON TER
SEQUENCE 471 AA; 54506 MW; E0DA685C374A9760 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, MS12017637, AAH17637.1, -.
MGD, MG1:215441, G115672.
SEQUENCE 484 AA, 55835 MW; BBB45F3B4BB02A36 CRC64;
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"Role of mobile DNA in the evolution of vancomycin-resistant
                                                                       EMBL; AE016947; AA079943.1; -.
TIGR; EF0063; -.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000437; Prok lipoprot_S.
InterPro; IPR00914; SEP_bac_S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1399 AA
                                                                                                                                                                                                                                                                                                                                                                                                  2, Mismatches
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                               Enterococcus faecalis.";
Science 299:2071-2074(2003).
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66...
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Best Local Similarity 60...
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 LIPEGMSYS 359
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581 QVVPAGLSY
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-C3784683; PubMed=12466851;

The FANTOM Consortium,

the RIKEN Genome Exploration Research Group Phase I & II Team;

the RIKEN Genome Exploration Research Group Phase I & II Team;

the RIKEN Genome Exploration Research Group Phase I & II Team;

"Analysis of the mouse transcriptome based on functional annotation of

60,770 full-length CDNAs.";

Nature 420:653-573 (2002).

ENBL; AK077741; BAC36760.1;

ENBL; AK077741; Gltscr2.

SEQUENCE 484 AA; 55792 MW; EB67949BCBB92D44 CRC64;
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STRAIN=V883 / ATCC 700802;
MEDLINE=2250857; PubMed-12663927;
MEDLINE=2250857; PubMed-12663927;
Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madugu R., Nelson W.,
Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBL_TaxID=1351;
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                    69.2%; Score 36; DB 11; Length 484; 60.0%; Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 24, Last annotation update)
01-UIN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to glioma tumor suppressor CANDIDATE region gene
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL, AKO89461; BAC40357.1; -.
MGD; MGI:2154441; Gltscr2.
SEQUENCE 484 AA; 55806 MW; B3056425B5EECAD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      083979;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pheromone binding protein, putative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   559 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                  484 AA
                                                                                                                                                                                                      2; Mismatches
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                                                                                                                                                      Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                     239 EVIPAGASYN 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                               Q8BK35,
Q8BK35;
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Q839T9
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STAGENER FROM: N.A.

STAGENER FROM: N.A.

Berry K. Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,

Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,

Berry K., Utterback T., Van Aken S., Feldblyum T.,

Berry K., Utterback T., Van Aken S., Feldblyum T.,

Brinkac L., Beanan M., Haff D., Selengut J., Nelson W., Davidsen T.,

Mite O., Fraser C., Collmer A., Kolonay J., Madupu R., Davidsen T.,

White O., Fraser C., Collmer A., Kelonay J., Nelson W., Davidsen T.,

White O., Fraser C., Collmer A., Kelonay J., Nelson W., Davidsen T.,

White O., Fraser C., Collmer A., Kelonay J., Nelson W., Davidsen T.,

Submitted (MAR. 2003) to the EMBL/GenBank/DDBJ databases.

BMBL, ARO16859; AAO54162.1; -

BMBL, ARO16859; AAO54162.1; -

BMBL, ARO16859; Pinna binding; IEA.

GO; GO:000530; Pitranscription; IEA.

GO; GO:000530; Pitranscription; IEA.

GO; GO:000530; Pitranscription; IEA.

GO; GO:000530; Pitranscription; IEA.

InterPro; IPR007065; RNA_DOl_Rpbl.3.

InterPro; IPR007065; RNA_DOl_Rpbl.3.

InterPro; IPR007081; RNA_DOl_Rpbl.3.

InterPro; IPR007081; RNA_DOl_Rpbl.3.

InterPro; IPR007081; RNA_DOl_Rpbl.3.

InterPro; IPR007081; RNA_DOl_Rpbl.3.

Bfam; PF04999; RNA_DOl_Rpbl.3.

Refam; PF04999; RNA_DOl_Rpbl.4; 1.

Pfam; PF04999; RNA_DOl_Rpbl.6; 1.

Pfam; PF04999; RNA_DOl_Rpbl.6; 1.

Pfam; PF04999; RNA_DOl_Rpbl.6; 1.

Pfam; PF04999; RNA_DOl_Rpbl.6; 1.
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                                                                                                                                                                                                                                                                                                                                Gaps
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Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 1.7e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                       69.2%; Score 36; DB 16; Length 559; 66.7%; Pred. No. 62;
Pfam; PF00496; SBP_bac_57_1.—
PROSTITE; PS00011; PROKĀR_LIPOPROTEIN; 1.
CCMplete Droteome.
SEQUENCE 559 AA; 61476 MW; CCI5418D33D53DE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
DNA-directed RNA polymerase, beta' subunit.
RPOC OR PSPTO0620
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Best Local Similarity 60.0
Matches 6; Conservative
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Q9XVK4;
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Q9XVK4
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
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MEDLINE-22825698; PubMed=12917642;
MEDLINE-22825698; PubMed=12917642;
Ablgren G., Larimer F.W., Lamerdin D., Malfatti S., Chain P.,
Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
Shaw S.L., Sreglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb E.A., Zinser B.R., Chisholm S.W.;
"Genome divergence in two Prochlorococcus ecotypes reflects oceanic
niche differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A MILLINGAN S.B., CABBER C.S.;

INTILINGAN S.B., CABBER C.S.;

Plant Mol. Biol. 28:691-711(1995).

R EMBL, USCOS2, AAAB00497.1;

R EMBL, USCOS2, AAAB00497.1;

R GO, GO:000486; F:endopeptidase inhibitor activity; IEA.

R INTERPOR, IPROOLSO, Kunitz_legume.

R PRINTS, PROOLS91, KUNITZINHERR.

R PRODOM; PROOLS91, KUNITZINHERR.

R PRODOM; PROOLS91, KUNITZ_INGUME; 1.

R PROSTIFS, PROOLS91, KUNITZ_INGUME; 1.

R PROSTIFS, PROOLS91, KUNITZ, 1.

R PROSTIFS, PROOLS91, STJ 1.

R PROSTIFS, PROOLS91, STJ 1.

R PROSTIFS, PROOLS93, SOTSBAN KUNITZ; 1.

R PROSTIFS, PROOLS93, SOTSBAN KUNITZ; 1.

T SIGNAL 1 20 UNKNOWN.

C CHAIN 21 225

UNKNOWN.

C SEQUENCE 225 AA; 25188 MW; 1074C261D20CFDAD CRC64;
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01-007-2003 (TrEMBLrel. 25, Last sequence update)
01-007-2003 (TrEMBLRel. 25, Last annotation update)
Phospholipid and glycerol acyltransferase (From 'motifs_6.msf').
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococaceae;
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EMBL: BX572098; CAE21267.1; -.

Acyltransferase; Transferase; Complete proteome.

SEQUENCE 245 AA; 26907 MW; 106F7C4CBE2C6427 CRC64;
                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein precursor.
Lycopersicon esculentum (Tomato).
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                                                                                  225 AA
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STRAIN=VF16; TISSUE=Pistil;
STRAIN=S95195533; PubMed=7647301;
Milligan S.B., Gasser C.S.;
"Nature and regulation of pistil-e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 54.5.
Thes 6; Conservative
                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4081;
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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GO: GO:0005524; F:ATP binding; IEA.

GO: GO:0016470; F:transferase activity; IEA.

GO: GO:0016468; F:protein kinase activity; IEA.

GO: GO:0016468; P:protein amino acid phosphorylation; IEA.

HIGEPPO: J:PROWOT9; Protein amino acid phosphorylation; IEA.

FroDom; PROWOGO; Protein amino acid phosphorylation; IEA.

ProDom; PROWOGO; Prote kinase; 1.

ProDom; PSOWOOI; Prote kinase; 1.

PROSITE: PSOWOII; RROFEIN KINASE_DOM; 1.

ATP-binding; Transferase.

SEQUENCE 425 AA; 49410 MW; 5D96E29B08C8B9D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome sequence of the nematode C.elegans: A platform for
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67.3%; Score 35; DB 5; Length 425;
Best Local Similarity 50.0%; Pred. No. 75;
Matches 5; Conservative 3; Mismatches 2; Indels
                              2; Indels
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                     425 AA.
60.0%; Pred. No. 41;
tive 2; Mismatches
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MEDLINE=99069613; PubMed=9851916;
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Science 282:2012-2018(1998).
EMBL; Z81109; CAB03241.1; -.
PIR; T24111; T24111.
                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel, 12, 01-NOV-1999 (TrEMBLrel, 12, 01-OCT-2003 (TrEMBLrel, 25, R10D12.10 protein.
                                                                                                                                                                                                                                                                     PRELIMINARY;
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
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                                                                                         Hepatitis
                                                                                                                    Hepatitis
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                                  Abb80542 Abb80543 Abb80538 Abb80539 Abb80539 Abb80540 Abb80549 Abb80549 Abb80544 Abb80547 Abb80556 Abb80557 Abb80556 Abb80557 Abb80557
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Abb80553 R
Abb80552 R
Abb80545 R
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ABB80553
ABB80552
ABB80552
ABB80526
ABB80566
ABB80566
ABB80536
ABB80542
ABB80543
ABB80543
ABB80540
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Misc-difference
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 Synthetic
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Abb80537 Hepatitis
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Abb80546 Hepatitis
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         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                     Sequence 11 AA;
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                                                                                                           Synthetic.
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                                                                                                                                                                                                                    protease
                                                                                                    virucide
                                    Matches
                                                           RESULT 2
ABB80558
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Length 11; DB 5; Le 96.4%; Score 54; DB 100.0%; Pred. No. 0.0 ive 0; Mismatches note= "N-terminal acetyl" /note= "C-terminal amide" 'note= "D-form residue" /note= "D-form residue" 'note= "Oxymethionine" Location/Qualifiers Brunck TK; ABB80560 standard; peptide; 11 AA. Claim 17; Page 65; 69pp; English. 19-JUL-2001; 2001WO-US023169 21-JUL-2000; 2000US-0220101P. 11; Conservative 1 EEVVPXGMHYS 11 ᇽ Lim-Wilby M, Levy OE, (CORV-) CORVAS INT INC EEVVPXGMHYS WPI; 2002-361643/39. Query Match Best Local Similarity Matches 11; Conserv Misc-difference Misc-difference Sequence 11 AA; WO200208251-A2 Key Modified-site Modified-site Modified-site Modified-site 08-OCT-2002 31-JAN-2002 Synthetic. ABB80560; virucide protease RESULT 3 δ å ö invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha **Etoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus "Norvalyl carbonyl forming keto-amide linkage with 7" Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus Gaps Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #38. ö Score 54; DB 5; Length 11; Pred. No. 0.00071; 0; Mismatches 0; Indels 'note= "N-terminal acetyl" /note= "C-terminal amide" 'note= "Oxymethionine" Location/Qualifiers Brunck TK; ABB80558 standard, peptide, 11 AA. Claim 17; Page 65; 69pp; English 96.4%; Scallarity 100.0%; P. Conservative 0; 19-JUL-2001; 2001WO-US023169 21-JUL-2000; 2000US-0220101P (first entry) /note= "1 residue ' 1 EEVVPXGMHYS 11 EEVVPXGMHYS 11 Levy OE,

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llarity 100.0%; Pred. No. 0.0
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RESULT 4

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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
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                                                                                   Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #17
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Pred. No. 0.0069;
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                                                                                                                                                                                                        Location/Qualifiers
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90.9%;
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Matches 10; Conservative
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Modified-site
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                    ABB80537;
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                                                                                                                                                                                                                                                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                          Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #7.
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hes 0; Indels
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                                                                                                                  ABB80527 standard; peptide; 11
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EEVVPXGMHYS 11
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Best Local Similarity
Matches 11; Conserv
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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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Ity useful for treating disorders associated with hepatitis C
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Pred. No. 0.011;
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es 10; Conservative
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                                                                                                                                                    /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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Pred. No. 0.006
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90.9%;
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           WPI; 2002-361643/39
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                                                                                                                                                                                     The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprrising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                forming keto-amide linkage with
                                                                                                                      Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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Pred. No. 0.011;
0; Mismatches 1; Indels
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residue 7"
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                                                                            Brunck TK;
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                                                                                                                                                                                                                                                                                                                                                                                                                          ABB80550 standard; peptide; 11 AA
                                                                                                                                                              Claim 17; Page 65; 69pp; English.
           19-JUL-2001; 2001WO-US023169.
                                 21-JUL-2000; 2000US-0220101P.
                                                                                                                                                                                                                                                                                                 85.7%;
ilarity 90.9%;
Conservative (
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                                                                            Levy OE,
                                                      (CORV-) CORVAS INT INC.
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                                                                                                WPI; 2002-361643/39.
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Best Local Similarity
Matches 10; Conserv
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Modified-site
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                                                                          Lim-Wilby M,
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                               C virus
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Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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Pred. No. 0.011;
0; Mismatches 1; Indels
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                                                                                                                             Claim 17; Page 65; 69pp; English
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90.9%;
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Length 11; 1; Indels

Score 48; DB 5; Pred. No. 0.011; 0; Mismatches 1

85.7%;

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
                                  The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                          ABB80532 standard; peptide; 11 AA
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            Claim 17; Page 65; 69pp; English.
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Matches 10; Conservative
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activity usefu
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'note= "N-terminal acetyl"

Location/Qualifiers

(first entry)

/note= "C-terminal amide" 'note= "D-form residue"

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pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                      Length 11;
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                                                                       Score 46; DB 5;
Pred. No. 0.027;
                                                                                                     0; Mismatches
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ilarity 90.9%;
Conservative
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                                                                                       Similarity
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Best Local Simi
Matches 10;
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19-JUL-2001; 2001WO-US023169
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90.9%;
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   ABB80561;
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                                                                                                                                          Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5
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Pred. No. 0.042
0; Mismatches
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BB80561
D ABB80561 standard; peptide; 11 AA.
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                                                                      ABB80525 standard; peptide; 11 AA.
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90.9%;
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Modified-site
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Best Local S:
Matches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
Hepatitis C virus NS3/NS4a serine protease inhibitor pepțide #41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1.
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Pred. No. 0.042;
0; Mismatches
                                                                                                                                                                                                                                                                                                         'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Oxymethionine"
                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB80521 standard; peptide; 11
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                               /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
Hepatitis C virus, HCV, serine protease, inhibitor, alpha-ketoamide, virucide.
                                                                                                'note= "N-terminal acetyl"
                                                                                                                                                                    /note= "C-terminal amide"
                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                        Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                21-JUL-2000; 2000US-0220101P.
                                                                                                                                                                                                                                                     19-JUL-2001; 2001WO-US023169.
                                                                                                                                                                                                                                                                                                                                        Lim-Wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                           (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-361643/39.
                                                                                                                                                                                               WO200208251-A2
                                                                     Key
Modified-site
                                                                                                            Modified-site
                                                                                                                                                      Modified-site
                                                                                                                                                                                                                          31-JAN-2002.
                                          Synthetic
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Gaps ö 80.4%; Score 45; DB 5; Length 11; 90.9%; Pred. No. 0.042; 1; Indels tive 0; Mismatches 1; Indels Local Similarity 90.9 Sequence 11 AA; Query Match Best Loca Matches

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1 EEVVPXGMHYS 11

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1 EEVVPXGMSYS 11

Search completed: June 3, 2004, 11:48:22 Job time : 45.9333 secs

28 32 32 31 31 32 32 34 34 35 35 37 37 37 37 37 37 37 37 37 37 37 37 37	,	32	RESULT 1	US-09-114-001C-4794 ; Sequence 4794, Applicat ; Patent No. 6380370 ; GENERAL INFORMATION:	APPLICANT: LYIN DOUGE TITLE OF INVENTION: NU TITLE OF INVENTION: E FILE REFERENCE: GTC-00 CURRENT APPLICATION NU PRIOR APPLICATION NUMB PRIOR PILLING DATE:	FAIOR FILING DATE: 1991 NUMBER OF SEQ ID NOS: 5 SEQ ID NO 4794 FEMALE: 1994	TYPE: PRT CRGANISM: Staphylococ	US-09-134-001C-4794	OJ L	Db 199 KEVVSNGLHYS	RESULT 2 US-09-252-991A-21444 ; Sequence 21444, Applica ; Patent No. 6551795	GENERAL INFORMATION: APPLICANT: Marc J. Ru TITLE OF INVENTION: N TITLE OF INVENTION: N	FILE REFERENCE: 10719 CURRENT APPLICATION NU CURRENT FILING DATE:	; PRIOR APPLICATION NUMB ; PRIOR FILING DATE: 19 ; PRIOR APPLICATION NUMB	PRIOR FILING DATE: 19 ; NUMBER OF SEQ ID NOS: ; SEO ID NO 21444	, LENGTH: 856 , TYPE: PRT
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. M protein - protein search, using sw model Run on: June 3, 2004, 11:36:47; Search time 11.7333 Seconds (without alignments)	Title: US-09-909-164-7 Perfect score: 56 Sequence: Sequence: Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	, ', ', ', ', ', ', ', ', ', ', ', ', ',	finimum DB seq length: 0	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	<pre>Database : Issued Patents AA:* 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:* 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:* 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:* 4: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:* 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:* 6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*</pre>	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	\$	Wesult Query No. Score Match Length DB ID Description	69.6 1037 4 US-09-114-001C-4794 Sequence 66.1 856 4 US-09-252-991A-21444 Sequence 60.7 323 4 US-09-543-681A-7304 Sequence 60.7 600 2 US-08-821-119-19 Sequence 60.7 600 2 US-08-821-118-2 Sequence	33 58.9 277 4 US-09-252-991A-26615 Sequence 33 58.9 385 4 US-09-252-991A-27834 Sequence 33 58.9 747 4 US-09-724-864-36 Sequence	33 58.9 3472 4 US-09-408-020-4 32 57.1 70 4 US-09-134-001C-3350 Sequence 32 57.1 101 4 US-09-621-976-6096 Sequence 32 57.1 102 2 US-08-880-988A-23 Sequence	32 57.1 126 2 US-08-879-995A-3 32 57.1 126 3 US-09-215-096-3 32 57.1 152 2 US-08-46-694-4	52 57.1 152 3 US-08-480-744-4 Sequence 4, 32 57.1 173 1 US-08-1977 Sequence 4, 32 57.1 189 2 US-08-464-517-21 Sequence 21,	32 57.1 189 2 US-08-246-361A-21 Sequence 32 57.1 189 3 US-08-453-772-21 Sequence 32 57.1 189 5 PCT-US93-05000-21 Sequence	32 57.1 236 2 US-08-464-517-22 Sequence 22, 32 57.1 236 2 US-08-246-361A-22 Sequence 22, 32 57.1 236 2 US-08-464-7772-23 Seminance 22	32 57.1 236 5 PCT-US93-05000-22 Sequence 22, 32 57.1 280 2 US-08-464-517-6 Sequence 6,

Sequence 6, Appli Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 24, Appli Sequence 8, Appli Sequence 8, Appli Sequence 19, Appli Sequence 19, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl		CAMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS DIAGNOSTICS AND THERAPEUTICS ,001C 64	Length 1037; ; Indels 0; Gaps 0;		QUENCES RELATING TO PSEUDOMONAS THERAPEUTICS
3 US-08-463-772-6 2 US-08-246-361A-4 5 PCT-US93-05000-4 5 PCT-US93-05000-4 2 US-08-46-517-23 2 US-08-46-361A-2 3 US-08-46-361A-2 1 US-08-46-361A-2 1 US-08-46-361A-2 2 US-08-46-361A-2 2 US-08-46-517-19 2 US-08-46-517-20 2 US-08-46-517-20 2 US-08-46-517-20 3 US-08-46-361A-19 2 US-08-46-361A-20 3 US-08-46-361A-20 3 US-08-46-361A-20 3 US-08-46-361A-20	ALIGNMENTS	1001 al ind indis	39; DB 4; No. 24; Ematches 2		ation US/09252991A ubenfield et al. NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS TUMBER: US/09/252,991A 1999-02-18 1988-02-18 1988-02-18 1988-02-18 1988-02-18 1938-07-27
57.1 289 57.1 289 57.1 289 57.1 291 57.1 292 57.1 292 57.1 295 57.1 295 57.1 295 57.1 295 57.1 295 57.1 295 57.1 295 57.1 295		ULT 1 09-134-001C-4794 equence 4794, Application US/09134001C atent No. 6380370 APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: WUCLEIC ACID AND AI TITLE OF INVENTION: DPIDERMIDIS FOR D FILE REFERENCE: GTC-007 CURRENT APPLICATION NUMBER: US/09/134, CURRENT PILING DATE: 1999-08-13 PRIOR APPLICATION NUMBER: US 60/064,96 PRIOR APPLICATION NUMBER: US 60/064,96 PRIOR APPLICATION NUMBER: US 60/055,77 PRIOR PILING DATE: 1997-10-8 PRIOR PILING DATE: 1997-11-08 PRIOR PILING DATE: 1997-13-14 NUMBER OF SEQ ID NOS: 5674 LENGTH: 1037 TYPE: PRT TYPE: PRT GRACH: 1037 TYPE: PRT	1 69.6%; Similarity 63.6%; 7; Conservative	BEVVPXGMHYS 11 : : KEVVSNGLHYS 209	S. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15
20000000000000000000000000000000000000		RESULT 1 Sequence 4794, Appl; Sequence 4794, Appl; Retent No. 6386370 GENERAL INFORMATION TITLE OF INVENTION TITLE OF INVENTION FILE REFERENCE: GTV CURRENT APPLICATION CURRENT PILING DATH; PRIOR FILING D	Query Match Sest Local S Matches	Qy 1 BE : Db 199 KI	RESULT 2 Sequence 21444, Appl Patent No. 6551795 GENERAL INFORMATION: TITLE OF INVENTION: THE OF INV
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us-09-909-164-7.rai

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Sequence 2, Application US/08821118

Sequence 2, Application VS 598989

GENERAL INFORMATION:
APPLICANT: Rey, Michael
APPLICANT: Golightly, Elizabeth
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES
TITLE OF INVENTION: ATTIVITY
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:

                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                               Length 600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Comparible
COMPUTER: IBM Comparible
OPPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,118
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4107.400-US
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                               60.7%; Score 34; DB 2; 75.0%; Pred. No. 1.2e+02; tive 0; Mismatches 2
                                                           TELEX:
INPORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 600 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLOGY: linear
MOLECULE TYPE: protein
FRAGRENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 600 amino acide TYPE: amino acid
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
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Best Local Similarity 75.0%
....hes 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 VPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 VPKGWHYS 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-821-118-2
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                                                                                                                                                                                                                                                                                                                                                               RESULT 3
US-09-543-681A-7304
US-09-543-681A-7304
US-09-543-681A-7304
INSORMATION:
PAPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 2000-04-05
FILE REPERENCE: 2709-1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
FILE REPERENCE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
SEQ ID NO 7304
LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19, Application US/08821119;
Sequence 19, Application US/08821119;
Patent No. 5821104

GENERAL INFORMATION:
APPLICANT: Holm, Kaj Andre
APPLICANT: Halkier, Torben
APPLICANT: Halkier, Torben
APPLICANT: Lehmbeck, Jan
ITLE OF INVENTION: Tripeptidyl Aminopeptidase
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS;
ADDRESSEE: No. 58211040 No. 5821104disk of No. 5821104th America, Inc.
STREET: A65 Lexington Avenue
STREET: NY
SCHALE: NY
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                                                                                           Score 37; DB 4; Length 856; Pred. No. 48; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,119
FILING DATE: 1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENE/DOCKET NUMBER: 4107.204-US
TELECOMMUNICATION INFORMATION:
   ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21444
                                                                                               66.1%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7304
                                                                                        Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                        1 REVVPXGMHY 10
                                                                                                                                                                                                                                                                             64 EAVVPGGEHY 73
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75 DVCPAGVHY 83
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US-08-821-119-19
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US-09-134-001C-3950

Sequence 3950, Application US/09134001C

Sequence 3950, Application US/09134001C

Sequence 3950, Application US/09134001C

Sequence 3950, Application US/09134001C

SEREAL INFORMATION:

TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: B99-08-13

FILE REFERENCE: GTC-007

CURRENT FILING DATE: 1999-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR PELING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

NUMBER OF SEQ ID NOS: 5674

TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-408-020-4
) Sequence 4, Application US/09408020
) Sequence 4, Application US/09408020
) Partent No. 6632937
; GENERAL INFORMATION:
) APPLICANT: Swanson, Ronald V.
) APPLICANT: Feldman, Robert A.
) APPLICANT: Feldman, NUCLEIC A.
) APPLICANT: Feldman, Robert A.
) APPLICANT: Schleper, Christa
) TITLE OF INVENTION NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
) FILE REFERRICE: DCORP. 002A
) CURRENT FILING DATE: 1999-09-29
) PRIOR APPLICATION NUMBER: 60/102,294
) PRIOR FILING DATE: 1998-09-29
) PRIOR FILING DATE: 1998-09-29
) NUMBER OF SEQ ID NOS: 123
) SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
TITLE OF INVENTION: by the polymucleotides and methods for their use. FILE REPRENCATION 105001
CURRENT PELLICATION NUMBER: US/09/724,864
CURRENT FILING DATE: 2000-11.28
PRIOR PRIOR PELLING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3 66
LENGTH: 747
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                                                                                                                                                                                                                                                                                                                                                    Query Match 58.9%; Score 33; DB 4; Length 747; Best Local Similarity 71.4%; Pred. No. 2.5e+02; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:|:| |: :|
2294 EDVIPRGISFS 2304
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Best Local Similarity 45.E
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    627 PGGLHÝS 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 PXGMHYS 11
                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 3472
                                                                                                                                                                                                                                                                                                     US-09-724-864-36
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Sequence 27834, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
APPLICATION:
APPLICATION UNMERS: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27834
LENGTH 385
                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: APPLICATION NUMBER: US/09/252,991A
CURRENT PAPLICATION NUMBER: US 60/074,788
PRIOR PALING DATE: 1999-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

ERNGTH: 277
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1S-09-724-864-36

Sequence 36, Application US/09724864

Sequence 36.808362

Patent No. 6580862

GENERAL INFORMATION:
APPLICANT: Watson, James D
APPLICANT: Warison, James G.

APPLICANT: Murison, James G.

APPLICANT: Murison, Polynucleotides, polypeptides expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 58.9%; Score 33; DB 4; 18est Local Similarity 44.4%; Pred. No. 1.2e+02; Matches 4; Conservative 3; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 4
Pred. No. 83;
0; Mismatches
                                                                                                                        Sequence 26615, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EEVVPXGMHYS 11
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     31 VPKGWHYS 38
                                                                                                      IS-09-252-991A-26615
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Sequence 23, Application US/08580988A

Patent No. 585461

Patent No. 585461

APPLICANT: Aggarwal et al.

TITLE OF INVENTION: Tumor Necrosis Factor

TITLE OF INVENTION: For Its Use

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRES: 2

ADDRESSE: ADDRESSE: ADDRESS:
ADDRESSE: ADDRES
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CTHER INFORMATION: Xaa = * ,Ala,Glu,Gly,Ile,Lys,Leu,Arg,Ser,Thr,Val
US-09-621-976-6096
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                                                                                                     Query Match 57.1%; Score 32; DB 4; Length 70; Best Local Similarity 62.5%; Pred. No. 29; Matches 5; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-09-621-976-6096

Sequence 6096, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: JODERT, S.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT PILLING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SEQ ID NO 6096

LENGTH: 101

LENGTH: 101
; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 83.3
---nhes 5; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                             36 MPKGFHYS 43
                                                                                                                                                                                                                                                            4 VPXGMHYS 11
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Gaps
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Pred. No. 44;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIWA TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
COMPUTER: DISKETCE
COMPUT
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Patent No. 598506
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Reser, Matthew R.
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCES: 4
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
COUNTRY: CA
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REPERENCE/DOCKET NUMBER: D5721CIP2
TELEPHONE: 713-777-2321
TELEPHONE: 713-777-6908
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 60.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
DESCRIPTION: protein
HYPOTHETICAL: no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: no
FRAGMENT TYPE: i
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS
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US-08-879-995A-3
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Pred. No. 55;
1; Mismatches 2; Indels
                                                                                                            Score 32; DB 2; Length 126;
Pred. No. 55;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STREET: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONTUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM COmpatible
COMPUTER: 1BM COmpatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEM for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECHONE: 415-855-055
TELEPHONE: 415-855-055
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09215096
Patent No. 6008194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                              57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                        Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                            28 EQVVPGGGH 36
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 163590
JS-08-879-995A-3
                                                                                                                                                                                    1 EEVVPXGMH 9
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CLONE: 163590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                             RESULT 14
JS-09-215-096-3
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28 EQVVPGGGH 36

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RESULT 15

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June 3, 2004, 11:57:42; Search time 33.7333 Seconds (without alignments) 91.741 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1155919 seqs, 281338677 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                               M protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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56
1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                              fitle:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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                                                                                                                                                                                                  tun on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 15 Sequence 7, Sequence 3 Sequence 3 Sequence 3 Sequence Description Sequence Sequence Sequence Sequence Sequence Sequence Sequence US-09-909-164-7 US-09-909-164-21 US-09-909-164-21 US-09-909-164-25 US-09-909-164-34 US-09-909-164-34 US-09-909-164-39 US-09-909-164-44 US-09-909-164-44 US-09-909-164-16 Query Match Length Score Result

Segmence 9, Appli		2 6	77	Sequence 13, Appl	equence 47,	48	е 4	20	51	52,	19,	20,	22,	equence 23,	24,	26,	27,	Sequence 28, Appl	29,	31,	32,	33,	equence 35,	36,	37,				equence 45,	46,
12 118-09-909-164-9	12 170 00 00 00 11	#BT-606-60-81 21	12 US-09-909	12 US-09-	12 US-09-	12 US-09-909-16	-60-SD	12 US-09-	12 US-09-909-	12 US-09-909-16	12 US-09-909-16	US-09-909-16	12 US-09-909-	US-09-909-16	US-09-909-16	US-09-909-16		-164-2	12 US-09-909-164	12 US-09-909-16	US-09-909-16	12 US-09-909-164-3;	OS-09-909-16	12 US-09-909-16	an	12 US-09-9	12 US-09-909-1	12 US-09-909-16	12 US-09-909-16	
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ALIGNMENTS

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Sequence 7. Application US/09909164
; Publication No. US20020068702A1
; GENERAL INFORMATION:
    APPLICANT: Corvas International, Inc.
    APPLICANT: Lewy, Odile E
    APPLICANT: APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEBATITIS C
    TILLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEBATITIS C
    TURRENT APPLICATION NUMBER: US/09/909,164
    CURRENT PLILATION NUMBER: 60/220,101
    PRIOR PILING DATE: 2000-07-21
    NUMBER OF SEQ ID NOS: 62
    SOFTWARE: PATENTIN Version 3.1
    SEQ ID NO 7
    LEMGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: 11-mer synthesized according to example 1
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OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAMESTRY: MISC FEATURE
LOCATION: (9)...(9)
OTHER INFORMATION: D-amino acid
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
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NAME/KEY: MISC FEATURE
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NAME/KEY: MOD RES
LOCATION: (11)..(11)
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Sequence 25, Application US/09909164

publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Levy, Odile B

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINB PROTEASE INHIBITORS OF HEFATITIS C

FILE REFERENCE: ILUN1192-US

FILE REFERENCE: 10101192-US

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT FILING DATE: 2003-03-25

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SEQ ID NOS: 62

LENGTHA: 11

LENGTH: 11
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                                                                                                                                                                                                                                                                     OTHER INFORMATION: 11-mer synthesized according to example 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49; DB 12; Length 11; Pred. No. 0.0067; 0; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE PATENTIN version 3.1
SEQ ID NO 21
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MISC FEATURE LOCATION: (6)...(6) OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (9)...(9) OTHER INFORMATION: D-amino acid US-09-909-164-21
                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: MOD RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
FRATURE:
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: artificial sequence
                                                                                                                                                                                                    TYPE: PRT ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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LOCATION: (11√..(11)
OTHER INFORMATION: AMIDATION
FEATURE:
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Sequence 11, Application US/09909164

Sequence 11, Application US/09909164

Publication No. US202020068702A1

GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lin-Wilby, Marguerita
APPLICANT: Bunds, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN0192-US
CURRENT APPLICATION NUMBER: (6/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
NUMBER OF SEQ ID NOS: 62
SEQ ID NO 11
LENGTH: 11
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Publication No. US20020068702A1

GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Notile E
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
APPLICANT: Brunck, Terence K
APPLICANT: INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
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OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
                                                                                  Length 11;
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; Pred. No. 0.0007;
                                                                                                                              0; Indels
                                                                             Query Match 96.4%; Score 54; DB 12; Best Local Similarity 100.0%; Pred. No. 0.0007; Matches 11; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

96.4%; Score 54; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 11; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       iocation: (8). (8) OTHER INFORMATION: D-amino acid US-09-909-164-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IYPE: PRT
ORGANISM: artificial sequence
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
          ; OTHER INFORMATION: AMIDATION US-09-909-164-7
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NAME/KEY: MISC_FEATURE
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US-09-909-164-21
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Sequence 18, Application US/0990164

Federace 18, Application US/0990164

Fublication No. US20020068702A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Order International, Inc.
APPLICANT: Lim.Wilby, Marguerita
APPLICANT: Stranck, Terence K
TITILE OF INVENTION: NOVEL PETIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C'
TITILE OF INVENTION: NOVER: 60/220,101

RIGHT APPLICATION NUMBER: 60/220,101

RIGHT APPLICATION NUMBER: 60/220,101

RIGHT APPLICATION OF SECOND NOS: 62
SOFTWARE: Patentin version 3.1

FENCIN NO 38
SEQ ID NO 38
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ORGANISM: artificial sequence
PERTURE:
OTHER INFORMATION: 11-mer_synthesized according to example 1
PERTURE:
                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
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Pred. No. 0.01;
0; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/09/909,164
                                CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION WNDRER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 34
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
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CCATION: (9)...(9)
CTHER INFORMATION: D-amino acid
US-09-909-164-34
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LOCATION: (1) ...(1)
OTHER INFORMATION: ACETYLATION
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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Best Local Similarity 90.9%;
Matches 10; Conservative (
                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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OTHER INFORMATION: AMIDATION
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NAME/KEY: MOD RES
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US-09-909-164-38
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IS-SULT 5
IS-SULT 5
IS-099-164-30
Sequence 30, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lorva, Codile E
APPLICANT: INFOING: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2000-03-25
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFFWARE: PARCENT PRIOR NOS: 62
SOFFWARE:
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1S-09-909-164-34
Squared 34, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Terence K
TILE REPERENCE: INVIL92-US
FILE REPERENCE: INVIL92-US
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87.5%; Score 49; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0067;
Matches 10; Conservative 0; Mismatches 1; Indels
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Pred. No. 0.01;
0; Mismatches
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
1S-09-909-164-30
OTHER INFORMATION; norvaline-(CO)
                                FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (8)...(8)
OTHER INFORMATION: D-amino acid
S-09-909-164-25
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: artificial sequence
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Best Local Similarity 90.9%;
Matches 10; Conservative
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INFORMATION: AMIDATION
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LOCATION: (11)..(
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Sequence 44, Application US/09909164

| Sequence 44, Application US/09909164
| Publication No. US20020068702A1
| GENERAL INFORMATION:
| APPLICANT: Lim-Wiby, Marguerita
| APPLICANT: Lim-Wiby, Marguerita
| APPLICANT: Lim-Wiby, Marguerita
| APPLICANT: Lim-Wiby, Movel PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C CURRENT APPLICATION NUMBER: US/09/909,164
| CURRENT APPLICATION NUMBER: 60/220,101
| PRIOR PILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SEQ ID NO 44
| LENGTH: 11
| LENGTH: 11
          PEDLICANT: Brunck, Terence K

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINB PROTEASE INHIBITORS OF HEPATITIS C
PILE REPERENCE: INOIN192-US

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT FILING DATE: 2003-03-03-03

PRIOR PELLING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PATENTIN OS: 62

SOFTWARE: PATENTIN OS: 62

LENGTH: 11
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Pred. No. 0.01
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MISC FEATURE LOCATION: (6). (6) OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MOD_RES
LOCATION: (1)...(1)
CTHER INFORMATION: ACETYLATION
FRATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1). (1)
OTHER INFORMATION: ACETYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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Levy, Odile E
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LOCATION: (11)...(11)
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Sequence 39, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Novic PEPTIDES AS NS-3-SERINB PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
SEQUENCE PEOPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
SOFTWARE PREDILING VERSION 3.1
SEQUENCE APPLICATION NOVE APPLICATION NUMBER: 00/220,101
SEQUENCE APPLICATION NOVE APPLICATION NUMBER: 00/220,101
SEQUENCE APPLICATION NOVE APPLICATION
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                                                                                                                                                                                                                              Score 48; DB 12; Length 11;
Pred. No. 0.01;
0; Mismatches 1; Indels
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Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
PEATURE:
| PEATURE:
| NAME/KEY: MISC. FEATURE
| LOCATION: (6)...(6)
| OTHER INFORMATION: norvaline-(CO)
| JS-09-909-164-38
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OTHER INFORMATION: norvaline-(CO)
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OTHER INFORMATION: D-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: artificial sequence
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Best Local Similarity 90.9
Matches 10; Conservative
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Sequence 5, Application US/09909164

Bequence 5, Application US/09909164

Publication No. US2020068702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Wilby, Marguerita

CURRENT PILING DATE: 2003-03-25

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQ ID NO 5

LENGTH: 11

TRYEP PRI

TRYEP PRI

CRANISM: artificial sequence

FRATURE:

FRATURE:
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: COTVAS International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, odlle E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPREMENTE: 1000-101-25
GURRENT APPLICATION NUMBER: 06/20,101
PRIOR PRILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTION NOS: 62
SOFTWARE: PATENTION NUMBER: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTION NUMBER: 111
ELENGTH: 11
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ORGANISM: artificial sequence
PERATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
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Pred. No. 0.026;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; IOCATION: (9) -- (9) OTHER INFORMATION: D-amino acid US-09-909-164-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KRY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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90.9%;
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NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.5
Matches 10; Conservative
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NAME/KEY: MOD_RES
LOCATION: (1)..(1)
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S-09-164-15
Sequence 15, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: NOWER: 100/09/909,164
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3:1
SEQ ID NO 15
LIMCTH: 11
LIMCTH: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12; Length 11;
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Pred. No. 0.01;
0; Mismatches
   OTHER INFORMATION: AMIDATION
FERVICES:
LOCATION: (8)..(9)
OTHER INFORMATION: D-amino acids
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
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'S-09-909-164-16
Sequence 16, Application US/09909164
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NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
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OTHER INFORMATION: ACETYLATION
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                            NAME/KEY: MISC FEATURE
LOCATION: (8).7(8)
OTHER INFORMATION: Met(0)
S-09-909-164-44
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GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilbly, Marguerita
APPLICANT: Lim-Wilbly, Marguerita
APPLICANT: Lim-Wilbly, Marguerita
APPLICANT: Lim-Wilbly, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Evy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PREPITIES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 11
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NAME/KEY: MOD_RES
LOCATION: (1) -. (1)
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Pred. No. 0.041;
0; Mismatches 1; Indels
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Job time : 33.7333 secs
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OTHER INFORMATION: ACETYLATION
FRATURE:
MAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MISC_FEATURE
LOCATION: (9)...(9)
OTHER INFORMATION: D-amino acid
FEATURE:
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ORGANISM: artificial sequence
FRATURE:
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Best Local Similarity 90.9%;
Matches 10; Conservative
Publication No. US20020068702A1
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APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERENCE: INOLID-2-18
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENT OF SEQ ID NOS: 62
LENGTHARE: PATENT OF SEQ ID NOS: 62
LENGTH: 11
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ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
                                                                                                                                                                                                                                                                 Query Match

80.4%; Score 45; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 1; Indels
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80.4%; Score 45; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 1; Indels
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-09-909-164-6
Sequence 6, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
                  FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
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OTHER INFORMATION: ACETYLATION
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CCATION: (11)...(11)
CTHER INFORMATION: AMIDATION
US-09-909-164-6
                                                                                                                                 ; NAME/KEY: MOD RES
; LOCATION: (11)...(11)
; OTHER INFORMATION: AMIDATION
US-09-909-164-5
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RESULT 15 US-09-909-164-8 ; Sequence 8, Application US/09909164

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

June 3, 2004, 11:35:47 ; Search time 9 Seconds Run on:

(without alignments) 117.567 Million cell updates/sec

US-09-909-164-7 56 1 EEVVPXGMHYS 11 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cription	ftsH proteinase ac	phospha	V1 protein - tobac			hypothetical prote	conserved hypothet	DNA binding protei	GMP synthetase, su	hypothetical prote	TSIB.1 protein - A	diphthine synthase	hypothetical prote	3-dehydroquinate s	probable DNA ligas	cell division prot	thetical I		P.		hypothetical prote	polyamine transpor		m	d anti	finger protein (cl	come-c3	F420-qui	hypothetical prote
SUMMARIES	_	A72207	σ	A42452	AE2001	\$69046	S38143	D82618	T02590	H69194	T24111	G86430	G69117	C75538	B75478	T35025	E69086	C83903	S58132	T28717	AF3286	S54619	E83607	G82253	G71542	H81697	S65811	HODVLB	A69284	T08564
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10 0 0	\$36851 T31308 A25905 D71640	S57810 E97120 T07215 C95881	T25737 JC4011 158372 A41984 A42822
242	0000	0000	00000
627 716 1257	1396 3472 126 197	225 233 267 270	7 5 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
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ALIGNMENTS

ftsH proteinase activity modulator HflK - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: In-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: A72207
R;Nelson, K.B.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicker Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.

Nature 399, 323-329, 1999
A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome set A,Teference number: A72200; MUID:99287316; PMID:10360571
A,Accession: A72207
A,Accession: A72207
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-308 cARN>
A,Accessives: 1-308 cARN>
A,Esidues: 1-308 cARN>
A,Experimental source: strain MSB8

C, Genetics

A;Gene: TM1822 C;Superfamily: erythrocyte band 7 integral membrane protein

ö Gaps .. 0 Query Match 66.1%; Score 37; DB 2; Length 308; Best Local Similarity 75.0%; Pred. No. 10; Matches 1; Indels Matches 1; Indels

3 VVPXGMHY 10 - 41 VVPSGIHY 48 ଚ 셤

RESULT 2

carbamoyl-phosphate synthase large chain [imported] - Staphylococcus aureus (strain N31:

C;Species: Stabhylococcus aureus
C;Species: Stabhylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: F68892
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
R;Kuroda, M.; Ohta, T.; Hobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Titles Miole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1057 «KUR» A;Crosa-references: GB:BA000018; PID:g13701002; PIDN:BAB42298.1; GSPDB:GN00149 A;Experimental source: strain N315

C;Genetics: A;Gene: pyrAB C;Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain; biotin

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Conserved hypothetical protein XF1950 [imported] - Xylella fastidiosa (strain 9a5c) cypecies: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Dacesslon: 985418
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Afference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
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A;Cross-references: EMBL:Z28292; NID:G486536; PIDN:CAA82146.1; PID:G486537; MIPS:YKR067
A;Experimental source: strain S288C
                          A;Accession: S69046
A;Molecule type: DNA
A;Residues: 1-460 <HAL>
A;Cross-references: EMBL:U43703; NID:g1244769; PIDN:AAB68221:1; PID:g1244776; MIPS:YPL1
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein YBL011w homolog YKR067w - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevision 03-May-1994 #text_change 19-Apr-2002
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-Apr-2002
C;Accession: S38443
R;van Vliet-Reedijk, J.C.; Planta, R.J.
Submitted to the Protein Sequence Database, March 1994
A;Reference number: S38130
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Best Local Similarity 75.0%; Pred. No. 43;
Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                    / Match 64.3%; Score 36; DB 2; Length 460; Local Similarity 62.5%; Pred. No. 25; 1; Indels nes 5; Conservative 2; Mismatches 1; Indels
                                                                                                        A)Cross-references: SGD:S0001775
A,Map position: 11R
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||| |:||
294 VVPCGLHY 301
A; Reference number: S69040
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85 IVPLGLHY 92
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A;Molecule type: DNA
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R,Kaneko, T., Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
NA Res. 8, 205-213, 2001
A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A,Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                            C)Accession: A44452
R)Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.B.
R)Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.B.
Virology 187, 633-642, 1992
A;Reference number: A42452; MUID:92188538; PMID:1546458
A;Accession: A44452
A;Molecule type: DNA
A;Redues: 1-102 < MOR>
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C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 17-Mar-2000
C;Accession: 869046
RFHall, J:; DePaulo, T.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.;
Submitted to the EMBL Data Library, December 1995
A;Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein alr1563 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
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AjStatus: preliminary
AjMolecule type: DNA
AjMolecule type: DNA
AjRosidues: 1-252 «KUR»
AjCross-references: GB:BA000019; PIDN:BAB77929.1; PID:g17135383; GSFDB:GN00179
AjExperimental source: strain PCC 7120
AjGenetics:
AjGene: alr1563
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hypothetical protein YPL139c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                C;Species: tobacco yellow dwarf virus
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
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                          Length 1057;
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64.3%; Score 36; DB 2; Length 102;
Best Local Similarity 60.0%; Pred. No. 5;
Matches 6; Conservative 3; Mismatches 1; Indels
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50.0%; Pred. No. 13;
ive 3; Mismatches 2; Indels
                                                                                 2; Indels
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                                .,
'
                                Score 37; DB
Pred. No. 39;
                                                                                 2; Mismatches
                                66.1%;
                                Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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190 EIVSNGLHYS 199
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Matches 5; Conserv
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Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 2000
A, Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A, Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A,Authors: Salzberg, S.L.; Schwarz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Reference and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: G86430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EWBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-25 < WILL
A;Cesidues: 1-25 < WILL
A;Cesidues: 1-25 < WILL
A;Cesidues: 25 < WILL
A;Experimental source: clone R10D12
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                                                                                                                                                                                                                                               C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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C;Species: Arabidopsis thaliana (## 2002)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C;Accession: G86430
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C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 25-Aug-2003
C; Accession: G69117
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diphthine synthase - Methanobacterium thermoautotrophicum (strain Delta H)
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Pred. No. 45;
2; Mismatches 2; Indels
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    Caenorhabditis elegans

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Pred. No. 37;
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A;Map position: 5
A;Introns: 23/3; 56/3; 113/3; 257/2
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50.0%;
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Best Local Similarity 60.0%;
Matches 6; Conservative
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                                                                                                                                                                                                      hypothetical protein R10D12.10
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Les 5; Conservative
            219 EEVVESGLHES 229
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EEVKPPGIHF 21
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                          C; Accession: T24111
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Matches
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R;Smith, D.R.; Doucetee-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
R;Smith, D.R.; Doucetee-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
R;Smith, D.R.; Doucetee-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Ri, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A; Thile: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID: 98037514; PMID: 9371463
A;Accession: H65134
A;Accession: H651
A, Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A Kodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A, Authors: da Silva, A.C.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, A.M.; Tsuhako, M.H.; Vallada, H.; Van Silva, F.R.; da Silvai, A.M.; Silva Jr., W.A.; da Silvai, A.R.; deference number: A59328
A, Reference number: A59328
C, Genetics: A, Contents: annotation
A, Gene: XF1950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Ohme-Takagi, M.; Shinshi, H. Plant Cell 7, 173-182, 1995
A;Title: Ethylene-inducible DNA binding proteins that interact with an ethylene responsi A;Feference number: Z14671; MUID:95276459; PMID:7756828
A;Accession: T05590
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA binding protein EREBP-2 - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-233 <CMM>
A;Residues: 1-233 <CMM>
A;Cross-references: EMBL:D38126; NID:g790362; PIDN:BAA07324.1; PID:g1208498
A;Experimental source: strain BY4; tissue-type leaf
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63.6%; Pred. No. 27;
ive 1; Mismatches 3; Indels
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Best Local Similarity 63.6
Matches 7; Conservative
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Best Local Similarity 55.6
Matches 5, Conservative
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QAVVPKGRHY 99
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A;Start codon: GTG
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A;Cross-references: GB:AE001932; GB:AE000513; NID:g6458481; PIDN:AAF10353.1; PID:g64584 A;Experimental source: strain R1 C;Genetics: A;Gene: 10777 A;Map position: 1 C;Superfamily: 3-dehydroquinate synthase, 3-dehydroquinate synthase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.Seeger, S.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.submitted to the EMBL Data Library, June 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Mosediduse: 1.355 GSBE.
A;Resediduse: 1.355 GSBE.
A;Cross-references: EMBL;AL079355; PIDN:CAB45581.1; GSPDB:GN00070; SCOEDB:SC4C6.17c
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable DNA ligase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T35025
                                                                                                                                                                                                                            y Match 60.7%; Score 34; DB 2; Length 350; Local Similarity 60.0%; Pred. No. 48; local Similarity 1; Mismatches 3; Indels
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71.4%;
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Best Local Similarity 71.4
Matches 5, Conservative
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A; Accession: T35025
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20 IPPGMHY 26
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C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: B75478
R;White, 0.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1995
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Saccession: C;SS38
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma; Sinith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
Science 286, 1571-1577, 1999
A;Fitle: Gannome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
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A;Molecule type: DNA
A;Resides 1-279 <MHI>
A;Resizeferences: GB:AE001889; GB:AE000513; NID:g6457944; PIDN:AAF09867.1; PID:g645795
A;Experimental source: strain R1
                 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Out. D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997.

A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUD:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                              A;Residues: 1-264 <MTH>
A;Cross-references: GB:AE000940; GB:AE000666; NID:g2623011; PIDN:AAB86340.1; PID:g262301
A;Experimental source: strain Delta H
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A;Map position: 1
C;Superfamily: Deinococcus radiodurans hypothetical protein DR0271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 60.7%; Score 34; DB 2; Length 264; Best Local Similarity 62.5%; Pred. No. 35; Mismatches 1; Indels Matches 5; Conservative 2; Mismatches 1; Indels
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Pred, No. 38;
0; Mismatches
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Best Local Similarity 75.v.
6; Conservative
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A)Status: preliminary
A,Molecule type: DNA
A)Residues: 1-350 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene: MTH1874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
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Gaps ; 0

Length 355;

Score 34; DB 2; Pred. No. 49; 1; Mismatches

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SEQUENCE FROM N.A.
STRAIN=ATCC 12228;
PubMed=12950922;
                                                                                                                                                                                         NCBI_TaxID=1282;
                                                                                                                         087gx9 vibrio para
099ur5 staphylococ
P58940 tobacco yel
003010 saccharomyc
03586 mestcharomyc
027902 methanobact
09156 deaulfovibr
P46231 vibrio para
P4335 caenorhabdi
P3330 baccillus su
P3330 baccariopha
P3330 baccariopha
P6858 bos taurus
076217 anopheles g
08766 clostridium
P56351 chlorella v
09766 clostridium
P56351 chlorella v
090209 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                        gallus gall
xenopus lae
gallus gall
homo sapien
homo sapien
mus musculu
                                                                                                                                                                                                                                                               Q8cpj4 staphylococ
Q8rg86 fusobartani
                                                                                                                                                                                                                                                                                                                                                                                                                                            brachydanio
                                                                                                                                                                                                                                                                                                                                                                                                                                                   xenopus lae
                                      June 3, 2004, 11:32:06 ; Search time 4.86667 Seconds (without alignments) 117.693 Million cell updates/sec
                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P55169
P30281
P24385
P25322
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P49706
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                                                                                                                               141681
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                141681 seqs, 52070155 residues
                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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MOUSE
BRARE
XENLA
CHICK
                          - protein search, using sw model
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YEAST
MESAU
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Gapop 10.0 , Gapext 0.5
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DPHBT
SLS1
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UMB1
YK47
IDI1
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PHSL
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TKNK
PE1 P
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                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                              1 BEVVPXGMHYS 11
                                                                 US-09-909-164-7
56
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11396
126
153
212
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Match 1
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99888778
                                                                                             Scoring table:
                                                                 Title:
Perfect score:
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                                                                                                                                                                                          Database :
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                                                                                                                Searched:
                                      Run on:
                                                                                                                                                                                                                                                                                  Result
                                                                                                                                                                                                                                                       No.
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P39948 rattus norv P40595 azotobacter	P19887 bacillus an Q9vwp4 drosophila Q89a96 buchnera ap	P32784 saccharomyc 074377 schizosacch	Q9KVZ9 VIDTIO Chol P15822 homo sapien P20273 homo sapien	P17280 chimpanzee P97885 rattus norv
CGD1_RAT HYPE_AZOVI	T2BA_BACAR SUOX_DROME MDLB_BUCBP	SCT1_YEAST SULH_SCHPO	KPOC VIBCH ZEPI_HUMAN CD22 HUMAN	REV SIVCZ SZOS_RAT
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295 341	353 573 578	877	2717 2717 847	124
57.1	57.1 57.1 57.1	57.1		
2 8	2 2 2 8	222	32 32 31.5	. TE
3.4 4.6	337 337	39 40	4 4 4 4 5 6	4. 4. 4. ቢ

ALIGNMENTS

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 186394;

MEDLINE=21886394;

Nablane=1086394;

Nablane=1086394;

Nablane=1086394;

Nablane=1086394;

Nablane=1086109;

Nasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,

Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,

Larsen N., D'Souza M., Overbeek R.;

Larsen N., D'Souza M., Overbeek R.;

Nablane=1086109;

Nablane=1086109;

Nablane=10886109;

Nablane=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
CARB FUSNN STANDARD; PRT; 1058 AA.
Q8RG86;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-
                                                                                                                                                                                                                                                  ATP (POTENTIAL).

184 MANGANESE 1 (BY SIMILARITY).

185 MANGANESE 2 (BY SIMILARITY).

186 MANGANESE 2 (BY SIMILARITY).

187 MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 1; Length 1057; Pred. No. 7.3; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusobacterium nucleatum (subsp. nucleatum).
Bacteria, Fusobacteria, Fusobacterales, Fusobacteriaceae;
                                                                                                                                                                                                                                  ATP (POTENTIAL)
ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphate synthetase ammonia chain).
                                                                                                                                                                                                                                                                                                                                                                                                                       63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 BEVVPXGMHYS 11
                                                                                                                              546
929
1057
1057
210
352
284
298
300
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153 21
202 35
208 29
209 20
300 30
832 832
1057 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=76856;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusobacterium
                                                                                                                                                                                                                                                                                                                                   METAL
METAL
SEQUENCE
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NP BIND
NP BIND
METAL
METAL
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CARB_FUSNN
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EMBL; AE010554; AAL94625.1; ALT_INIT.

RAMAP; MF 01210; ...; 1

RIGEPTO; IPRO0643; Cara_L glu.

RIGEPTO; IPRO05480; CPase_L D2.

RIGEPTO; IPRO05480; CPase_L D2.

RIGEPTO; IPRO05480; CPase_L D3.

RIGEPTO; IPRO0480; CPase_L D3.

RIGEPTO; IPRO0480; CPase_L D3.

RIGEPTO; IPRO0480; CPase_L D3.

REAM; PF021780; CPase_L D3; 1.

REAM; PF021780; CPase_L D3; 1.

REAM; PF021780; CPASSE_L D3; 1.

REAM; PF021780; CPASSE_L D3; 1.

REAM; REAM; REAM; REAM; REAM; REPEAR; REPEAR; REPEAR; REAM; MAGARIAE SYNTHETIC DOMAIN.

TOMAIN 402 546 OUIGOMAIN.

POMAIN 501 CPASSE COMPLEATE SYNTHETIC DOMAIN.

POMAIN 501 CPASSENTE COMPLEATE SYNTHETIC DOMAIN.

POMAIN 501 CPASSENTE COMPLEATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-RIMD 2210633 / Serctype 03:K6;
STRAIN-RIMD 2210633 / Serctype 03:K6;
STRAIN-RIMD 2210633 / Serctype 03:K6;
Makino K., Oshima K., PubMed=12620739;
Makino K., Oshima K., Makano M., Yamashita A., Kubota Y., Kimura S., Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T., Rimura S., Gasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. choleres.";
Lancet 361:743-749[2003).
-!- CATALYIC ACTIVITY: Phosphoenlpyruvate + 3-phosphoshikimate = phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate pathway;
-!- PATHWAY: Aromatic amino acids blosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
13-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPs).
                                                                                                                                                                                                                                                                                                                                                                                                 ATP (POTENTIAL).

ATP (POTENTIAL).

ATP (POTENTIAL).

ATP (POTENTIAL).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

AGAGENESE 3 (BY SIMILARITY).

AGAGENESE 3 (BY SIMILARITY).

AGAGENESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 1; Length 1058;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrio parahaemolyticus.
Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales,
Vibrionaceae, Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sixth step.
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLUTAR LOCATION: Cytoplasmic (Probable).
                                                                                                                                                                                                                                                                                                                                                     ALLOSTERIC DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 60.0
es 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 EIVPNGLNYS 199
                                                                                                                                                                                                                                                                                                                      546
929
1058
546
1058
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Q87QX9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
NP BIND
NP BIND
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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DOMAIN
DOMAIN
REPEAT
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ID AROA V
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Matches
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or send an email to license@isb-sib.ch)
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60.0%;
                                EMBL; AP003361; BAB57365.1;
EMBL; AP003132; BAB42298.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      832 83
1057 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=196620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARB STAAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
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NP_BIND
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     요
                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the burspean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lancet 357:1225-1240(2001).

Lancet 357:1225-1240(2001).

CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + phosphate + L-glutamate + carbamoyl phosphate.

CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + COORCION: Binds 3 manganese ions per subunit (By similarity).

PATHWAY: Arginine biosynthesis;
PATHWAY: Pyrimidine biosynthesis; first step.

PATHWAY: Pyrimidine biosynthesis; first step.

SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=MISO / ATCC 700699, and N315;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsuman H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Samehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba '
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                             HAMAP, MF_00210; -; 1.
InterProf; IRROD1986; EPSP_synth.
Pfam; PF00275; EPSP_synthase; 1.
PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
PROSITE; PS00886; BRSP_SYNTHASE_2; 1.
Aromatic amino acid biosynthasis; Transferase; Complete proteome.
SEQUENCE 426 AA; 46094 MW; 373D39CC5BA1F70F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamcyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamcyl-phosphate synthase ammonia chain).
CARB OR PYRAB OR PATAL03 OR SA1046.
Staphylococcus aureus (strain Mu50 / ATCC 700699), and
Staphylococcus aureus (strain N315).
Bacteria, Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                              66.1%; Score 37; DB 1; Length 426; 60.0%; Pred. No. 7.3;
                                                                                                                                                                                                                                                                                                                                               3; Indels
-!- SIMILARITY: Belongs to the EPSP synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Selongs to the carB family.
                                                                                                                                                                                                                                                                                                                               Pred. No. 7.3;
1; Mismatches
                                                                                                                                                              EMBL; AP005076; BAC59283.1; -.
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                             223 EFVIPAGOHY 232
                                                                                                                                                                                                                                                                                                                                                                              1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                            Local Similarity
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ID CARB STAAM
                                                                                                                                                                                                                                                                                                                Query Match
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Matches
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-!- CAPLYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP
-!- CAPLYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP
phosphate + L-glutamate + carbamoyl phosphate.
-!- CORACTOR: Binds 3 manganese ions per subunit (By similarity).
-!- PATHWAY: Arginine biosynthesis.
R HSSP; P00968; 1CSO.

R HSSP; P00968; 1CSO.

R HARD; ME 01210; 1.

R InterPro; IPR00548; CPase_L.

R InterPro; IPR005483; CPase_L.

R InterPro; IPR005481; CPase=L.

R InterPro; IPR006481; CPase=L.

R InterPro; IPR006481; CPase=L.

R Ffam; PF02787; CPase=L.

R Ffam; PF02787; CPase=L.

R RINTS; PR00681; CPSASE I.

R RINTS; PR00687; CPSASE I.

R RYSTIT; PS008667; CPSASE I.

R ATGINION blosynthesis; Ligase; Repeat;

M ATGINION Manganese; Complete proteome.

M ATGINION Manganese; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P58940;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
26-FEB-2004 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oguchi A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP (POTENTIAL).

ATP (POTENTIAL).

ATP (POTENTIAL).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

ANANGANESE 3 (BY SIMILARITY).

117171 MW; B3E179EF0591F0F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE-2040/17; PubMed=12044378; Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K.; Naimi T., Ruroda H., Cui L., andennome and virulence determinants of high virulence community-acquired MRSA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 1; Length 1057;
Pred. No. 19;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus (strain MW2).
Bacteria, Firmicutes, Bacillales, Staphylococcus.
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of the infectious cloned DNA component of

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                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its work by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
PATHWAY: Pyrimidine biosynthesis; first step.
SUBINIT: Composed of two chains; the small (or glutamine) chain promores the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome.
CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-92188538; PubMed-1546458;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0098; CPSASE.
TIGREAMS; TIGR01369; CPSASE.1 Lrg; 1.
PROSITE; PS00866; CPSASE 1; 2.
PROSITE; PS00867; CPSASE 1; 2.
ARGININE blosynthesis; Pyrimidine biosynthesis; Ligase; Repeat; ATP-binding; Manganese; Complete protecome.
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MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND Z (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 1; Length 1057;
Pred. No. 19;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D8E3B09F9BC6F152 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                  similarity).
-1- SIMILARITY: Belongs to the carB family.
                                                                                                                                                                                                                                                                                                                             HAMAR, MF 01210; -; 1.
InterPro; IPR006575; CarA L glu.
InterPro; IPR006575; CarA L glu.
InterPro; IPR005483; CPase L D2.
InterPro; IPR005480; CPase L D3.
InterPro; IPR005480; CPase L D3.
InterPro; IPR005481; CPase L D3.
InterPro; IPR004362; MS2 Ilike.
Pfam; PP00289; CPSase L Chain; 2.
Pfam; PP02786; CPSase L D3; 1.
Pfam; PP02186; CPSase L D3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117185 MW;
                                                                                                                                                                                                                                                                                                           EMBL; AP004825; BAB94951.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.1%;
60.0%;
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nes 6; Conservative
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546
1057
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153 21
302 35
284 298
298 29
300 30
820 82
832 83
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    -!- PATHWAY:
-!- SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYDVA
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SEQUENCE
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NP_BIND
NP_BIND
METAL
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P31619;
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DOMAIN
DOMAIN
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ID YILK TYDVA

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    SOLUTION TO THE STATE ST
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 7780 V.A.B.

SEQUENCE 7780 V.A.B.

SEQUENCE 77813271; PubMed=9169875;

MINITES-97313271; PubMed=9169875;

Bussey H., Storma R.K., Ahmed A., Albermann K., Allen E., Ansorge W., Araujo R., Aparicio A., Barcell B.G., Badcock K., Bense V.J.

A araujo R., Aparicio A., Barcell B.G., Badcock K., Cherry J.M., Carpenter J., Cherry J.M., Chung B., Churcher C.M., Coster F., Davis K., Davis R.W., A. Dietrich F.S., Delius H., DiPaolo T., Dubois B., Duesterhoeft A., Dietrich F.S., Delius H., DiPaolo T., Dubois B., Duesterhoeft A., Annicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K., A., Hall J., Hebling U., Haumann K., Hibbert H., Hillier L.W., Annicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K., A. Marathe R., Messenguy F., Mewes H.-W., Mittipati S., Moestl D., Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J., Kan Marathe R., Messenguy F., Mewes H.-W., Mittipati S., Moestl D., RA, Marathe R., Messenguy F., Mewes H.-W., Scharfe M., Winnett B., Winnett R., Wang Y., Wedler B., Vissers S., Voss H., Walle S., Vos M., Wille S., Vos M., Wille S., Scharfe M., Winnett B., Radiong W.W., Zollner A., Vo D.H., Hani J.;

Nathe nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";

REGULATION: TRANSCRIPTIONAL MODULATOR WITH ROLES IN MEIOTIC REGULATION SURVERNIANCE MEATURE REGULATOR OF MEIOSIS.
                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its way by non-profit institutions as long as its existent is in no way modified and this statement is not removed, usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONTROL 1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Meiosis negative regulator UNE1.
UMEI OR WIM3 OR YFL139C OR LPI7C.
Saccharomyces cerevisiae (Baker's speat).
Eukaryota, Fungi; Ascomycota, Saccharomyceties; Saccharomyces ascoharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
"The nucleotide sequence of the infectious cloned DNA compone cloaccy bellow dwarf virus reveals features of geminiviruses infecting monocotyledonous plants."; Virology 187:633-642(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.3%; Score 36; DB 1; Length 102; 60.0%; Pred. No. 2.7; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=A364A;
Mallory M.J., Strich R.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, M81103; AAA47947.1; -.
PIR, A42452; A42452.
InterPro; IPR002621; Gemini mov.
Pfan, PF01708; Gemini mov. 1.
Hypothetical protein.
SEQUENCE 102 AA; 11178 MW; A40ECFIEOAF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 4 WD repeats.
-!- SIMILARITY: STRONG, TO YEAST WIM1 AND WIM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          460 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EVVPXGMHYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UME1 YEAST S:
Q03010; P87330;
01-NOV-1997 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4932;
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UMB1 YEAST
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us-09-909-164-7.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   van Vliet-Reedijk J.C., Planta R.J.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: STRONG, TO YEAST YBL011W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
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01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 83.6 kDa protein in CCPI-MET1 intergenic region.
                                                                                                                                                                                                                            GO, GO:0005634, C:nucleus; IDA.
GO; GO:0005634, C:nucleus; IDA.
GO; GO:0003714; F:transcription co-repressor activity; IDA.
GO; GO:0003714; F:transcription of meiosis; IGI.
InterPro; IPRO400; WD40; WD40.
Ffam; PRO6400; WD40; 3.
FRANT; SM00320; WD40; 4.
FROSITE; PS00032; WD REPEATS 1; FALSE NEG.
PROSITE; PS50034; WD REPEATS 2; FALSE NEG.
PROSITE; PS50294; WD REPEATS 7EGION; FALSE NEG.
Transcription regulation; Meiosis; Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.3%; Score 36; DB 1; Length 460; 62.5%; Pred. No. 13; cive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           51022 MW; AA6F60448B7BCBA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                743 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z28292; CAA82146.1; -.
PIR; S38143; S38143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                             M M D 1.
M M D 2.
M D 3.
                                                                                                                                Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 VVPXGMHY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                          411 4
460 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GermOnline; 140046;
SGD; S0001775; GPT2.
                                                                                                                                                                                                                    SGD; S0006060; UME1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
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ID _YK47_Y
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GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:000436; F:ellycerol-3-phosphate O-acyltransferase acti. . .; IDA.
GO:00004366; F:ellycerol-3-phosphate O-acyltransferase acti. . .; IDA.
InterPro; IPR002123; Acyltransferase.
InterPro; IPR0553; Acyltransferase; 1.
SMART; SM00563; Plsc; 1.
Hypothetical protein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97373600; Pubmed=9228075;
Paton V.G., Shackelford J.E., Krisans S.K.;
Paton V.G., Shackelford J.E., Krisans S.K.;
Paton V.G., Shackellular localization of hamster and rat isopentenyl
"Cloning and subcellular localization of hamster and rat isopentenyl
diphosphate dimethylallyl diphosphate isomerase. A PTS1 motif targets
the enzyme to peroxisomes.";
J. Biol. Chem. 272.18945-18950(1997).
-!- FUNCTION: CATALYZES THE 1.3 ALLIVIIC REARRANGEMENT OF THE
HOMOBALIVIIC SUBSTRAPE ISOPENTENYL (IPP) TO ITS HIGHLY
BLECTROPHILIC ALLIVIIC ISOMER, DIMETHYLALLYL DIPHOSPHATE (DMAPP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
11-CCT-2003 (Rel. 42, Last annotation update)
11-Copentenyl-diphosphate delta-isomerase 1 (EC 5.3.3.2) (IPP isomerase 1) (Isopentenyl pyrophosphate isomerase 1)
                                                                                                                                                                                                                                                                                                                            Gaps
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Proflow; PD004109; 1. IPP isomerase; 1.
Carotenoid biosynthesis; Cholesterol biosynthesis;
Isoprene biosynthesis; Sterol biosynthesis; Isomerase; Peroxisome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- COPACTOR: Magnesium.
-!- COPACTOR: Magnesium.
-!- PATHWAY: Isoprenoid biosynthetic pathway whose end products include dolichols, vitamins A, D, E, and K, steroid hormones, carotenoids bile acids and cholesterol.
-!- SUBCELLULAR LOCATION: Peroxisomal.
-!- SIMILARITY: Belongs to the IPP isomerase type I family.
                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                              Score 36; DB 1; Length 743;
Pred. No. 21;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                        84B9946E56B82F15 CRC64;
                                                                                                                                                    POTENTIAL. POTENTIAL.
                                                                                                                                                                                              POTENTIAL. POTENTIAL.
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InterPro; IPR000086; NUDIX hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mesocricetus auratus (Golden hamster)
                                                                                                                                                31 55 PO
69 85 PO
502 85 PO
539 554 PO
743 AA; 83644 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF003836; AAC53283.1; -.
                                                                                                                                                                                                                                                                                64.3%;
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                294 VVPCGLHY 301
                                                                                                                                                                                                                                                                                                                                                                      3 VVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDI1 MESAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Magnesium.
                                                                                                                                                                                                 TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                    TRANSMEM
                                                                                                                                                                       TRANSMEM
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IDI1 MESAU
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1 REVVPXGMHYS 11
                                                                                        DPHB METTH
027902;
                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                              RESULT 11
DPHB_METTH
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                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98037514; PubMed=9371463; MEDLINE=98037514; PubMed=9371463; MEDLINE=98037514; PubMed=9371463; MEDLINE=98037514; Dubois J., Smith D.R., Dubois J., Smith D.R., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Mang Y., Widerzbowski J., Gibson R., Spadafora R., Vicare R., Mang Y., Widerzbowski J., Gibson R., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum planting and commarative genomics."
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  deltaH: functional analygis and comparative genomics.;
J. Bacteriol. 179:1135.7155(1997).
-!- CATALYTIC ACTIVITY: ATP + xanthosine 5'-phosphate + L-glutamine H(2)O = AMP + diphosphate + CAMP + L-glutamate.
-!- PATHMAY: GMP biosynthesis.
-!- SUBMUT: Heterodimer composed of a glutamine amidotransferase subunit (A) and a GMP synthase subunit (B) (Potential).
-!- SIMILARITY: Belongs to the GMP synthase family.
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                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
18-PCT-2003 (Rel. 41, Last annotation update)
GMP synthase [glutamine-hydrolyzing] subunit B (EC 6.3.5.2)
synthetase).
                                                                                                                                                                                                                                                                                                                        Methanobacterium thermoautotrophicum.
Achbaea, Buryarchaeota, Methanobacteria; Methanobacteriales;
Methanobacteriacee, Methanothermobacter.
MCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam, PF00958; GMP synt C; 1. TIGREAMs; TIGRE00884; guaA Cterm; 1.
Ligase; GMP biosynthesis; Purine biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 1; Length 308;
Pred. No. 13;
1; Mismatches 3; Indels
                                                           Score 35; DB 1; Length 227;
Pred. No. 9.8;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GMP-BINDING (BY SIMILARITY).
                           TARGETING SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP (BY SIMILARITY).
F2DCF6ED202CAEC1 CRC64;
                                      26317 MW; F500A6586385E803 CRC64;
                                                                                                                                                                                                              308 AA
 BY SIMILARITY.
BY SIMILARITY.
MICROBODY TARG
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InterPro; IPR001674; GMP_gynth_C.
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29 35 A
308 AA; 34403 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.5%;
                                                                62.5%;
                                                                             Local Similarity 70.0
                                                                                                                                                                                                              STANDARD;
                                                                                                                                              121 EEVDPNEMHY 130
                                                                                                                    1 EEVVPXGMHY 10
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  86
148
225
227 AA;
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                           GUAAB OR MTH710.
                                                                                                                                                                                     RESULT 10
GAAB_METTH
ID GAAB_METTH
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SEQUENCE
 ACT_SITE
ACT_SITE
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SEQUENCE
                                                                Query Match
Best Local S
Matches 7
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Gaps

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Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable diphthine synthase (BC 2.1.1.98) (Diphthamide biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98037514; FubMed=9371463; Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois Jantedge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safter H., Patvell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Moo J.-I., Rice P., Noelling J., Reeve J.N.; Complete genome sequence of Methanobacterium thermoautotrophicum Complete Genomal analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biosynthesis (By similarity).
-!- CATALYTIC ACTIVITY: S-denosyl-L-methionine + 2-(3-carboxy-3-aminopropyl-L-histidine = 8-adenosyl-L-homocysteine + 2-[3-carboxy-3-(methylammonio)propyl]-L-histidine.
-!- PATHWAY: Diphthamide biosynthesis; second step.
-!- SIMILARITY: Belongs to the diphthine synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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NCBI_TaxID=187420;
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PIR, GG9117; G
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                                                                                                                                                                                                                                                                                                                                     264 AA
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ID SLS1_YARLI STANDARD;
AC Q99158;
DT 01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-OCT-2003 (Rel. 42, Created)
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hes 5; Conservative
216 EEVVESGLHES 226
                                                                                                                                                                                                                                                                                                                                            STANDARD;
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235 WVPAGLHF 242
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DPHB OR MTH1874.
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01-JAN-1990 (Rel. 13, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Periplasmic [NiFeSe] hydrogenase large subunit (EC 1.12.99.6) (NiFeSe hydrogenlyase large chain).
Desulfovibrio baculatus (Desulfomicrobium baculatus).
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-88058744; PubMed=3316183;
Menon N.K., Peck H.D. Jr., le Gall J., Przybyla A.E.;
"Cloning and sequencing of the genes encoding the large and small
subunits of the periplasmic (NIPeSe) hydrogenase of Desulfovibrio
                                                                                                                                                                                                                    "MotY, a component of the sodium-type flagellar motor.";
J. Bacteriol. 176:4219-4225(194).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: STRONG, TO H.INFLUENZAB H10325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 1; Length 441;
Pred. No. 50;
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451969FE307E4D46 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            513 AA
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EMBL; U06949; AAA21571.1; -.
InterPro; IPR004770; Antiport_nhaC.
InterPro; IPR001991; Na/dico_symport.
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PRINTS; PR00173; EDTRNSPORT.
                                                                                                                                                   MEDLINE=94292449; PubMed=8021208;
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54.5%;
                                    [2]
SEQUENCE OF 1-140 FROM N.A.
    Lancet 361:743-749(2003).
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Best Local Similarity 5%...
6; Conservative
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419
441 AA;
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                                                                                                                                                                                        McCarter L.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swise Institute of Bioinformatics and the EMBL outstation the buspean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 7046076; PubMed=8662639;

MEDLINE=96216076; PubMed=8662639;

Boistane A.A. Beckerlich J.-M., Gaillardin C.;

Boistane A.A. Beckerlich J.-M., Gaillardin C.;

Boistane A.B. Beckerlich J.-M., Gaillardin C.;

Boistane A.B. Beckerlich J.-M.

"Slalp, an endoplasmic reticulum component, is involved in the protein the yeast Yarrowia lipolytica.";

J. Biol., Chem. 271-11668-11675 (1986).

-I- FUNCTION: Involved in the protein translocation process. May interact directly with translocating polypeptides to facilitate their transfer and/or help their folding in the ER. It is not required for viability but is essential for optimal growth at elevated temperatures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=RIMD 2210633 / Serotype 03:K6;
STRAIN=RIMD 2210633 / Serotype 03:K6;
STRAIN=RIMD 2210633 / Serotype 03:K6;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Iijima Y., Oshima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Stsunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vihito parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLS1 PROTEIN.
PREVENT SECRETION FROM ER (POTENTIAL).
OACD7EF17540B8E2 CRC64;
                                                                                                      Yarrowia lipolytica (Candida lipolytica).
Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.7%; Score 34; DB 1; Length 426; 44.4%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
SLS1 protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Hypothetical protein VP2115 (ORF3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  441 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
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InterPro; IPR008886; ER target_S.
PROSITE; PS00014; ER_TARGET; I.
Endoplasmic reticulum; Signal.
SIGNAL
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10-OCT-2003 (Rel. 42, Last seqt)
10-OCT-2003 (Rel. 42, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z50154; CAA90516.1; -. PIR; S58132; S58132.
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52 DQVIPAGLH 60
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P46231;
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Pred. No. 58;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUTL BACSU

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MUTL BACSU

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MOTL_BACSU

MOTL_BACSU

MOTL_COTT-1996 (Rel. 34, Created)

MOTL-COTT-1996 (Rel. 34, Last sequence update)

MOTL-COTT-2003 (Rel. 42, Last annotation update)

MOTL_COTT-2003 (Rel. 42, Last annotation update)

MOTL_COTT-2003 (Rel. 42, Last annotation update)

MOTL_COTT-2003 (Rel. 42)

MOTL_COTT-2004 (Rel. 42)

MOTL_COTT-2004 (Rel. 42)

MOTL_COTT-2004 (Rel. 43)

MOTL_COTT-200
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Best Local Similarity 71.4%;
Matches 5, Conservative 1
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513 AA;
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   \\ \text{C} 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DR EMBL; M18271; AAA23375.2; DR PIR; A33101; HQDVLB.
DR PIR; A33101; HQDVLB.
DR PDB; 1CC1; 01.7UN-9;
DR Pfam; PP00374; NiFeSe Hase; 1.
DR PROSITE; PS00507; NI HGENASE L. 1; 1.
DR PROSITE; PS00508; NI HGENASE L. 1; 1.
W Oxidoreductase; Periplasmic; Metal-binding; Nickel; Iron; Selenium; T INTT MET 0
T INTT MET 51
T NETAL 51
T NETAL
                                                                                                                                                                                                                                                                                                                                                                                                                          ligands.
-!- SUBDATT: Heterodimer of a large and a small subunit.
-!- SUBDATT: Heterodimer of a large and a small subunit.
-!- SUBCELLUAR LOCATION: PERHAPS THE LEADER OF THE SMALL SUBUNIT SERVES AS A TANASPORT VEHICLE FOR BOTH SUBUNITS.
-!- SIMILARITY: Belongs to the [Nife]/[NifeSe] hydrogenase large subunit family.
                                                          X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS).
MEDLINE=99306038; PubMed=10378275;
Garcin E., Vernede X., Hatchikian E.C., Volbeda A., Frey M.,
Garcin E., Vernede X., Hatchikian E.C., Volbeda A., Frey M.,
Fontecilla-Camps J.C.;
Rontecilla-Camps J.C.;
North Portogenase upon reduction with H2, as revealed by X-ray
structure analysis at 1.4-A resolution.";
Structure analysis at 1.4-A resolution.";
-1- CATALYTIC ACTIVITY: H(2) + acceptor = 2 H(+) + reduced acceptor
-1- CATALYTIC ACTIVITY: H(2) + acceptor = 2 H(+) + reduced acceptor
-1- COFACTOR: Nickel, 2 irons and selencysteine. Iron 1 has three
-1- CYALIG and carbon monoxide ligands. Iron 2 has three water
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NICKEL.
IRON 1.
NICKEL.
IRON 2 (VIA CARBONYL OXYGEN).
IRON 1.
NICKEL.
IRON 1.
      Bacteriol. 170:4429-4429(1988)
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HELIX
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Minst F., Ogssawara N., Moszer P., Bolotin A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessiers P., Bolotin A., Borchett S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Borniss R., Boursier L., Comerton I.F., Cummings N.J., Daniel R.M.,
A bonizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Entian K.D., Errington J., Pabret C., Ferrari E., Foulger D.,
Entian K.D., Errington J., Pabret C., Ferrari E., Foulger D.,
A chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
A chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
A chiseppi G., Guy B.J., Haga K., Haicch J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
Kobayashi Y., Koetter P., Koningsfein G., Krogh S., Kumano M.,
Aurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medique C.,
Medina N., Mellado R.P., Mizuo M., Moestl D., Nakai S., Noback M.,
Norle S., Laying A., Liu H., Masuda S., Barksi S.H.,
Persecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
Rieger M., Tavconi E., Packal E., Roche B., Rose M., Sadale Y.,
Sarot T., Scanlan E., Schleich S., Schroeter P., Shin B.S.,
Takeuchi M., Tamakoshi A., Tanaka T., Takamashi H., Takemaru K.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vasamoto K., Yasawotti A.,
Tosato V., Wohlyama S., Vandenbol M., Vannier P., Waltan A., Yamanoto E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Danchin A.,
The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                    MEDLINE-56349107; PubMed-8760914;
Ginetti F., Perego M., Albertini A.M., Galizzi A.;
"Bacillus subtilis muts mutL operon: identification, nuclectide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                         sequence and mutagenesis.";
Microbiology 142:2021-2029(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                    SEQUENCE FROM N.A.
NCBI_TaxID=1423;
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FUNCTION: This protein is involved in the repair of mismatches in DNA. It is required for dam-dependent methyl-directed DNA mismatch repair. May act as a "molecular matchmaker", a protein that promotes the formation of a stable complex between two or more DNA-binding proteins in an ATP-dependent manner without itself being part of a final effector complex (By similarity). SIMILARITY: Belongs to the DNA mismatch repair mutl/hexB family.
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TIGREAMS; TIGRO0585; mutl; 1.
PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
EMBL; U27343; AAB19236.1; --
FIRE, Z99112; CAB13578.1; --
PIR; A69663; A69663.
HSSP; P23367; LBKN.
SubtiList; BG11402; mutl.
HAWAP; MF 00149; --
INTERPO; IPR003594; ATPbind ATPase.
INTERPO; IPR003594; ATPbind ATPase.
Ffam; PF01119; DNA mis repair; Pfam; PF0218; HATPase c; 1.
SWART; SM00387; HATPase c; 1.
TIGRFAMS; TIGR00585; mutl; 1.
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Gaps ö 58.9%; Score 33; DB 1; Length 627; 54.5%; Pred. No. 71; 4; Indels ive 1; Mismatches 4; Indels DNA repair, Complete proteome. SEQUENCE 627 AA; 70431 MW; 068A0509CC265343 CRC64; Query Match
Best Local Similarity 54.0.,
Branches 6; Conservative

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488 EMIVPLIFHYS 498 1 EEVVPXGMHYS 11 ઠે g Search completed: June 3, 2004, 11:49:51 Job time : 5.86667 secs

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Q98A71 arabidopsis
QPEA71 arabidopsis
QPL207 methanopyru
Q7L195 gallus gall
Q9FAD9 deinococcus
Q9FAD1 deinococcus
Q9FAD1 deinococcus
Q9FAD1 bacillus ha
Q9FAD1 arabidus ha
Q9FAD1 arabidus ha
Q9FQ1 arabidus
Q9FQ1 arabid herpe
Q9FV01 arabid herpe
Q9VQ17 drosophila
Q9VQ17 drosophila
Q12479 saccharomyc
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Q8pibo xanthomonas
O99011 prototheca
Q96n44 homo sapien
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Q8ktq4 candidatus
Q9rdc1 streptomyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitteed (UTW-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032195; AAH32195.1; -.
MGD; MGJ:1915724; Tada11.
GO; GO:003074; F:ligand-dependent nuclear receptor transcrip. . .; IDA.
GO; GO:0005515; F:protein binding; IPI.
SEQUENCE 413 AA; 46621 MW; A9B8AlDC70CDA0D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similar to expressed sequence A1987856.

TADA31 OR 1110004B19RIK.

Bukar musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

MCBI_TaxID=10090;
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Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                   Q9KBA1
Q8CAL1
Q16912
Q876Z9
Q9Y0Y6
Q9E1X6
                                                                                                                                                                                                                                                                                                                        Q8C6X2
Q9VQL7
Q12479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                    Q7T1G5
Q9RXN9
Q98HU6
Q9RW92
Q9XAM3
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QBKTQ4
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Q8PIB0
O99011
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QBBNL0
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                                                                01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2003 (TrEMBLrel. 25,
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                                                                     1 EEVVPXGMHYS 11
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SEQUENCE FROM N.A.
OBCEJ4;
01-MAR-2003
01-MAR-2003
01-OCT-2003
 Query Match
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 Q8K289
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                                                                                                                 June 3, 2004, 11:35:06 ; Search time 29.8667 Seconds (without alignments) 116.206 Million cell updates/sec
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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Q8CPV4
Q9CED4
Q9HLH8
Q9HLH8
Q8YWP1
Q9AW4
Q5A489
Q9PC35
Q9PC35
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sp human:*
sp nammal:*
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sp organelle:*
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56
1 EEVVPXGMHYS 11
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115:
17:
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Perfect
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Query Match
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Sest Conservative
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                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 75.0
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STRAIN=MSB8 / DSM 3109,
MEDLINE=99287316; PubMed=10360571;
MEDLINE=99287316; PubMed=10360571;
Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Redenard A.M., Cotton M.D., Fratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
                                                                                                                                                                                        STRAIN=ATCC 12228;
Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Chen Z., Wen Y.;
                                                                                                                                                                                                                                                A CHEN Z., WEN X., MEN X., MEN X., WEN X., A GOOG STATE C. CYCTOPLASM.; IEA.

REMBL, AEOLSTAGE C. CYCTOPLASM.; IEA.

GO, GO:0005524; F:ATP binding; IEA.

GO; GO:0004197; F:ATP binding; IEA.

GO; GO:0004197; F:Cysteine-type endopeptidase activity; IEA.

GO; GO:0006524; F:ATP binding; IEA.

GO; GO:0006526; F:ATP pindine biosynthesis; IEA.

GO; GO:0006506; P:ATP pindine biosynthesis; IEA.

RO; GO:0006507; P:Nitrogen metabolism; IEA.

RO; GO:0006508; P:Prorecolysis and peptidolysis; IEA.

RICEPPO: IPRO06548; CPase_L.

RICEPPO: IPRO05489; CPase_L.

RICEPPO: IPRO05489; CPase_L.

RICEPPO: IPRO05481; CPase_L.

RICEPPO: IPRO0369; REASE_L.

RICEPPO: IPRO0369; REASE_L.

RICEPPO: IPRO0369; CPase_L.

RICEPPO: IPRO0369; CPase_L.

REMBL: PERMINERATOR CPASE L.

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Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga
NCBI_TaxID=2336;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1057 AA; 117391 MW; 8944D7D8DB1CAE59 CRC64;
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                          Staphylococcus epidermidis.
Bacteria, Firmicutes, Bacillales, Staphylococcus.
NCBI_TaxID=1282,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
Carbamoyl-phosphate synthase large chain.
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THORPAMS; THORD1369; CPSASELI Lrg; 1.
THORPAMS; PRODS 66; CPSASE 1; 2.
PROSITE; PSODS67; CPSASE 2; 2.
PROSITE; PSODS67; CPSASE 2; 2.
COMPLOLE PLOCEOME.
SEQUENCE LOST AA; 117391 MW; 8944D7D
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01-NOV-1999 (TrEMBLrel. 12, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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les 7; Conservative
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                                                                                                                                                                 SEQUENCE FROM N.A.
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Q9X2E2
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WARDLINE=20479972; PubMed=11029001;

Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,

Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,

Ruepp A., Graml W., Stocker S., Lupas A.N., Baumeister W.;

Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;

"The genome sequence of the thermoacidophilic scavenger Thermoplasma cridophilum.""

"The genome sequence of the thermoacidophilic scavenger Thermoplasma are adjointum.", P. Stocker S., Lupas A.N., Baumeister W.;

Nature 407:508 513 (2000).

BMBL; AL445063; CAC11395-1; -.

BMBL; AL445063; CAC11395-1; -.

ROGOGO1494; P. Soddorductase activity; IEA.

ROGOGO1618; P. Selectron transport; IEA.

ROGOGO1618; P. Selectron transport; IEA.

ROGOGO1649; P. SOGOON MOCA.

ROGOGO1649; P. SOGOON MOCA.

ROGOGO1649; P. SOGOON MOCA.

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Thermoplasmataceae, Thermoplasma
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SEQUENCE 308 AA; 34778 MW; ADE03603E5101A9D CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Multidarug efflux transporter.
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Nature 399;323-329(1999).

EMBL; AE001819; AAD36885.1; -
PIR; A72207; A72207.

TIGR; TM1822; -
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016023; F:peptidase activity; IEA.
InterPro; IPR001107; Band, 7.
InterPro; IPR001972; Stomatin.
PRINTS; PR00721; STOWATIN.
SMART; SM00244; PHB; 11.
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STRAIN=cv. Alaska;
MEDILNE-21231727; bubMed=11333309;
Sassa N., Mateushita Y., Nakamura T., Nyunoya H.;
"The Molecular Characterization and in situ Expression Pattern of Pea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pisum sativum (Garden pea).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I; Fabales, Fabaceae, Papilionoideae, Vicieae, Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=1595285; PubMed=11758840; MEDLINE=1595285; PubMed=11758840; MEDLINE=1595285; PubMed=11758840; Maranabe A., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Simura T., Kanada A., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., Nakazaki M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Tabata S., Sugimoto P., Takazawa M., Yamada M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Pasuda M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Tabata S., Sugimoto M., Takazawa M., Yamada M., 
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc
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Plant Cell Physiol. 42:385-394 (2001).

EMBL, ABGNETA, BB39155.1; -.

TRANSFAC, T05513, -.

GO; GO:0009288; C:flagellum (seneu Bacteria); IEA.

GO; GO:0005174; F:nertor activity; IEA.

GO; GO:0005188; F:seructural molecule activity; IEA.

GO; GO:0005189; F:seructural molecule activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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           Pred. No. 36;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       252
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                                                                                                                                                                                                                                                                                                                                                                   PRT;
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           50.08;
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2003 (TrEMBLrel. 25,
       Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                     130 DVIPEGKHYA 139
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                                                                                                                2 EVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Cyanobact
NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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MEDLINE=20194806; PubMed=10732668;
Tauch A., Krieft S., Kalinowski J., Puhler A.;
"The 51,409-bp R-plasmid prplof from the multiresistant clinical
"The 51,409-bp R-plasmid prplof from the multiresistant clinical
isolate Corynebacterium striatum M82B is composed of DNA segments
initially identified in soil bacteria and in plant, animal, and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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SPECIES=C.xerosis; STRAIN=M82B;
MEDLINE=56117603; PubMed=555980;
TAUCH A.; Kassing F., Kalinowski J., Puhler A.;
"The Corynebacterium xerosis composite transposon Tn5432 consists of two identical insertion sequences, designated is1249, flanking the erythromycin resistance gene ermCX.";
                                                                                                                                                                                     Sasamoto S.,
                                                                                                                           MEDLINE-2225144; PubMed=12240834;
A Matanabe A., Iriquchi M., Katoh H., Sasamoto S.,
A Watanabe A., Iriquchi M., Kawashima K., Kimura T., Kishida Y.,
Kiyokawa C., Kohara M. Matsumoto M., Matsumo A., Nakazaki N.,
Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
I "Complete genome structure of the thermophilic cyanobacterium
Intermosynachococcus elongatus BP-1.";
DNA Res. 9:123-130(2002).
R EMBL; Ap065344; BAC09170.1; -.
R GO; GO:0016021; Crintegral to membrane; IEA.
GO; GO:0016021; Crintegral to membrane; IEA.
R GO; GO:0016021; Ritransporter activity; IEA.
R GO; GO:00160103; Acfivin_res.
R InterPro; IPR00103; Acfivin_res.
R InterPro; IPR00103; Acfivin_res.
R InterPro; IPR00103; Acfivin_res.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterium striatum.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
NCBI_TaxID=1725, 43770;
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, Last sequence update)
, Last annotation update)
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TIGREAMS; TIGRO915; 2A0602; 1.
Complete proteome.
SEQUENCE 1044 AA; 113205 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium xerosis, and
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01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
Hypothetical protein (GcrA).
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Best Local Similarity 63.6
Matches 7; Conservative
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843 EEVLPNGIGYS 853
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                                                                 FROM N.A.
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NCBI_TaxID=32046;
                                                                                                    STRAIN=BP-1
                                                                     SEQUENCE
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Q46486
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Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
                                 Xanthomonadaceae; Xylella.
                                                      NCBI_TaxID=2371;
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SEQUENCE 1
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087D36
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A Katz M.E., Rood J.I.;
Billington S.J., Sinistaj M., Cheetham B.F., Ayres A., Moses B.K.,
A Katz M.E., Rood J.I.;
Indentification of a native Dichelobacter nodosus plasmid and
implications for the evolution of the vap regions.";
Indentification of a native Dichelobacter nodosus plasmid and
implications for the evolution of the vap regions.";
Indentifications for interestable in the vap regions.";
Indentifications for interactions of the vap regions.";
Indentifications for interactions of the vap regions.";
Indentifications for the evolution of the vap regions.";
Indentifications for the evolution of the vap regions.";
Indentifications for the evolution of the vap regions.";
Indentification of a native profile in the profile in
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MEDILE=96020672; PubMed=7476204;
MEDILE=96020672; PubMed=7476204;
Moses B.K., Good R.T., Sinistaj M., Billington S.J., Langford C.J.,
Rood J.I.,
"A multiple site-specific DNA-inversion model for the control of Ompl
phase and antigenic variation in Dichelobacter nodosus.";
Mol. Microbiol. 17:183-196(1995).
                                                                                                                                                                                                                              Gaps
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Cardiobacteriaceae; Dichelobacter.
NCBI TaxID=870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                  64.3%; Score 36; DB 10; Length 819; 45.5%; Pred. No. 1.5e+02; ive 4; Mismatches 2; Indels
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55.6%; Pred. No. 37;
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   InterPro; IPR001444; Flag_bb_rod.
InterPro; IPR005202; GRAS.
Pfam, PF03514; GRAS, IPROSTITE, PS00588; PLAGELLA BB ROD; 1.
SEQUENCE 819 AA; 90372 WW; 41B67BD5DC72ADFA CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Xf1950.
XF1950.
Xylella fastidiosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q57489;
01-NOV-1196 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
DNA ligase (Fragment).
Bacteroides nodosus (Dichelobacter nodosus).
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                                                                                                                                                                  Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                      343 DDVVPTSLHFS 353
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21 IVPAGVHWS 29
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Best Local Similarity
Matches 5; Conserv
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SEQUENCE
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Q9PC35;
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09PC35
ID 09PC3
DT 01-OC
DT 01-OC
DT N1-OU
DD N1-OU
DD XF190C1
OS XY10L1
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REAL MEDILINE-2036517; Publication F.C., Arruda P., Abreu F.A., Acencio M., Arives LUN.C., Arruda P., Abreu F.A., Acencio M., Alwes LUN.C., Arraya J.E., Baia G.S., Baptista C.S., Alvaenda R., Alves L.M.C., Arraya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonaccorai E.D., Bordin S., Carraro D.M., Carrer H., Bueno M.R., Canaaroo A.A., Camaroo L.E.A., Carraro D.M., Carrer H., Colauto N.E., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M., Franca S.C., Franca E.F., Costa M.C.R., Ferro J.A., Franca S.C., Franco M.C., Fronme M., Furlan L.R., Frieger J.S., Franca S.C., Franco M.C., Fronme M., Furlan L.R., R. Freger J.S., Kuramae E.E., Langer E.L., Kitajima J.P., Krieger J.S., Kuramae E.E., Langer E.L., Kitajima J.P., Krieger J.S., Mardela M.B.N., Madela M.B.N., Madela M.B.N., Madela M.B.N., Madela M.B.N., Madela M.B.N., Mattino C.L., Sha Machado M.A., Madela A.B.B.N., Martino E.M., Mattino E.C., Miyaki C.Y., Monteliaro-Vitorello C.B., Monn D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Maria M. M. Maraca B.C., Miyaki C.Y., Monteliaro-Vitorello C.B., Roberto P.G., Nunes L.R., Oliveira M.A., Perior G.B., Pereira G.A.G., Pereira H.A. Jr., Paris A., Paris A. C. de Sa R.G., Santelli R.V., Sawasaki H.E., A da Silveira J.F., Silveira M.C., Sautelli R.V., Sawasaki H.E., A da Silveira J.F., Silveira M.C., Tasils M.A., Verjovski-Almeida S., Vettore A.L., The Renome Sequence of the plant pathogen Kylella fastidiosa.";

REMBL, Accourance of the plant pathogen Kylella fastidiosa.";

REMBL, Accourance of the plant pathogen Kylella fastidiosa.";

REMBL, Accourance of the plant FEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=22421331; PubMed=12533478;
Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xylella fastidiosa (strain Temeculal / ATCC 700964).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
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Pred. No. 42;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l protein; Complete proteome.
156 AA; 17144 MW; D8358619C6671A5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Conserved hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005622; C:intracellular; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0006935; P:chemotaxis; IEA.
GO; GO:0007165; P:signal transduction; IEA.
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SEQUENCE FROM N.A.
STRAIN=9a5c;
MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.5%;
55.6%;
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PROSITE; PS50851; CHEW; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 55.6
les 5; Conservative
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Takita M.A., Lemos B.G.M., Machado M.A., Ferro M.I.T., da Silva F.R., Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M., Carrer H., Carraro D.M., de Olivaira K.C., Nunes L.R., Siqueira W.J., Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E., Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M., Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V., Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.I., Kishi L.T., Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.I., Sena J.A.D., Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C., Kitajima J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
lamiids, Solanales, Solanaceae, Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                 disease and citrus variegated chlorosis strains of Pierce's fastidiosa.";

J. Bacteriol. 185:1018-1026 (2003).

GO, GO:000622; C:intreallular; IEA.

GO; GO:0006421; F:signal transducer activity; IEA.

GO; GO:0006315; P:chemotaxis; IEA.

GO; GO:0007165; P:signal transduction; IEA.

HODEROY: IPR002545; CheW.

PROSITE: PS50851; CHEW; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor activity; IEA.
transcription, DNA-dependent; IEA.
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MEDLINE=92276459; Pubmed=7756828;
MEDLINE=92276459; Pubmed=7756828;
Chme-Takagi M., Shinshi H.;
Ethylene-inducible DNA binding proteins that interact with an ethylene responsive element.";
Plant Cell 7:173-182(1995).
Plant Cell 7:173-182(1995).
Plant rol590; T02590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.5%; Score 35; DB 16; Length 156; 55.6%; Pred. No. 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Complete proteome.
SEQUENCE 156 AA; 17130 MW; D83583B9CG671A5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00380; AP2; 1.
SEQUENCE 233 AA; 25563 MW; 6CD16783582C0CB5 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
EREBP-2.
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TRANSFAC; T02654; -...
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005370; F:transcription fa
GO; GO:000635; P:regulation of tr
InterPro; IPR001471; TF BRP.
PRINTS; PR00367; BTRRSPELEMNT.
ProDom; PD001423; TF_BRF; 1...
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Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity
Matches 6; Conserv
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Nicotiana.
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STRAIN=22827954; PubMed=12910271;
BAEDLINE=22827954; PubMed=12910271;
Parkhill J., Sebainia M., Perston A., Murphy L.D., Thomson N.,
Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
Achtman M., Atkin R., Baken D., Bason N., Cherevach I.,
Chillingworth T., Collins M., Cronin A., Davis P., Dogget J.,
Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
Leather S., Morberzak H., O'Neil S., Ormond D., Price C.,
Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
Sharp S., Simmonds M., Skelton J., Squares S., Stevens K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kitajima S., Koyama T., Olime-Takagi M., Shinshi H., Sato F.;
"Characterization of gene expression of NeERFs, transcription factors
of basic PR genes from Nicotiana sylvestris.";
Plant Cell Physiol. 41:817-824(2000).
#RSSP, O80337; 2GCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro: IPR001471; TF ERF.
PFINTS; PR00167; AP2-domain; 1.
PRINTS; PR00167; ETHRSPELEMNT.
PRINTS; PR00167; TF ERF; 1.
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.5%; Score 35; DB 10; Length 237; 60.0%; Pred. No. 66; 3; Indels ive 1; Mismatches 3; Indels
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SRQUENCE 237 AA; 26243 MW; 01BC35EB51E46298 CRC64;
                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Environe-responsive element binding factor.
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01-0cT-2003 (TrEMBLrel. 25, Last sequence update)
01-0cT-2003 (TrEMBLrel. 25, Last annotation update)
Putative enoyl-COA hydratase.
                                                                                                                                                                                                                                       237 AA
                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                       PRT;
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MEDLINE=20399450; PubMed=10945353;
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01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2003 (TrEMBLrel. 24,
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Duery Match
Best Local Similarity 60.00,
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94 QAVVPKGRHY 103
                                                             90 OAWPKGRHY 99
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1 EEVVPXGMHY
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MEDLINE=22827954; PubMed=12910271;

MEDLINE=22827954; PubMed=12910271;

A Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,

A Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

A Achtman M., Arkin R., Baker S., Basham D., Bason N., Cherevach I.,

A Achtman M., Arkin R., Baker S., Basham D., Bason N., Cherevach I.,

A Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Reliable A., Morbercask H., Olveil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Slamonda M., Skelton J., Squares R., Squares S., Stevens K.,

Unwin L., Whitchead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

I'm Nat. Genet. 35:32-40(2003).

EMBL; BX640425; CAE40321.1; -.

ROMPLE PROTOCOME.
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Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
"Comparative analysis of the genome sequences of Bordetella pertussis,
Bordetella parapartussis and Bordetella bronchiseptica.";
Nat. Genet. 35:32-40(2003).
BMBL, BX640440, CAR31621.1; -.
Complete protecome.
SEQUENCE 262 As; 28907 MW; B3CA29331CB776B2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella parapertussis.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
NCBI_TaxID=519;
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                                                                                                                                                     Score 35; DB-16; Length 262;
Pred. No. 73;
1; Mismatches 2; Indels
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Q7W023;
Q1-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                         62.5%;
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
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182 QEVVPYGQH 190
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5.1.6 Compugen Ltd.	Search time 45.933 Seconds (without alignments) 67.664 Million cell updates/sec			S	irs: 1586107				ð.			,	ted by chance to have a of the result being printed,	score distribution.		Description		Hepatiti	Hepatiti		Hepatiti		Hepatiti	Hepatiti Hepatiti	Hepatiti Hepatiti	Hepatiti Hepatiti	Hepatiti Hepatiti		Abb80568 Hepatitis Abb80523 Hepatitis
GenCore version 5. Copyright (c) 1993 - 2004 Co	3, 2004, 11:31:01 ;	Title: US-09-909-164-8 Perfect score: 54 Sequence: 1 EEVVPXGMDYS 11	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 1586107 seqs, 282547505 residue	Total number of hits satisfying chosen parameter	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	A Geneseq 29Jan0	: geneseqpi980s : geneseqp1990s	geneseqp2000s geneseqp2001s	 geneseqp2003as:* geneseqp2003as:* 	8: geneseqp2004s:*	 No. is the number of res re greater than or equal to 	of the		Result No. Score Match Length DB ID	52 96.3 11 5 ABB80	52 96.3 11 5 ABB80	4 52 96.3 11 5 ABB80	6 47 87.0 11 5 ABB80	47 87.0 11 5 ABB80	0 46 85.2 11 5 ABB80	1 46 85.2 11 5 ABB80	3 46 85.2 11 5 ABB80 4 46 85.2 11 5 ABB80	5 46 85.2 11 5 ABB80 6 46 85.2 11 5 ABB80	7 46 85.2 11 5 ABB80 8 46 85.2 11 5 ABB80	9 46 85.2 11 5 ABB80 0 46 85.2 11 5 ABB80	1 46 85.2 11 5 ABB80 2 46 85.2 11 5 ABB80 3 46 85.2 11 5 ABB80	46 85.2 11 45 83.3 11

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                      Gaps
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                                                                                                                                                        ch 96.3%; Score 52; DB 1 Similarity 100.0%; Pred. No. 0.0 11; Conservative 0; Mismatches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7^{\rm n}
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Best Local Similarity 100.0%; Pred. No. 0.0024;
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  96.3%; Score 52; 100.0%; Pred. No.
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"Norvaly1 carbony1 forming keto-amide linkage with ? 7"
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                                                                                                Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #42
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(first entry)

08-OCT-2002

RESULT 5 ABB80562 ID ABB80562 standard; peptide; 11 AA.

Matches

8 셤 ABB80542

Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have invincide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                    "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                      Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                            Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 5; Length 11;
Pred. No. 0.023;
0; Mismatches 1; Indels
                                                                                                                'note= "N-terminal acetyl"
                                                                                                                                                                                                /note= "C-terminal amide"
                                                                                                                                                                          'note= "D-form residue"
                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                           TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 17; Page 65; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB80543 standard; peptide; 11
                                                                                                                                                                                                                                                                                                                                            Brunck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.0%;
                                                                                                                                                                                                                                                                       19-JUL-2001; 2001WO-US023169
                                                                                                                                                                                                                                                                                             21-JUL-2000; 2000US-0220101P
                                                                                                                                                 residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 REVVPXGMDYS 11
                                                                                                                                        note=
                                                                                                                                                                                                                                                                                                                    (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                            Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEVVPXGQDYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11 AA;
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                                                                                          Key
Modified-site
                                                                                                                                                                                       Modified-site
                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                            Lim-Wilby M,
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                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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Matches
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Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;

Synthetic

virucide

Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #23.

(first entry)

08-OCT-2002

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                                                                                                                                                                                                                                                                                                                                                                                       The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV procease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                          "Norvaly1 carbony1 forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                   virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                    ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #18.
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Pred. No. 0.023;
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                   'note= "N-terminal acetyl"
                                                                                                                              /note= "C-terminal amide"
                                                                              'note= "D-form residue"
                                                                                                     'note= "D-form residue"
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                                                                                                                                                                                                    19-JUL-2001; 2001WO-US023169
                                              /note= "No
residue 7"
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                           Misc-difference
                                                                    Misc-difference
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                                                                                                                                                                                                                                                                                                                                                  protease
                                                                                                                                                                                                                                                                                                                           Novel
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ABB80538
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/note= "C-terminal amide"

Brunck TK,

Levy OE,

'note= "D-form residue"

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoanide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C r protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                               21-JUL-2000; 2000US-0220101P
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Misc-difference
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                                                                                                                            WO200208251-A2
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Modified-site
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Matches
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Gaps

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87.0%; Score 47; DB 5; Length 11; 90.9%; Pred. No. 0.023; 1; Indels ive 0; Mismatches 1; Indels

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(first entry)

'note= "N-terminal acetyl"

Location/Qualifiers

/note= "C-terminal amide"

note= "D-form residue"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Norvalyl carbonyl forming keto-amide linkage with 7"
                                                                                                                                                                            Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
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Pred. No. 0.036;
0; Mismatches
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                                                                                                             Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB80548 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                             Claim 17; Page 64; 69pp; English.
               19-JUL-2001; 2001WO-US023169.
                                             21-JUL-2000; 2000US-0220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                          85.2%;
Local Similarity 90.9%;
les 10; Conservative (
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                                                                                                              Levy OE,
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                                                                             (CORV-) CORVAS INT INC
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Modified-site
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Matches
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                                                                                                                                                                                                                                                                                                                             virus
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compound having hepatitis C virus protease inhibitory il for treating disorders associated with hepatitis C virus

useful

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
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                                                                                                                                                                                                                                                                                                                                                               ABB80521 standard; peptide; 11 AA.
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                                                                                 Claim 17; Page 65; 69pp; English
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                                                                                                                                                                                                                                                                            1 EEVVPXGMDYS 11
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          WPI; 2002-361643/39
                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                       Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200208251-A2
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Modified-site
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activity usefu
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                                                          protease
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(first entry)

'note= "Norvaly1 carbony1 forming keto-amide linkage with

'note= "C-terminal amide'

residue 7"

note= "N-terminal acetyl"

Location/Qualifiers

The sequence represents a peptide compound of the invention having

Brunck

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Norvalyl carbonyl forming keto-amide linkage with
hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 virus
                                                                                                                                                           Gapa
                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2.
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                                                                                                                              Length 11
                                                                                                                                                         1; Indels
                                                                                                                            Score 46; DB 5;
Pred. No. 0.036;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "N-terminal acetyl"
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EEVVPXGTDYS 11

Score 46; DB 5; Length 11; Pred. No. 0.036;

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RESULT 13 ABB80547

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/note= "2-aminoisobutyryl carbonyl residue forming a keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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                                                                                                                        Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46.
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                            ABB80566 standard; peptide; 11
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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7^{\rm m}
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Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
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Query Match 85.2%; Score 46; DB 5; Length 11; Best Local Similarity 90.9%; Pred. No. 0.036; Matches 10; Conservative 0; Mismatches 1; Indels

Search completed: June 3, 2004, 11:48:23 Job time: 46.9333 secs

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OTHER INFORMATION: Cys, Gln, Glu, Gly, His, Ile,
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2: /cgn2 6/ptodata/2/iaa/5B_COMB.pep:*
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5: /cgn2 6/ptodata/2/iaa/PdTUS_COMB.pep:*
6: /cgn2 6/ptodata/2/iaa/PdTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 7, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 22, Appli Sequence 21, Appli	SEQUENCES RELATING TO DIAGNOSTICS AND THERAPEUTICS	Length 181; ; Indels 0; Gaps 0;	CITRUS AND DNA ENCODING a, Arg, Asn, Asp, u, Lys, Met, Phe,
883 4 US-09-667-373-4 65 6 5177197-51 10.2 2 US-08-580A-23 15.2 2 US-08-694-4 15.2 3 US-08-460-694-4 17.3 1 US-07-67-7118-4 17.3 1 US-08-193-977-7 18.9 2 US-08-246-361A-21 18.9 3 US-08-464-517-21 18.9 3 US-08-464-517-21 18.9 3 US-08-464-517-22 18.9 3 US-08-464-517-22 23.6 2 US-08-463-772-2 23.6 2 US-08-463-772-2 23.6 2 US-08-463-772-2 23.6 3 US-08-463-772-2 23.6 3 US-08-463-772-2 23.6 3 US-08-463-772-2 23.6 3 US-08-463-772-2 23.6 5 US-08-246-3772-2 23.6 5 US-08-246-3772-2 23.7 US-08-246-3772-2 23.7 US-08-246-3772-2 23.7 US-08-246-3772-2 23.7 US-08-26-8428-2 23.7 US-08-26-8428-2 24.0 3 US-08-463-772-2 24.0 3 US-08-463-772-2 24.0 3 US-08-926-8428-2 24.0 3 US-08-926-8428-2	S ACIE FOR	faecalis 66.7%; Score 36; DB 4; 70.0%; Pred. No. 11; ive 0; Mismatches 0	cation US/08853948B 3. 3. AMA, TOYOTA ON: THE SAME ON: THE SAME O049-0235-0 ION NUMBER: US/08/853,948B ATE: 1997-05-09 ATE: 1997-05-09 LIN Ver. 2.1 S unshiu ON: Xaa at position 109 is one of Ala, ON: Cys, Gln, Glu, Gly, His, Ile, Leu,
28 33 23 23 23 23 23 23 23 23 23 23 23 23 2	RESULT 1 US-09-134-000C-4848 Sequence 4848, Application US/09134000C Patent No. 6617156 GENERAL INFORMATION: TITLE OF INVENTION: NUCLEIC ACID AND ANINO; TITLE OF INVENTION: NUCLEIC ACID AND ANINO; PILE REPERENCE: 032796-032 CURRENT APPLICATION NUMBER: US/09/134,000C PRIOR PLIANG DATE: 1999-08-13 PRIOR PLIANG DATE: 1997-08-15 NUMBER OF SEQ ID NOS: 6812 SOFTWARE: Patentin Version 3.1 SEQ ID NO 4848		RESULT 2 US-08-853-48B-4 Sequence 4, Application US/06 Patent No. 6210943 GENERAL INFORMATION: APPLICANT: AKTHAWA, TOYOTA TITLE OF INVENTION: SUCROSE; TITLE OF INVENTION: TITLE OF INVENTION: TITLE SAD: FILE REFERENCE: 0049-023-04 CURRENT FILING DATE: 1997-05 SOFTWARE: PatentIN Ver. 2.1 SEQ. DN O. 4 LENGTH: 341 TYPE: PRT TYPE: PRT GRANIEN: Citrus unshiu FEATURE: OTHER INFORMATION: Xaa at E

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08853948B
Sequence 5, Application US/08853948B
Patent No. 6210044
GENERAL INFORMATION:
APPLICANT: AKKHAMA, TOYOTA
TITLE OF INVENTION: THE SAME
TITLE OF INVENTION: THE SAME
FILE REPERENCE: 0049-0235-0
CURRENT FILING DATE: 1997-05-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGIH: 348
TYPE: PRT

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Pred. No. 24;
2; Mismatches 1; Indels
                                                                                                           Score 36; DB 3; Length 341;
Pred. No. 22;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 3; Length 348; Pred. No. 22; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Geguence 24, Application US/09697367
Fatent No. 6323015
GENERAL INFORMATION:
APPLICANT: COZCO Jr., Emil M.
APPLICANT: CAIMI, Perry G.
APPLICANT: CAIMI, Perry G.
APPLICANT: TAICZYNEKİ, Mitchell
TITE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: BB1166 US NA
CURRENT APPLICATION NUMBER: US/09/697,367
CURRENT APPLICATION NUMBER: 60/084,529
PRIOR PLING DATE: 1998-MAY-07
PRIOR APPLICATION NUMBER: PCT/US99/09865
PRIOR APPLICATION NUMBER: PCT/US99/09865
PRIOR APPLICATION NUMBER: PCT/US99/09865
PRIOR APPLICATION NUMBER: PCT/US99/09865
SPRIOR APPLICATION NUMBER: PCT/US99/09865
SOFTWARE: Microsoft Office 97
SOFTWARE: Microsoft Office 97
LENTH: 368
; OTHER INFORMATION: Pro, Ser, Thr, Trp, Tyr, or Val
US-08-853-948B-4
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                                                                                                               Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative 2
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Best Local Similarity 66.7%;
Matches 6; Conservative ;
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                             228 VIPPGMDFS 236
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; ORGANISM: Zea mays
US-09-697-367-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-08-853-948B-5
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US-09-697-367-24
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THE OF INTERNATION TO APPLICATION US/09394272

PREALE NO. 6472896

PREALE NO. 6571726

PREALE NO. 6772976

PREALE NO. 67729778

PREALE NO. 6772979

PREALE NO. 6772970

PREALE NO. 6772970

PREALE NO. 67729
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Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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435 VIPPGMDFS 443
                        435 VIPPGMDFS 443
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CITY: Palo Alto
STATE: California
COUNTRY: USA
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                                                                                 RESULT 8
US-09-051-341-7
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Pred. No. 81;
                                                                                                                                                                                                                                                           1; Indels
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ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,777
FILING DATE: NOT YET ASSIGNED
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,471
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BADDATE: Z2-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BADDATE: COMPLET
SECTIORALION NUMBER: CGNE.072.02US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B: Law Offices of Barbara Rae-Venter
260 Sheridan Avenue, Suite 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Van Assche, C.
APPLICANT: Lando, D.
APPLICANT: Bruneau, J. M.
APPLICANT: Gervais, M.
TITLE OF INVENTION: MODIFICATION OF SUCROSE
TITLE OF INVENTION: PHOSPHATE
TITLE OF INVENTION: SYNTHASE IN PLANTS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEBE: Law Offices of Barbara Rae-Venter
                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08718777
Patent No. 5981852
GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 1068
                                                                                                                                                                                                                    66.7%;
                                                                                                                                                                                                                                    Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                               TYPE: Amino acia
STRANDEDNESS: Single
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
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MOLECULE TYPE: protein
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435 VIPPGMDFS 443
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STREET: 26v C.
CITY: Palo Alto
TMATE: California
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Gaps
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US-09-394-272-8

Sequence 8, Application US/09394272

Sequence 8, Application US/09394272

Sequence 8, Application

APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, A. Scott

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

FILE REFERENCE: 201304/1000

CURRENT APPLICATION NUMBER: US/09/394,272

CURRENT FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 14
Sequence 7, Application US/09051341
Patent No. 6124528
DEBREAL INPORMATION:
APPLICANT: Shewmaker, C. K.
TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING
TITLE OF INVENTION: BUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rae-Venter Law Group, P.C.
STREET: 260 Sheridan Avenue, Suite 440
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Pred. No. 81;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                          ZUENTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/051,341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:

CLASSIFICATION: 800

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/17351

FILING DATE: 25-0CT-1996

APPLICATION NUMBER: US 08/549,016

FILING DATE: 27-0CT-1995

PRIOR APPLICATION NUMBER: US 08/372,200

FILING DATE: 12-JAN-1995
ATORNEY/ABENT INFORMATION:
REGISTRATION NUMBER: 32,750

REGISTRATION NUMBER: 32,750

REGISTRATION NUMBER: 32,750

TELEPHONE: (415)328-4400

TELEPHONE: (415)328-4400

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3 VVPXGMDYS 11

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US-08-569-147-76
                                                                                                                                                                                                                                                                                                            SEQ ID NO 9
LENGTH: 1084
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Sequence 4, Application US/09394272

Patent No. 6472588

GENERAL INFORMATION:
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/100 NUMBER: US/09/394,272

CURRENT APPLICATION NUMBER: US/09/394,272

CURRENT FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4
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APPLICANT: Haigler, Candace H.

APPLICANT: Haigler, Candace H.

APPLICANT: Holaday, A. Scott

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

CURRENT APPLICATION NUMBER: US/09/394,272

CURRENT FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 11

LENGTH: 1083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

66.7%; Score 36; DB 4; Length 1081;
Best Local Similarity 66.7%; Pred. No. 83;
Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                         Score 36; DB 4; Length 1068;
Pred. No. 81;
2; Mismatches 1; Indel8 ·
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT , ORGANISM: Craterostigma plantagineum US-09-394-272-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/09394272
Patent No. 6472588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Arabidopsis thaliana US-09-394-272-11
                                                                                                                                           66.7%;
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 1068
                                                                                                                                                Query Match
Best Local Similarity 66.73
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          483 VIPPGMDFS 491
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445 VIPPGMDFS 453
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                                                                                                                                                                                                                                     3 VVPXGMDYS 11
                                                             TYPE: PRT
; ORGANISM: Zea mays
US-09-394-272-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1081
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US-09-394-272-11
                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-09-394-272-4
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Sequence 9, Application US/09394272
Sequence 9, Application US/09394272
Sequence 9, Application US/09394272
Patent No. 6472588
GENERAL INFORMATION:
APPLICANT: Haidday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE FILE REPERENCE: 1013047/100
CURRENT APPLICATION NUMBER: US/09/394,272
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOPTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
ZONDTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
APPLICATION NUMBER: US/08/569,147
FILIGATION TOWNER: 25-March-1996
CLASSIFICATION: S36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
TITLE OF INVENTION: HUMANISED ANTIBODIES
NUMBER OF SEQUENCES: 95
NUMBER OF SEQUENCES: 95
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 6180377ris, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
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Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INPOSMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION UNBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPAK: (215) 568-3439
INPORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 76, Application US/08569147; Patent No. 6180377; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 140 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       453 VIPPGMDFS 461
                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-394-272-9
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US-09-252-991A-31637

Sequence 31637, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT:
APLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION:
FILE REFERENCE:
107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE:
1998-02-18

PRIOR FILING DATE:
1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 31637

LENGTH: 1065
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STATE: PAA COUNTRY: U.S.A.

COUNTRY: U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floopy disk
COMPUTER: IBM PC COMPATIBLE
OPERATURG SYSTEM: PC COMPATIBLE
OFFICIAL NUMBER: S3 (99, 147
FILING DATE: S36
ATTORNEY/AGENT INFORMATION:
NAME: TTUJILO, DORGEN YALKO
REGISTRATION NUMBER: 35, 719
REFERENCE/POCKET NUMBER: 35, 719
REFERENCE/POCKET NUMBER: 35, 719
REFERENCE/POCKET NUMBER: 35, 719
RELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
SEQUENCE CHARACTERISTICS:
TENETHY 140 amino acids
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63.0%; Score 34; DB 3; Length 140;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                           RESULT 14
US-08-569-147-82
S-G9-569-147-82
S-GREEN No. 6180377
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: HUMANISED ANTIBODIES
NUMBERS OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: One Liberty Place - 46th Floor
CITY:
CITY:
CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                    122 VVPTGFDY 129
VVPXGMDY 10
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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
is ORGANISM: Pseudomonas aeruginosa
is ORGANISM: Pseudomonas aeruginosa
is ORGANISM: Pseudomonas aeruginosa
is ORGANISM: 63.0%; Score 34; DB 4; Length 1065;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 PXGMDYS 11
Db 324 PQGMDYS 330
Search completed: June 3, 2004, 12:03:07
Job time: 12.8 secs
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June 3, 2004, 11:57:42; Search time 33.7333 Seconds (without alignments) 91.741 Million cell updates/sec
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/ cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1155919 segs, 281338677 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                    US-09-909-164-8
54
1 EEVVPXGMDYS 11
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                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 8, Appli	Sequence 12, Appl	Sequence 13, Appl	Sequence 22, Appl	Sequence 26, Appl	Sequence 27, Appl	Sequence 5, Appli	Sequence 6, Appli	Sequence 9, Appli	Sequence 10, Appl	Sequence 31, Appl	Sequence 32, Appl	Sequence 35, Appl	Sequence 40, Appl	Sequence 41, Appl
	D	US-09-909-164-8	US-09-909-164-12	US-09-909-164-13	US-09-909-164-22	US-09-909-164-26	US-09-909-164-27	US-09-909-164-5	US-09-909-164-6	US-09-909-164-9	US-09-909-164-10	US-09-909-164-31	US-09-909-164-32	US-09-909-164-35	US-09-909-164-40	US-09-909-164-41
		12	12	12	12	12	13	12	12	12	12	12	12	12	12	12
	Length DB	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11
ф	Query Match	96.3	96.3	96.3	87.0	87.0	87.0	85.2	85.2	85.2	85.2	85.2	85.2	85.2	85.2	85.2
	Score	52	52	25	47	47	47	46	46	46	46	46	46	46	46	4.6
	Result No.	7	2 (2)	3	4	ഗ	9	7	80	a	10	11	12	13	14	12

Sequence 45, Appl Sequence 46, Appl Sequence 47, Appl Sequence 48, Appl Sequence 49, Appl	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Sequence 39, Appl Sequence 36, Appl Sequence 36, Appl Sequence 43, Appl Sequence 37, Appl Sequence 34, Appl Sequence 34, Appl Sequence 38, Appl Sequence 42, Appl Sequence 42, Appl
12 US-09-908-164-45 12 US-09-909-164-46 12 US-09-909-164-47 12 US-09-909-164-49 12 US-09-909-164-49	12 US 09-909-164 12 US 09-909-164	нанананан
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ALIGNMENTS

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Secure A Application US/09909164

Sequence A Application US/09909164

Settle No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Brunck, Terence K

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: IN01192-US

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT APPLICATION NUMBER: 60/220,101

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SEQ ID NO 8

SEQ ID NO 8

MENTAL APPLICATION AND APPLICATION NUMBER: 10/220,101

PRIOR FILING DATE: 2000-07-21

SEQ ID NO 8

MENTAL APPLICATION NUMBER: 10/220,101

PRIOR FILING DATE: 2000-07-21

SEQ ID NO 8

MENTAL APPLICATION NUMBER: 10/220,101

PRIOR FILING DATE: 2000-07-21

SEQ ID NO 8

MENTAL APPLICATION NUMBER: 10/220,101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (6)...(6)
TOTHER INFORMATION: norvaline-(CO)
FRATURE:
NAME/KEY: MISC_FRATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (9). (9)
OTHER INFORMATION: D-amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)..(11)
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Sequence 22, Application US/09909164
Sequence 22, Application US/09909164
Sequence 22, Application US/09909164
Sequence 22, Application No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: CATURE International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terce K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFREENCE: INO1192-US
FILE REFREENCE: 1001192-US
CURRENT APPLICATION NUMBER: 05/220,101
PRIOR PLILING DATE: 2000-07-21
PRIOR PLILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTHWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
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OTHER INFORMATION: 11-mer synthesized according to example 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 96.3%; Score 52; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.00097; Matches 11; Conservative 0; Mismatches 0; Indels
  CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRATURE:
NAME/KEY: MISC_FRATURE
LOCATION: (8). (9)
OTHER INFORMATION: D-amino acids
                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
                                                                                                                                                                                                             TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (11)..(11)

OTHER INFORMATION: AMIDATION
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OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EEVVPXGMDYS 11
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NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MISC_FEATURE
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NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: MOD RES
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US-09-909-164-22
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LENGTH: 11
                                                                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/0990164
| Publication No. US2020068702A1
| Sequence 12, Application US/0990164
| Publication No. US2020068702A1
| GENERAL INFORMATION:
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lone | Reprint Lim-Wilby, Marguerita
| CURRENT APPLICANTON NUMBER: 60/220,101
| PRIOR FILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SOFTWARE: Patentin version 3.1
| LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
PILE REFERENCE: IN01192-US
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                                                                         Query Match 96.3%; Score 52, DB 12, Length 11; Best Local Similarity 100.0%; Pred. No. 0.00097; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.3%; Score 52; DB 12; Length 11; 100.0%; Pred. No. 0.00097; tive 0; Mismatches 0; Indels
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NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: MISC_FEATURE
) COCATION: (8)..(8)
. OTHER INFORMATION: D-amino acid
US-09-909-164-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: MOD RES
LOCATION: (1) ... (1)
OOTHER INFORMATION: ACETYLATION
FEATURE: NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
; OTHER INFORMATION: AMIDATION US-09-909-164-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 96.3
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                    1 EEVVPXGMDYS 11
                                                                                                                                                                                        1 EEVVPXGMDYS 11
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US-09-909-164-13
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TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C TITLE OF INVENTION: NOVEL PEPTIDE SERVER APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PARENT APPLICATION NUMBER: 03.1
SOFTWARE: PETING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PARENT NOS: 62
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                                                                                                                                                                                                                                                                                      FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB 12;
Pred. No. 0.0097;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (6).7(6) OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MISC FEATURE

: LOCATION: (8)...(9)

: OTHER INFORMATION: D-amino acids

US-09-909-164-27
                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FRATURE:
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                  ORGANISM: artificial sequence
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.9
Matches 10; Conservative
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Sublication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim Wilby, Marguerita

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Novue PEFTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REPERENCE: IN01192-US

CURRENT APPLICATION NUMBER: US/09/09,164

CURRENT PILING DATE: 2003-03-25

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR PILING DATE: 2000-07-21
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OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
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Pred. No. 0.0097;
0; Mismatches 1; Indels
                                                                                                                                        Score 47; DB 12; Length 11;
Pred. No. 0.0097;
0; Mismatches 1; Indels
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Publication No. US20020068702A1
GENERAL INFORMATION
APPLICANT: Corves International, Inc.
APPLICANT: Lim-Wilby, Marguerita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (6). (6) OCHER INFORMATION: norvaline-(CO)
OTHER INFORMATION: norvaline-(CO)
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; OTHER INFORMATION: D-amino acid
US-09-909-164-26
                 FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (9)...(9)

OTHER INFORMATION: D-amino acid
US-09-909-164-22
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
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Best Local Similarity 90.9%;
Matches 10; Conservative (
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SOFTWARE: Patentin version 3.1
SEQ ID NO 5
EARCTH: 11
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ORGANISM: artificial sequence
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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NAME/KEY: MISC_FEATURE
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Best Local Similarity
Matches 10; Conserv
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Sequence 10, Application US/09909164

Sequence 10, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:
APPLICANT: Cirvamilby, Marguerita
APPLICANT: Lir, Whilby, Marguerita
APPLICANT: Lir, Whilby, Marguerita
APPLICANT: Lir, Vodie B
APPLICANT: L
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE Brunck, Terence K
TITLE LOUIS BRUNCK, TERENCE INVESTIVE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERBNCE: INOI192-08
CURRENT APPLICATION NUMBER: 105/09/101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 11
TYPE: PRI
CREANISM: artificial sequence
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OTHER INFORMATION: ACETYLATION
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OTHER INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
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OTHER INFORMATION: AMIDATION
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NAME/KEY: MOD RES
LOCATION: (11)..(11)
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LOCATION: (1) .. (1)
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NAME/KEY: MOD_RES
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APPLICANT: Lim.Wilby, Marguerita
APPLICANT: Levy, Odie E
APPLICANT: Levy, Odie E
APPLICANT: Levy, Odie E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: INDI192-US
FILE REFERENCE: INDI192-US
FILE REFERENCE: SOUS-03-25
PRIOR APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 05/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VERSION 3.1
ENGTHAR: 11
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Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
   OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: MISC FEATURE
LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
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OTHER INFORMATION: D-amino acid
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OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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                              FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)
COTHER INPORMATION: AMIDATION
US-09-909-164-5
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NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORWATION: AMIDATION
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## Sequence 35, Application US/09909164

| Sequence 35, Application No. US20202068702A1
| Publication No. US20202068702A1
| Publication No. US20202068702A1
| GENERAL INFORMATION:
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Brunck, Terence K
| TITLE OF INVENTION: NOVEL PEFTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEDATITIS C
| TITLE OF INVENTION: NUMBER: US/09/909,164
| CURRENT APPLICATION NUMBER: 60/220,101
| PRIOR FILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 35
| LENGTH: 11
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS (
PILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT PILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
SUUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENT VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MISC_FEATURE
| LOCATION: (9)...(9)
| CTHER INFORMATION: D-amino acid
| US-09-909-164-32
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
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ORGANISM: artificial sequence
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NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.9
Matches 10; Conservative
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US-09-909-164-35
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Sequence 31, Application US/09909164
Sequence 31, Application US/09909164
Sequence 31, Application US/09909164
Sequence 31, Application US/0909164
Sequence 31, Application No. US2020068702A1
GENERAL INFORMATION:
APPLICANT: Lim-Wilby, Marguerita
FILIR OF PRICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFWARE: Patentin version 3.1
LENGTH: 11
LENGTH: 11
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                                                                                                                                                                                                                                                                                     85.2%; Score 46; DB 12; Length 11; 90.9%; Pred. No. 0.015;
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US-09-909-164-32
US-09-909-164-32
; Publication No. US20020068702A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
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COTHER INFORMATION: norvaline-(CO)
US-09-909-164-31
        OTHER INFORMATION: AMIDATION
FEATURE:
MAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                  LOCATION: (9). (9); OTHER INFORMATION: D-amino acids US-09-909-164-10
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NAME/KRAY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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90.9%;
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ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: MOD RES
LOCATION: (11);..(11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.4
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                        10; Conservative
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                                                                                                                                                          NAME/KEY: MISC FEATURE
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 10; Conserva
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Publication No. US20020068702A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MISC FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 40, Application US/09909164

| Sequence 40, Application US/0909164
| Publication No. US20020068702A1
| GENERAL INFORMATION:
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Env., cdile E
| APPLICANT: Env., cdile E
| APPLICANT: Brunck, Terence K
| TITLE OF INVENITION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
| TITLE OF INTENIT FILING DATE: 2003-03-25
| CURRENT APPLICATION NUMBER: 60/220,101
| PRIOR FILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 40
| LEADTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: 11-mer synthesized according to example 1 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46; DB 12; Length 11;
Pred. No. 0.015;
0; Mismatches 1; Indels
                                                                                                                                                                                                                    Score 46; DB 12; Length 11; Pred. No. 0.015; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-09-909-164-41
; Sequence 41, Application US/09909164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MISC_FEATURE LOCATION: (6)...(6) OTHER INFORMATION: norvaline-(CO) FEATURE:
                             FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: D-amino acid US-09-909-164-40
                                                                                                        FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (9). 7(9)

CTHER INFORMATION: D-amino acid
US-09-909-164-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: artificial sequence
          OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EEVVPXGMDYS 11
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                                                                                                                                                                                                                                                                                                           1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                             1 EEVVPXGSDYS 11
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APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Law, Allay, Margaerita
APPLICANT: Nonita Brain, 100132-US
CURRENT FILIATIO BARE: 2003-03-25
PRIOR PRINTO BARE: 2003-03-25
PRIOR PRINTO BARE: 2003-07-21
PRIOR FILIATION BARE: 2003-07-21
PRIOR FILIATION AND ARE
NONITER: MARGAERITAN AND APPLICANTON ACETYLATION
FRAUTRE: MOD RES
INGRAINS: ALLICATION ACETYLATION
FRAUTRE: MOD RES
INGRAINS: ```

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

using sw model OM protein - protein search,

Run on:

June 3, 2004, 11:35:47; Search time 9 Seconds (without alignments) 117.567 Million cell updates/sec

US-09-909-164-8 54 Perfect score:

1 EEVVPXGMDYS 11 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 78:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sucrose-phosphate unknown protein F2 sucrose-phosphate sucrose-phosphate sucrose-phosphate hypothetical prote peptidoglycan-bind probable alkaline hypothetical prote probable membrane hypothetical prote conserved hypothet V1 protein - tobac sucrose-phosphate facets (faf) s plastocyanin b - L plastocyanin precu plastocyanin b pre 6-0-methylguanine-06-methylguanine-D hypothetical prote probable hexosyltr i-lactate dehydrog phenylalanine-tRNA ABC transporter AT sucrose-phosphate sucrose-phosphate Description A42452 S72649 S72650 G96764 JC4783 JQ1329 T04103 T24111 \$38255 D98182 F72745 G69290 G69350 A70164 F81138 T48898 T09837 T04062 B49132 В 日日 Length Query Match 1 Score 

| disease resistance<br>RND multidrug effl | hypothetical prote<br>hypothetical 367K | partial transposas<br>hypothetical prote | fibroblast growth | hypothetical prote | hypothetical prote | conserved hypothet | unknown protein (i | transposase ISC105 | transposase ISC105 | hypothetical prote | pantoate-beta-alan | transposase ISC105 |
|------------------------------------------|-----------------------------------------|------------------------------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| T48899<br>F83335                         | T30830<br>T31308                        | A99427<br>A90471                         | 827021            | E90335             | S57810             | A96001             | A96546             | F90298             | C90307             | C64417             | G83055             | E90487             |
| 01 01                                    | 0 0                                     | 01 0                                     | 0                 | 7                  | N                  | N                  | N                  | ~                  | Ŋ                  | N                  | N                  | 7                  |
| 908<br>1062                              | 1062                                    | 128                                      | 172               | 184                | 225                | 247                | 257                | 262                | 267                | 276                | 283                | 299                |
| 63.0                                     | 63.0                                    | 61.1                                     | 61.1              | 61.1               | 61.1               | 61.1               | 61.1               | 61.1               | 61.1               | 61.1               | 61.1               | 61.1               |
| 3 34                                     | 3. 3.<br>4. 4.                          | e e                                      | 33                | 33                 | 33                 | 33                 | 33                 | 33                 | 33                 | 33                 | 33                 | 33                 |
| 30<br>31                                 | 3 B                                     | 6) 6)<br>4: (1)                          | 36                | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

|             |     | _         |
|-------------|-----|-----------|
|             |     | yeast     |
|             |     | 1         |
|             |     | YOR013w   |
|             |     | protein   |
| 1 1 1 1 1 1 | 619 | othetical |

hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae) N/Alternate names: hypothetical protein 02612; hypothetical protein YOL303.3

Cispecials: Saccharomydes Gerevisian Ol-Sep-1995 #text\_change 19-Apr-2002 Cispecials: Saccharomydes Gerevisian Ol-Sep-1995 #text\_change 19-Apr-2002 Cispecials: S4649; 866879
Ride Haan, M.; Maarse, A.C.; Grivell, L.A.
submitted to the EMBL Data Library, May 1995
A; Reference number: S54617
A; Reference number: S54617
A; Residues: S14619
A; Molecule type: DNA
A; Residues: 1-156 < DBH;
A; Cross - references: EMBL: X87331; NID: 91041652; PIDN: CAA60762.1; PID: 9829123
B; de Haan, M.; Grivell, L.A.; Maarse, A.C.
Submitted to the Protein Sequence Database, July 1996
A; Reference number: 866877

A;Accession: S66879
A;Molecule type: DNA
A;Residues: 1-156 <DEWA;Residues: 1-156 <DEWA;Cross-references: EMBL:Z74920; NID:g1420109; PIDN:CAA99201.1; PID:g1420111; MIPS:YOR0
A;Experimental source: strain S288C
C;Genetics:

A,Cross-references: SGD:S0005539 A,Map position: 15R C,Superfamily: hypothetical protein YOR013w

Length 156; ; DB . 14.1%; Score 40; ilarity 77.8%; Pred. No. Conservative 1; Mismatc Query Match Best Local Similarity Best Loc Matches

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Gaps

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Indels

Mismatches

EVVPXGMDY 10 N ઠે

EVMPLGMDY 58 20 셤

conserved hypothetical protein AF2411 - Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Date: 05-Dec-11997 #sequence\_revision 05-Dec-1997 #text\_change 22-Oct-1999

succinate dehydrog disease resistance

Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative

A;Molecule type: DNA A;Residues: 1-363 <KLE>

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Successions: Citrus unshiu (fragment)
C, Species: Citrus unshiu
C, Species: Citrus unshiu
C, Species: Citrus unshiu
C, Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
C, Accession: 872650
R, Komateu, A.; Takanokura, Y.; Omura, M.; Akihama, T.
Mol. Gen. Genet. 252, 346-351, 1996
A, Fittle: Cloring and molecular analysis of cDNAs encoding three sucrose phosphate synt A, Reference number: 872648; MUID:96439842; PMID:8842155
A, Accession: 872650
A, Retatus: number: acid sequence not shown
A, Molecule type: mRNA
A, Residues: 1-348 cKON's
A, Fittle: Cloring and molecular analysis of CDN:8842155
A, Fittle: Cloring and molecular analysis of CON's A, Residues: 1-348 cKON's
A, Molecule type: mRNA
A, Residues: 1-348 cKON's
A, Fittle: Contens and molecular sequence was submitted to the EMBL Data Library, August 1997
C, Genetics:
A, Genet
 Unknown procein F25P22.17 [imported] - Arabidopsis thaliana (species: Arabidopsis thaliana (mouse-ear cress) (spacession: G95764) (spac
 A)Description: catalyzes formation of sucrose-6-phosphate from UDPglucose and D-fructo A,Pathway: sucrose biosynthesis C,Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase homology C,Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis F;1-348/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <SSFS>
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 A; Cross-references: GB: AE005173; NID: 96692750; PIDN: AAF24856.1; GSPDB: GN00141
 Gaps
 Gaps
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0
 Length 460;
 66.7%; Score 36; DB 2; Length 348; 66.7%; Pred. No. 17; cive 2; Mismatches 1; Indels
 3; Indels
 DB 2;
 0; Mismatches
 Score 36; DB
Pred. No. 23;
 sucrose-phosphate synthase (EC 2.4.1.14)
C;Species: Oryza sativa (rice)
 66.7%;
70.0%;
 Local Similarity 70.0
 Local Similarity 66.7
 1 EEVVPXGMDY 10
 |:| |||:|
234 VIPPGMDFS 242
 3 VVPXGMDYS 11
 218 EEDVPSAMDY
 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-460 <STO>
 A, Accession: G96764
 A;Gene: F25F22.17
A;Map position: 1
 Query Match
Best Local S
Matches 7
 Query Match
 Genetics:
 RESULT 6
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 Virgotein - tobacco yellow dwarf virus (strain Australia)
C.Species: tobacco yellow dwarf virus
C.Species: tobacco yellow dwarf virus
C.Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C.Accession: A42452
C.Accession: A42452
C.Accession: A. Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
Virology 187, 633-642, 1992
A.Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yello
 R;Komatsu, A.; Takanokura, Y.; Omura, M.; Akihama, T.
Mol. Gen. Genet. 252, 346-351, 1996
A;Title: Cloning and molecular analysis of cDNAs encoding three sucrose phosphate syntha
A;Reference number: S72648; MUID:96439842; PMID:8842155
 A; Description: catalyzes formation of sucrose-6-phosphate from UDPglucose and D-fructose A; Description: sucrose biosynthesis C; Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase; c; Superfamily: sucrose-phosphate synthase; c; Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis F;1-341/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <8SPS>
 A;Cross-references: GB:AE001109; GB:AE000782; NID:g2689432; PIDN:AAB91255.1; PID:g265068
 A;Cross-references: EMED:AB006319; NID:g2588891; PIDN:BAA23215.1; PID:g2588892
A;Experimental source: fruit, cv. Miyagawa-Wase
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1997
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 sucrose-phosphate synthase (EC 2.4.1.14) isoform 2 - Citrus unshiu (fragment)
 C;Species: Citrus unshiu
C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
C;Accession: S72649
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 A,Accession: A42452
A,Molacule type: DNA
A;Residues: 1-102 AMOR>
A,Cross-references: GB:M31103; NID:G335283; PIDN:AAA47947.1; PID:G335284
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 66.7%; Score 36; DB 2; Length 341;
66.7%; Pred. No. 16;
Live 2; Mismatches 1; Indels
 Score 36; DB 2; Length 102;
Pred. No. 4.3;
3; Mismatches 1; Indels
 Score 38; DB 2; Length 363;
Pred. No. 6.8;
3; Mismatches 2; IndelB
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66.78;

Query Match
Best Local Similarity 60.0
Matches 6; Conservative

|||| |::|| 7 OVVPSGINYS 16 2 EVVPXGMDYS 11

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A; Accession: S72649 A; Status: nucleic acid sequence not shown

A; Residues: 1-341 < KOM>

A; Molecule type: mRNA

Conservative

Query Match Best Local Similarity Matches 6; Conserv

228 VIPPGMDFS 236

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RESULT 5

3 VVPXGMDYS 11

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A;Map position: 4
A;Introns: 86/3; 116/3; 255/3; 322/2; 482/3; 526/3; 570/3; 629/3; 647/3; 668/3; 949/3; 5
A;Introns: 86/3; 116/3; 255/3; 322/2; 482/3; 526/3; 570/3; 629/3; 647/3; 668/3; 949/3; 5
A;Note: F28MIJ. 40
C;Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase homology F230-714/Domain: sucrose/sucrose-phosphate synthase homology <85PS>
 sucrose-phosphate synthase homolog F28M11.40 - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress) Cispecies: Arabidopsis thaliana (mouse-ear cress) Cispecies: Arabidopsis thaliana (mouse-ear cress) Cispecies: Arabidopsis transfer (Cispecies: A.Apr-1999 #sequence_revision 30-Apr-1999 #text_change 16-Jul-1999 Cispecies in T04062 #the Footesion: T04062 #the Frotesion S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.) A;Reference number: Z15184 #the Frotesion: T04062
 R.Sakamoto, M.; Satozawa, T.; Kishimoto, N.; Higo, K.; Shimada, H.; Fujimura, T. Plant Sci. 112, 207-217, 1995
Plant Sci. 112, 207-217, 1995
A;Title: Structure and RPLP mapping of a rice sucrose phosphate synthase (SPS) gene that A;Reference number: Z15212
 A;Title: Analysis of CDNA clones encoding sucrose-phosphate synthase in relation to sug:
A;Reference number: Z16874; MUID:97451773; PMID:9306694
A;Accession: T09837
 A)Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-frn A;Pathway: sucrose biosynthesis
C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology C;Keywords: glycosyltransferaes; hexosyltransferaes; sucrose biosynthesis
P;176-674/Domain: sucrose/sucrose-phosphate synthase homology <8SS>
 K.; Shimada, H.; Fujimura,
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1081 <ING>
A;Cross-references: EMBL:Y11795; NID:g2190349; PIDN:CAA72491.1; PID:g2190350
A;Experimental source: ABA-treated callus
C;Genetics:
 C.Species: Oryza sativa (rice)
C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
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Pred. No. 60;
2; Mismatches 1; Indels
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Pred. No. 60;
2; Mismatches 1; Indels
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A;Residues: 1-1003 <BEV>
A;Cross-references: BMBL:AL049487
A;Experimental source: cultivar Columbia; BAC clone F28M11
 A;Accession: T04103
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
 sucrose-phosphate synthase (EC 2.4.1.14) 1 - rice
 A,Residues: 1-1084 <SAK>
A,Cross-references: EMBL:D45890; PIDN:BAA08304.1
A,Experimental source: subsp. Japonica
 Match 66.7%;
Local Similarity 66.7%;
les 6; Conservative ;
 h 66.7%;
Similarity 66.7%;
6; Conservative
Plant Physiol. 115, 113-121, 1997
 445 VIPPGMDFS 453
 483 VIPPGMDFS 491
 3 VVPXGMDYS 11
 3 VVPXGMDYS 11
 Query Match
Best Local Similarity
Matches 6; Conserv
 C; Accession: T04103
 Query Match
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 A;Molecule type: mRNA
A;Residues: 1-1049 <VDL>
A;Cross-references: GB:U33175; NID:g1449931; PIDN:AAC49379.1; PID:g988270
A;Cross-references: GB:U33175; NID:g1449931; PIDN:AAC49379.1; PID:g988270
C;Comment: UDPGlucose-fructose-phosphate glucosyltransferase; Sucrosephosphate-UDPglucosylt
C;Comment: This enzyme catalyzes the formation of sucrose-phosphate form UDP-glucose and
 C;Accession: JQ1329; PQ0260
R;Morrell, A.C.; Bruneau, J.M.; Summerfelt, K.; Boersig, M.; Voelker, T.A.
Plant Cell 3, 1121-1130, 1991
A;Title: Expression of a maize sucrose phosphate synthase in tomato alters leaf carbohyd
A;Réference number: JQ1329; MUID:92338837; PMID:1840396
A;Accession: JQ1329
 Molecule type: protein
Residues: 71-74;206-212;471-481;872-892 <WOR1>
Residues: 71-74;206-212;471-481;872-892 Group from UDPglucose to fructose-6-phosph
Comment: This enzyme transfers the glucosyl group from UDPglucose to fructose-6-phosph
Comment: This enzyme is involved in the regulation of carbon partitioning in the leave
 4, Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fruct Pathway: sucrose biosynthesis
2, Superfamily: sucrose-phosphate synthase; sucrose-sucrose-phosphate synthase; sucrose-sucrose-sucrose-sucrose-biosynthesis
2, Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F;180-663/Domain: sucrose/sucrose-phosphate synthase homology <88PS>
 Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fruc
 B.; Herrera-Estrella
 Pathway: sucrose bissynthesis
Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
 Introns: 24/1; 103/3; 183/3; 205/3; 435/3; 475/3; 519/3; 578/3; 596/3; 617/3; 931/3;
 sucrose-phosphate synthase (EC 2.4.1.14) isoform 2 - Craterostigma plantagineum
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 JAccession: JC4783

(yValdez-Alarcon, J.J.; Ferrando, M.; Salerno, G.; Jimenez-Moraila, B.; Herre Sene 170, 217-222, 1996

JTtile: Characterization of a rice sucrose-phosphate synthase-encoding gene. J. Reference number: JC4783; MUID:96235138; PMID:8666248
 C.Species: Craterostigma plantagineum
C.Species: L-Uul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C.Accession: T09837
R.Ingram, J.; Chandler, J.W.; Gallagher, L.; Salamini, F.; Bartels, D.
 ;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 18-Jun-1999
 Species: Zea mays (maize)
Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 Gaps
 Gaps
 Molecule type: mRNA
Residues: 1-1068 <WOR>
Cross-references: GB:M97550; NID:g168625; PIDN:AAA33513.1; PID:g168626
 C, Keywords: glycosyltransferass, hexosyltransferass; sucross plosynu.
F;1178-666/Domain: sucrose/sucrose-phosphate synthase homology <8SPS>
 Score 36; DB 2; Length 1049;
Pred. No. 58;
2; Mismatches 1; Indels
 66.7%; Score 36; DB 1; Length 1068; 66.7%; Pred. No. 59; 1; Indels 1; Indels
 ucrose-phosphate synthase (EC 2.4.1.14) - maize
 66.7%;
 Query Match
Rest Local Similarity 60.,
f; Conservative
 6; Conservative
 443
 |:| |||:|
436 VIPPGMDFS 444
 3 VVPXGMDYS 11
 3 VVPXGMDYS 11
 |:| ||| VIPPGMDFS
 Best Local Similarity
Matches 6; Conser
 A; Accession: PQ0260
 Function:
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A; Map position: 1

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Accession: T24111

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C;Accession: H72784
R;Xawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka awa, H.; Takaniya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; DNA Res. 6, 83-101, 1999
A;Tile: Compilete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy A;Reference number: A72450; MUID:99310339; PMID:10382966
 A;Map position: S
A;Introns: 33/3; 63/3; 132/3; 169/3; 221/3; 299/3; 379/2; 423/2; 438/2; 471/1; 513/2; 6
 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-440 «KAA»
A;Residues: 1-440 «KAA»
A;Cross-references: DDBJ:AP000058; NID:g5103388; PIDN:BAA79178.1; PID:g5103657
A;Experimental source: strain K1
 A,Status: preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Rosidues: 1-1150 - 1150 - 440 - 4
 A;Cross-references: EMBL:Z78015; PIDN:CAB01437.1; GSPDB:GN00023; CESP:C53A5.2
A;Experimental source: clone R02D5
 probable alkaline proteinase APB0263 - Aeropyrum pernix (stráin Kl)
C;Species: Aeropyrum pernix
C;Date: 20-Aug_1599 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 hypothetical protein C53A5.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T20173; T23857
R;Mortimore, B.
 0; Gaps
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 Query Match 64.8%; Score 35; DB 2; Length 1150; Best Local Similarity 66.7%; Pred. No. 1e+02; Matches 6; Conservative 2; Mismatches 1; Indels
 64.8%; Score 35; DB 2; Length 440; 66.7%; Pred. No. 35; tive 2; Mismatches 1; Indels
 A)Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1150 <WI2>
 submitted to the EMBL Data Library, November 1996
 submitted to the EMBL Data Library, August 1996
A;Reference number: Z19808
A;Accession: T23857
 C; Superfamily: subtilisin; subtilisin homology
 Search completed: June 3, 2004, 12:00:00 Job time: 10 secs
 Query Match
Best Local Similarity 66...
Best Accessive 6, Conservative
 120 EVLPWGVDY 128
 562 VLPVGIDYS 570
 A;Reference number: Z19232
A;Accession: T20173
 2 EVVPXGMDY 10
 3 VVPXGMDYS 11
 A; Gene: CESP: C53A5.2
 A; Accession: H72784
 A; Gene: APE0263
 C; Genetics:
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R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Burkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolor
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Introns: 120/3; 200/2; 221/3; 452/3; 492/3; 536/3; 595/3; 613/3; 634/3; 946/3; 989/2 C;Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase homology C;Keywords: glycosyltransferase; hexosyltransferase
F;196-680/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
 Ripercy, C. submitted to the EMBL Data Library, October 1996
symmitted to the EMBL Data Library, October 1996
A,Recession: T24111
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: 1-425 AVIL.
A,Residues: 1-425 AVIL.
A,Residues: 1-425 AVIL.
A,Residues: ceferences: EMBL:281109; PIDN:CAB03241.1; GSPDB:GN00023; CESP:RIODI2.10
A,Experimental source: clone R10D12
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 A;Sratus: preliminary
A;Molecule (rpps: DM)
A;Residues: 1-433 <STO>
A;Cross.references: GB:AE005673; NID:q13425020; PIDN:AAK25284.1; GSPDB:GN00148
 hypothetical protein R10D12.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 peptidoglycan-binding protein, probable [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #text_change 20-Apr-2001
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 0; Gaps
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 Query Match 66.7%; Score 36; DB 2; Length 1084; Best Local Similarity 66.7%; Pred. No. 60; Matches 6; Conservative 2; Mismatches 1; Indels
 Owery Match
64.8%; Score 35; DB 2; Length 425;
Best Local Similarity 50.0%; Pred No. 34;
Marches 5; Conservative 3; Mismatches 2; Indele
 64.8%; Score 35; DB 2; Length 433; 54.5%; Pred. No. 35; ive 2; Mismatches 3; Indels
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A,Map position: 5 A,Introns: 23/3; 56/3; 113/3; 257/2

Genetics: Gene: CESP:R10D12.10

RESULT 13

Query Match
Best Local Similarity 54.5
Matches 6; Conservative

A, Gene: CC3322

| ::| | ||| 266 EVILPPGFDYS 276 1 EEVVPXGMDYS 11

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pseudomonas
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populus nig
borrelia bu
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 zea mays (m
craterostig
 homo sapien
oryza sativ
 daucus caro
 Q8rg86 fusobacteri
 tobacco yel
 oryza sativ
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 gallus gall
 pseudomonas
 (without alignments)
117.693 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 June 3, 2004, 11:32:06 ; Search time 4.86667 Seconds
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 P19102
P20422
Q88cg0
Q92bc5
Q8y6u8
 141681
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Potal number of hits satisfying chosen parameters:
 141681 seqs, 52070155 residues
 SUMMARIES
 CARB FUSNN
Y11K TYDVA
SPS ORYSA
SPS MAIZE
SPSZ CRAPL
FAF DROME
KHLL HUMAN
 ECB2_HALEL
ECB1_HALEL
ECB2_HUMAN
FGR3_MOUSE
CEK2_CHICK
SULH_SCHPO
ENV_SFY3L
SPPOG_VIBCH
ZEP1_HUMAN
 HORVU
POPNI
BORBU
ARATH
ARATH
ARATH
METJA
PSEAE
VIBCH
 ZEP1 HUMAN
ET2A XENLA
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 TPX_LISIN
TPX_LISMO
HES3_RAT
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 ACDM
 R81.4
 RP8H.
 RPP8
 Minimum DB seq length: 0 Maximum DB seq length: 2000000000
 US-09-909-164-8
54
1 EEVVPXGMDYS 11
 DB
 SwissProt_42:*
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63.9
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Perfect score:
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 Score
 Database :
 Sequence:
 Searched:
 Run on:
 Result
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NEW (III)

| P08203 escherichia P06190 salmonella Q9wzri thermotoga Q04827 rattus norv P30279 homo sapien P30280 mus musculu Q90459 brachydanio P50755 xenopus lae P53782 xenopus lae P55169 gallus gall P30281 homo sapien |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ARAD_SCOLI<br>ARAD_SALLY<br>HILS9_THENA<br>CGD2_RAT<br>CGD2_RAT<br>CGD2_HUMAN<br>CGD1_BRARE<br>CGD1_XENLA<br>CGD1_XENLA<br>CGD2_XENLA<br>CGD2_XENLA<br>CGD1_CHICK<br>CGD2_XENLA<br>CGD1_CHICK                  |
| нанананана                                                                                                                                                                                                     |
| 231<br>231<br>231<br>231<br>231<br>231<br>231<br>231<br>231                                                                                                                                                    |
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## ALIGNMENTS

```
REGUENCE FROM N.A.

REGUENCE FROM N.A.

REGUENCE STEAL STAGE C. 25586;

REGUENCE STEAL STAGE C. 25586;

RA Magatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,

RA Shatacharya A., Bartman A., Gardner W., Grechkin G., Zhu L.,

RA Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman B., Bernal A.,

RA Larsen N., D'Souza M., Walumas T., Pusch G., Haselkorn R.,

RA Larsen N., D'Souza M., Walumas T., Pusch G., Haselkorn R.,

RA Larsen N., D'Souza M., Walumas T., Pusch G., Haselkorn R.,

RT nucleatum strain ATCC 25586 i.,

RT nucleatum strain ATCC 25586 i.,

RT CAPALTYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + Dhosphate + L-glutamate + carbamoyl phosphate.

C. I CARCTOR: Binds 3 manganese ions per subunit (By similarity).

C. I PATHWAY: Pyrimidine biosynthesis; first step.

C. I PATHWAY: Pyrimidine biosynthesis; the small (or glutamine) chain

promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).
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 QBRGE6;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
 Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
 PRT; 1058 AA
 -!- SIMILARITY: Belongs to the carB family.
 EMBL; AE010554; AAL94625.1; ALT_INIT.
 HAWAP; MF_01210; -; 1.
InterPro; IPR006575; CarA_Lglu.
InterPro; IPR006549; CPase_L.
InterPro; IPR005499; CPase_L.D2.
InterPro; IPR005409; CPase_L.D2.
InterPro; IPR005409; CPase_L.D3.
InterPro; IPR005481; CPase_L.N.
InterPro; IPR004362; MGS_IIKe.
Pfam; PP020289; CPSase_L.D2; 2.
Pfam; PF02786; CPSase_L.D2; 2.
 STANDARD;
 NCBI_TaxID=76856;
 Fusobacterium
 FUSNN
RESULT 1
CARE_FUSNN
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us-09-909-164-8.rsp

7 QVVPSGINYS 16

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DR PEINTS; PRO0142; MGS; 1.

DR PRINTS; PR00088; CPSASE.

DR TIGREAMS; TIGRO1369; CPSASE.

DR PROSITE; PS00866; CPSASE.1; 2.

DR PROSITE; PS00867; CPSASE.1; 2.

DR Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

KW ATP-binding; Manganese; Complete proteome.

THE DOMAIN 1 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.

TAT 529 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

ALLOSTERIC DOMAIN.

ALLOSTERIC DOMAIN.
 Gaps
 MEDLINE=92188538; PubMed=1546458;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
"The nucleotide sequence of the infectious cloned DNA component of
tobacco yellow dwarf virus reveals features of geminiviruses
infecting monococyledonous plants.";
Virology 187:633-642(1992).
 153 210 ATP (POTENTIAL).
302 352 ATP (POTENTIAL).
302 352 ATP (POTENTIAL).
294 294 MANGANESE 1 (BY SIMILARITY).
298 298 MANGANESE 2 (BY SIMILARITY).
300 MANGANESE 2 (BY SIMILARITY).
820 MANGANESE 3 (BY SIMILARITY).
831 MANGANESE 3 (BY SIMILARITY).
832 MANGANESE 3 (BY SIMILARITY).
834 MANGANESE 3 (BY SIMILARITY).
 ö
 70.4%; Score 38; DB 1; Length 1058; 60.0%; Pred. No. 9.4; tive 3; Mismatches 1; Indel8
 Query Match
66.7%; Score 36; DB 1; Length 102;
Best Local Similarity 60.0%; Pred. No. 2.2;
Matches 6; Conservative 3; Mismatches 1; Indels
 l protein.
102 AA; 11178 MW; A40ECF1E0AF55B67 CRC64;
 Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
NCBI_TaxID=31599;
 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
 InterPro, IPR002621; Gemini mov. Pfam; PF01708; Gemini mov; 1. Hypothetical protein.
 EMBL; M81103; AAA47947.1; -.
 Local Similarity 60.0
tes 6; Conservative
 STANDARD;
 190 EIVPNGLNYS 199
 2 EVVPXGMDYS 11
 SEQUENCE FROM N.A.
 Y11K TYDVA
P31619;
 METAL
SEQUENCE
 SECUENCE
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NP BIND
METAL
 Query Match
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Y11K_TYDVA
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 ö
 -!- FUNCTION: Involved in the regulation of carbon partitioning in the leaves of plants. May regulate the synthesis of sucrose and therefore play a major role as a limiting factor in the export of photoassimilates out of the leaf.
-!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
 SUCTORE 6-phosphate.
-!- ENZYME REGULATION: Activity regulated by phosphorylation and moderated by concentration of metabolites and light.
-!- PATHWAY: Sucrose synthesis.
-!- SUBUNIT: Homodimer or homotetramer (By similarity).
-!- PTM: Phosphorylated, However, phosphorylation is not essential for enzyme function (By similarity).
-!- SIMILARITY: Belongs to the glycosyltransferase family 1.
 Gaps
 Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Bhrhartoideae, Oryzeae, Oryza.
 "Characterization of a rice sucrose-phosphate synthase-encoding
 ô
 66.7%; Score 36; DB 1; Length 1049; 66.7%; Pred. No. 24; tive 2; Mismatches 1; Indels
 775 779 POLY-ARG.
1049 AA; 116455 MW; ED862E2819AA4B04 CRC64;
 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14)
(UDP-glucose-finctose-phosphate glucosyltransferase).
 STRAIN=cv. Indica-IR36; TISSUE-Leaf;
MEDLINE-96235138; PubMed=8666248;
Valdez-Alarcon Ju., Perrando M., Jimenez-Moraila B.,
Herrera-Estrella L.;
 Gramels: V2500...
Interpro: V2500...
Pfam: PF00534; Glycos trans 1.
Transferase; Glycos transferase; Phosphorylation.
DOMAIN 695 698 POLY-GLY.
DOMAIN 695 698
 PRT; 1049 AA.
 PRT; 1068 AA.
 SPS MAIZE STANDARD; 18 191927; 01-JUL-1993 (Rel. 26, Created)
 EMBL; U33175; AAC49379.1; -.
PIR; JC4783; JC4783.
 STANDARD;
 6; Conservative
 gene.";
Gene 170:217-222(1996).
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436 VIPPGMDFS 444
 3 VVPXGMDYS 11
 Local Similarity
 SEQUENCE FROM N.A.
 Gramene; 043802; -
 NCBI_TaxID=4530;
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SPS ORYSA
ID SPS O
 RESULT 4
SPS_MAIZE
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Gaps

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2 EVVPXGMDYS 11

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Morrell A.C., Bruneau U.-M., Summerfelt K., Boersig M., Voelker T.A.;

"Expression of a maize sucrose phosphate synthase in tomato alters
I leaf carbohydrate partitioning.";

Plant Cell 3:1121-1130(1991).

- !- FUNCTION: Involved in the regulation of carbon partitioning in the leave of plants. May regulate the synthesis of sucrose and therefore play a major role as a limiting factor in the export of photoassimilates out of the leaf.

-!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP + sucrose 6-phosphate.

-!- RNZWE REGULATION: Activity regulated by phosphorylation and moderated by concentration of metabolites and light.

-!- SNEUNTI: Homodimer or homotetramer.

-!- SUBUNIT: Homodimer or homotetramer.

-!- SUBUNIT: Homodimer or homotetramer.

-!- PTM: Phosphorylated. However, phosphorylation is not essential for
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 Craterostigma plantagineum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledona; core eudicots; asterids;
 Gaps
 Zea mays (Maize).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
PACCAD clade, Panicoideae, Andropogoneae, Zea.
 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sucrose-phosphate synthase 2 (EC 2.4.1.14) (UDP-glucose-fructose-phosphate glucosyltransferase 2).
 SEQUENCE FROM N.A., AND SEQUENCE OF 71-74; 206-212; 471-481 AND
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14) (UDP-glucose-fructose-
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 -!- SIMILARITY: Belongs to the glycosyltransferase family 1.
 66.7%; Score 36; DB 1; Length 1068; 66.7%; Pred. No. 25; ive 2; Mismatches 1; Indels
 1068 AA; 118575 MW; 074679B5E9A1D282 CRC64;
 Malgeus; 25274; InterPro; IPR001296; Glyco_trans_1.
InterPro; IPR001296; Glycos_transf_1; 1.
Transferase; Glycosyltransferase; Phosphorylation.
DOMAIN 25 31
 PRT; 1081 AA.
 STRAIN=CV. PIONEER 3184; TISSUE=Leaf;
MEDLINE=92338837; PubMed=1840396;
 phosphate glucosyltransferase)
 EMBL; M97550; AAA33513.1; -.
 Local Similarity 66,7
les 6; Conservative
 STANDARD;
 435 VIPPGMDFS 443
 3 VVPXGMDYS 11
 PIR; JQ1329; JQ1329.
 NCBI_TaxID=4577;
 MaizeDB; 25294;
 CRAPL
 SEQUENCE
 Query Match
 SPS2_CRAPL
ID SPS2_CR
AC 004933;
 OC GENTAL OCC
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Ingram J., Chandler J.W., Gallagher L., Salamini F., Bartels D.;
Ingram J., Chandler J.W., Gallagher L., Salamini F., Bartels D.;
Ingram J., Chandler J.W., Gallagher Expressions especiated with dehydration in the
relation to sugar interconversions associated with dehydration in the
relation to sugar interconversions associated with dehydration in the
relation to sugar interconversions associated with dehydration in the
Plant Physiol. 115:113-121(1997).

I. FONGTION: Involved in the regulation of carbon partitioning in the
leaves of plants. May regulate the synthesis of sucross and
therefore play a major role as a limiting factor in the export of
photoassimilates out of the leaf.

I. CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
sucrose 6-phosphate.

I. PAZYME REGULATION: Activity regulated by phosphorylation and
moderated by concentration of metabolites and light.

I. PATHWAY: Sucrose synthesis.

I. PATHWAY: Sucrose synthesis.

I. PATHWAY: Phosphorylated. However, phosphorylation is not essential for
enzyme function (By similarity).

I. SIMILARITY: Belongs to the glycosyltransferase family 1.
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 PAR PSES 21 (2019) CONTRACTOR CON
 Gaps
 InterPro; IPR01256; Glyco_trans 1.
Pfam; PP00534; Glyco_transf 1; 1.
Pfam; PP00534; Glycos_transf 1; 1.
Pransferase; Glycosyltransferase; Phosphorylation; Multigene family.
DOWAIN 256 264 POLY-SER.
DOMAIN 256 264
 SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), AND TISSUE SPECIFICITY
 Score 36; DB 1; Length 1081;
Pred. No. 25;
2; Mismatches 1; Indels
 1081 AA; 120933 MW; DD142DC2F1A72900 CRC64;
lamiids; Lamiales; Lamiales incertae sedis; Lindernieae;
 PRT; 2778 AA
 TISUE-Eye imaginal diek,
MEDLINE-93202020; PubMed=1295747;
Fischer-Vize J.A., Rubin G.M., Lehmann R.;
 MEDLINE=97451773; PubMed=9306694;
 EMBL; Y11795; CAA72491.1; -. PIR; T09837; T09837.
 66.7%;
 STANDARD;
 Conservative
 |:| |||:|
445 VIPPGMDFS 453
 3 VVPXGMDYS 11
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=7227;
 NCBI_TaxID=4153;
 9
 FAF DROME
 SEQUENCE
 RESULT 6
FAF DROME
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 RXX COCCOSSION SERVICE ઠે
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The far facets gene is required for Drosophila eye and embryo R. Drevalopment. 1: 16:180-1000(1992).

Revalopment 1: 16:180-1000(1992).

Reverse 2: 16:180-1000(1992).

Revalopment 1: 16:180-1000(1992).

Revalopment 1: 16:180-1000(1992).

Reverse 2: 16:180-1000(1992).

Reverse 3: 16:180-1000(1992).

Reverse 3: 16:180-1000(1992).

Reverse 4: 16:180-1000(1992).

Reverse 5: 16:180-1000(1992).

Reverse 5: 16:180-1000(1992).

Reverse 6: 16:180-1000(1992).

Reverse 7: 16:180-1000(1992).

Reverse 7: 16:180-1000(1992).

Reverse 7: 16:180-1000(1992).

Reverse 7: 16:180-1000(1992).

Reverse 8: 16:180-1000(1992).

Reverse 9: 16:180-1000(1992).

Reverse 9: 16:180-1000(1992).

Reverse 9: 16:180-1000(199
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 | Machine | Mach
 Flyase, FBgn0005632; faf.

GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0007349; P:cellularization; IMP.
GO; GO:0007456; P:eye morphogenesis; IMP.
GO; GO:0001755; P:eye morphogenesis (sensu Drosophila); IMP.
GO; GO:0001755; P:eye morphogenesis (sensu Drosophila); IMP.
GO; GO:0001757; P:nuclear nigration; IMP.
GO; GO:0007097; P:nuclear nigration; IMP.
GO; GO:000757; P:protein deubiquitination; IDA.
GO; GO:0005211; P:ubiquitin-dependent protein catabolism; IGI.
 Isoīd=P55824-3; Sequence=VSP 005269;
-!- TISSUE SPECIFICITY: Eye disks and ovaries.
-!- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
-!- SIMILARITY: Belongs to peptidase family C19.
 Gaps
 function.
-!- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)0 ubiquitin + a thiol.
-!- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing, Named isoforms=3; Comment=Experimental confirmation may be lacking for some
 ô
 64.8%; Score 35; DB 1; Length 2778; 54.5%; Pred. No. 1.1e+02; ive 2; Mismatches 3; Indels
 Hydrolase, Thiol protease,
 IsoId=P55824-2; Sequence=VSP_005270;
 [soId=P55824-1; Sequence=Displayed;
 InterPro) IPR001394; Peptidase C19.
Pfam; PR00443; UCH; 1.
PROSITE; P800972; UCH 2 1; 1.
PROSITE; P800973; UCH 2 2; 1.
UDI conjugation pathway; Hydrolase;
 Local Similarity 54.5
nes 6; Conservative
 isoforms;
 Developmental RACT_SITE 1677
ACT_SITE 1978
ACT_SITE 1978
VARSPLIC 2709
 Name=1;
 CONFLICT
CONFLICT
SEQUENCE
 VARSPLIC
 Query Match
 Best Loc
Matches
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1394 EVIVPDĞQDFS 1404

RESULT 7

1 EEVVPXGMDYS 11

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 TISSUE-Brain;
MEDLINE=20277482; PubMed=10819331;
MEDLINE=20277482; PubMed=10819331;
Magase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
Prediction of the coding sequences of unidentified human genes. XVII.
The complete sequences of 100 new cDNA clones from brain which code
 Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
 SEQUENCE FROM N.A.
MEDLINE=20347694; PubMed=10888605;
Koob M.D., Nemes J.P., Benzow K.A.;
"The SCA8 transcript is an antisense RNA to a brain-specific
"Transcript encoding a novel actin-binding protein (KLHLI).";
Hum. Mol. Genet. 9:1543-1551(2000).
 KEICH 1.
KEICH 2.
KEICH 3.
KEICH 4.
KEICH 5.
KEICH 5.
ERLI HUMAN STANDARD; PRT; 748 AA. O9NR64; O9NR64; O9NR65; O9D838; 16-OCT-2001 [Rel. 40, Created) [16-OCT-2001 [Rel. 40, Last sequence update) 10-OCT-2003 [Rel. 42, Last annotation update) [Rel. 11ke protein 1. Kalti. OR KIAA1490. Homo sapiens (Human)
 EMBL; AF252283; AAF81719.1; -.
EMBL; AF552279; AAF81716.1; -.
EMBL; AB04023; BAA96014.1; ALT_INIT.
EMBL; AL353738; CAC16128.1; -.
Genew; HGNC:6352; KLHL1.
 for large proteins in vitro.";
DNA Res. 7:143-150(2000).
 MΜ
 82680
 555
601
649
701
748 AA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 DOMAIN
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
SEQUENCE
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 ï
 the
 Gaps
 Molecular cloning and characterization of plastocyanin precursor in
 Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Lillopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
 Therepro; IPR001235; BlueCul.

R InterPro; IPR001235; Copper_blue.

R InterPro; IPR001235; Copper_blue.

R Profile; PR00125; Copper_blue, 1.

R PRINTS; PR00125; Copper_blue; 1.

R PROSTINE; PR001186; COPPER_BLUE; 1.

R PROSTINE; PR001186; COPPER_BLUE; 1.

R Transit peptide.

F Transit peptide.

F Transit peptide.

F CHLOROPLAST.

F CHAIN.

F CHAIN.

F CHAIN.

F CHAIN.

F DOMAIN 58 154 PLASTOCYANIN.
Score 34.5; DB 1; Length 748; Pred. No. 35;
 Indels
 PLASTOCYANIN.
PLASTOCYANIN-LIKE.
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
 Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
 ő
 P20423; Q9SBB8;
01-FBB-1991 (Rel. 17, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Plastocyanin, chloroplast precursor.
 Ą
 1; Mismatches
 STRAIN-cv. Ilpoom; TISSUE-Leaf;
 EMBL; AF093636; AAC78108.1; -.
HSSP; P00289; 2PCF.
 15577 MW;
 63.9%;
 Query Match
Best Local Similarity 80.0
Matches 8; Conservative
 STANDARD;
 135
 57
1139
145
145
145
 2
 127 EEVVP-GMDF
 142
147
154 AA;
 1 EEVVPXGMDY
 SEQUENCE OF 58-154
 SEQUENCE FROM N.A.
 NCBI_TaxID=4530;
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 STRAIN=CV. NK 1558;
MEDLINE=94039081; PubMed=8223592;
Nielsen P., Gausing K.;
"In vitro binding of nuclear proteins to the barley plastocyanin gene
 Gaps
 Hordeum vulgare (Barley).
Makaryote, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Agnollophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
 STRAIN=Cv. Bomi;
Nielsen O.S., Gausing K.;
Nielsen O.S., Gausing K.;
"The precursor of barley plastocyanin: sequence of cDNA clones and gene expression in different tissues.";
FEBS Lett. 225:159-162(1987).
 ö
 PRINTS; PRO0156; COPPERBLUE.
PRODOM; PRO0125; COPPER BLUE; 1.
PROSITE; PS00196; COPPER BLUE; 1.
Chloroplast; Electron transport; Copper; Thylakoid; Membrane; Transit peptide.
TRANSIT 1 58 CHLOROPLAST.
 Score 34; DB 1; Length 154; Pred. No. 8.7; 2; Mismatches 3; Indels
 PLASTOCYANIN.
PLASTOCYANIN-LIKE.
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
 01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
28-FRE-2003 (Rel. 41, Last annotation update)
Plastocyanin, chloroplast precursor.
 PIR; S38255; S38255.

HSSP; P00289; 2PCF.
InterPro; IPR001923; BlueCu 1.
InterPro; IPR001235; Copper_blue.
InterPro; IPR08972; Cupredaxin.
Pfam; PF00127; copper-bind; 1.
 EMBL; Y00704; CAA68696.1; -. EMBL; Z28347; CAA82201.1; -.
 63.0%;
Query Match
Best Local Similarity 54.5%;
Marches 6; Conservative
 100 EDAVPSGVDVS 110
 STANDARD;
 1 EEVVPXGMDYS 11
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=4513;
 PLAS HORVU
 P0824B;
 CHAIN
 PLAS HORVU

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DT 01-AUG

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 Gaps
 Populus nigra (Lombardy poplar).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids I; Malbighiales; Sallcaceae; Sallceae; Populus.

NCPL_TaxID=1691;
 R BMBL, Z50186, CAA90565.1; -. RPIR, S20210; S02210; R PIR, S20208; S18208.

R HSCP; D00299; JEDC.

R InterPro; JFR001235; Copper_blue.

R PRINF; PR00127; copper_blue; I PR00127; copper_blue; I PR00127; COPPER_BLUE; I PR001235; COPPER_BLUE; I. R PROSITE; PS00196; COPPER_BLUE; I. R CALOCOPLAST; Copper_blue; I. R CALOCOPLAST; Capper_blue; I. R TANBIT TANBIT TRANSIT
 membrane surface in chloroplasts.
-- SIMILARITY: THERE ARE 12 DIFFERENCES BETWEEN THE SEQUENCE OF POPLAR PLASTOCYANINS A AND B.
-- SIMILARITY: Contains 1 plastocyanin-like domain.
 ó
 63.0%; Score 34; DB 1; Length 155; 54.5%; Pred. No. 8.7; tive 2; Mismatches 3; Indels
 STRAIN=Cv. Italica; TISSUD=Leaf;
Reichert J., Jenzelewski V., Haehnel W.;
Khuitted (ANG-1995) to the EMBL/GenBank/DDBJ databases.
120 120 T -> N (IN CV. NK 1558).
155 AA; 15709 MW; DAA7EABESF6F4F91 CRC64;
 PLASTOCYANIN B.
PLASTOCYANIN-LIKE.
 01-OCT-1989 (Rel. 12, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
 PRT; 168 AA.
 Plastocyanin B, chloroplast precursor
 COPPER.
 COPPER
 Local Similarity 54.5%;
les 6; Conservative
 STANDARD;
 101 EDAVPSGVDVS 111
 1 EEVVPXGMDYS 11
 SEQUENCE FROM N.A.
 PLAT POPNI
P11970:
VARIANT
SEQUENCE
 Query Match
 CHAIN
 Matches
 g
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566 AA; 65173 MW; 9D48C8B5D6D3B74B CRC64;
 R8L4 ARATH
Q9FJK8;
 SEQUENCE
 Tabata S.
 Query Match
 RESULT 12
R8L4 ARATH
 Matches
 FERRE BERNEL BER
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 ö
 SEQUENCE FROM N.A.
STRAINSATCS 35210 / B31;
STRAINSATCS 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Kerchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-P., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Ulterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujil C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.;
 similarity).
--- SUBCELLULAR LOCATION: Cytoplasmic.
--- SUBCELLULY: Belongs to the phenylalanyl-tRNA synthetase beta chain family. Subfamily 2.
 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FEB-2003 (Rel. 41, Last annotation update)
Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine--
 Pfam; PF03484; B5; 1.
TIGRADA; TIGROA71; pheT_arch; 1.
Aminoacy1-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
Complete protecome.
 Gaps
 [1] _
SQUENCE FROM N.A.
STRAIN=AUCC 35210 / B31;
STRAIN=AUCC 35210 / B31;
Barbour A.G., Hinnebusch J.;
Barbour A.G., Hinnebusch J.;
Fhenylalanyl-tRNA synthetase genes (alpha and beta subunits) and
Thioredoxin reductase gene of Borrelia burgdorferi.";
thioredoxin reductase gene of Borrelia burgdorferi.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
 Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia
 --- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP diphosphate + L-phenylalanyl-tRNA(Phe).
--- SUBUNIT: Tetramer of two alpha and two beta chains (By
 ö
 Length 168;
 "Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.";
Nature 390:580-586(1997).
 Indels
 16981 MW; F20DA6EA2038AEEA CRC64;
 63.0%; Score 34; DB 1;
54.5%; Pred. No. 9.5;
 566 AA
 2; Mismatches
 IIGR; BB0514; -; 1
HAMAP; MF 00284; -; 1
INCERPIC; IPR005147; B5.
INCERPIC; IPR004531; PheT_arch.
 EMBL; U82978; AAB41019.1; -.
EMBL; AE001153; AAC66870.1; -.
PIR; A70164; A70164.
TIGR; BB0514; -.
HAMAP; MF_00284; -; 1.
 tRNA ligase beta chain) (PheRS)
 6; Conservative
 STANDARD;
 112 EDAVPSGVDVS 122
 1 EEVVPXGMDYS 11
 168 AA;
 Best Local Similarity
Matches 6; Conser
 NCBI_TaxID=139;
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 Query Match
 SYFB BOR P94283;
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 .;
0
 **RPPB/HRT subfamily.
-!- SIMILARITY: Contains 3 leucine-rich (LRR) repeats.
-!- SIMILARITY: Contains 1 NB-ARC domain.
-!- DATABASE: NAME-NIB-LRRS.
-!- NAME-NIB-LRRS.
NOTE-Punctional and comparative genomics of disease resistance gene
 ŏ
 Gaps
 RPPBL4 OR ATSG48620 OR KISN18.9.
Arabidopsis thaliana (Mouse-ear cress).
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 SEQUENCE FROM N.A.
STRAIN=CV. Columbals
STELINE=99087489; PubMed=9872454;
Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
 "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned PI and TAC clones.";
DNA Res. 5:297-308(1998).
 ö
63.0%; Score 34; DB 1; Length 566; llarity 85.7%; Pred. No. 33; Conservative 0; Mismatches 1; Indels
 PRINTS; PR00364; DISEASRSIST.
Plant defense; ATP-binding; Repeat; Leucine-rich repeat.
DOWAIN
 10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable disease resistance RPP8-like protein
 908 AA.
 or send an email to license@isb-sib.ch).
 homologs;
WWW="http://niblrrs.ucdavis.edu".
 Interpro, IPR000767; Disease_resist.
Interpro, IPR001611; LRR.
Interpro, IPR002182; NB-ARC.
 EMBL; AX117163; BAB10695.1; -. EMBL; AX117163; BAC41841.1; -.
 Pfam; PF00560; LRR; 2.
Pfam; PF00931; NB-ARC; 1.
 STANDARD;
 169 VPFGMDY 175
 4 VPXGMDY 10
 Local Similarity
nes 6; Conserv
 SEQUENCE FROM N.A
 NCBI_TaxID=3702;
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ô
 SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, MUTANTS RPP8-1; RPP8-2 AND RPP8-3. AND VARIANTS.

STRAIN-cv. Columbia, and cv. Landsberg erecta;

MEDLINE-99030193; PubMed-9811794;

MCDOWell J.M., Dhandaydham M., Long T.A., Aarts M.G.M., Goff S., Hollub E.B., Dangl J.L.,

"Intragenic recombination and diversifying selection contribute to the evolution of downy mildew resistance at the RPP8 locus of
 Cooley M.B., Pathirana S., Wu H.-J., Kachroo P., Klessig D.F.; "Members of the Azabidopsis HRT/RPP8 family of resistance genes confer resistance to both viral and comycete pathogens."; plant Cell 12:663-676(2008)
 "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty Pl and TAC
 RPPB ARATH STANDARD; PRT; 908 AA.
QBW419; QBGWGS; Q9MSA1; Q9ZSY4;
10-OCT-2003 [Rel. 42, Created]
10-OCT-2003 [Rel. 42, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Disease resistance protein RPPB (Resistance to Peronospora parasitica
 Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
Karlin-Newmann G., Liu S.K., Lam B., Sakano H., Wu T., Yu G.,
Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
Arakawa T., Banho F., Bowser L., Brooks S.Y., Carninci P.,
Chao Q., Choy N., Eju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
 Gaps
 RPPS OR HRT OR AT5G43470 OR WWF20.19.

Arabidopsis thaliana (Mouse-ear cress).

Arabidopsis thaliana (Streptophyte; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 STRAIN=cv. Columbia;
MEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
 ö
 63.0%; Score 34; DB 1; Length 908; 60.0%; Pred. No. 54;
 2; Indels
 146 459 NB-ARC.
575 599 LRR 1.
600 623 LRR 3.
842 867 LRR 3.
192 199 ATP (POTENTIAL).
908 AA; 104448 MW; 3111991B17239693 CRC64;
 SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS.
 2; Mismatches
 STRAIN=cv. Di-17;
MEDLINE=20271766; Pubmed=10810142;
 STRAIN≈cv. Columbia;
MEDLINE=22954850; PubMed=14593172;
 SEQUENCE FROM N.A. (ISOFORM 1).
 SEQUENCE FROM N.A. (ISOFORM 1).
 Arabidopsis.";
Plant Cell 10:1861-1874(1998)
 Conservative
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883 EKLVPGGEDY 892
 clones.";
DNA Res. 7:31-63(2000).
 1 EEVVPXGMDY 10
 Similarity
 NCBI_TaxID=3702;
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 Tabata S.;
DOMAIN
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 MEDITE=20496823, PubMed=11041886;
Ren T., Qu F., Morris T.J.;
"HAT gene function requires interaction between a NAC protein and units gene function requires interaction between a NAC protein and plant Cell 12:1917-1926(2000).

-!- FUNCTION: Disease resistance protein. Resistance proteins guard the plant against pathogens that contain an appropriate avirulence protein via an indirect interaction with this avirulence protein. That triggers a defense system including the hypersensitive response, which restricts the pathogen growth. The interaction with TIP (TCV-interacting protein) may be essential for the recognition of the avirulence proteins, and the triggering of the
 Isode_0804.09-2; Sequence=vSP_007171, VSP_007172;
Note=Has been shown to exist only in cv. Columbia so far;
Note=Has been shown to exist only in cv. Columbia so far;
DOMAIN: The LRR repeats probably act as specificity determinant of
pathogen recognition.
POLYMORPHISM: The strong polymorphisms present in cv. Di-17 and
cv. Columbia are probably due to an unequal crossing-over between
the highly related RPPs and RPH8A genes present in cv. Landaberg
erecta. Such variations probably modify the specificity of
Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T., Satou M., Tamane R., Yaysberg M., Wallender E.K., Wong C., Yamamura Y., Yuan S., Shinozaki K., Davis R.M., Theologis A., Ecker J.R., "Empirical analysis of transcriptional activity in the Arabidopsis
 STRAIN=cv. Columbia,
Sexi M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
Hayashizaki Y., Shinozaki K.;
"Arabidopsis thaliana full-length cDNA.";
Submitted (NOV-2002) to the EMBL/GenBank/DDSJ databases.
 pathogen recognition.
MISCELLANEOUS: In cv. Columbia and cv. Landsberg erecta, RPP8
 Event=Alternative splicing; Named isoforms=2;
 SUBUNIT: Interacts with the NAC protein TIP. ALTERNATIVE PRODUCTS:
 IsoId=Q8W4J9-1; Sequence=Displayed;
 WWW="http://niblrrs.ucdavis.edu".
 EMBL; AF089711; AAC78631.1; -.
EMBL; AF24174; AAF56987.1; -.
EMBL; AB025638; BAA57426.1; -.
EMBL; AX062514; AAL32592.1; -.
EMBL; AX118862; BAC43449.1; -.
InterPro; IPR000767; Disease_resist.
 SEQUENCE FROM N.A. (ISOFORM 2).
 EMBL; AF089710; AAC83165.1; -.
 Science 302:842-846(2003).
 defense response.
 INTERACTION WITH TIP.
 Name=1;
 Name=2
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Substituting the control of the cont
 erecta.

N -> F (in cv. Di-17 and cv. Landsberg erecta).

DSZISTYSLFY -> YSKISAVDLFN (in cv. Landsberg erecta).

ELSTYS -> KITTOE (in cv. Di-17).

A -> V (in cv. Landsberg erecta).

DNYLSWQ -> NKYLEVH (in cv. Di-17).

DN -> NR (in cv. Landsberg erecta).

NQ -> SH (in cv. Landsberg erecta).

Y -> N (in cv. Landsberg erecta).

Y -> N (in cv. Landsberg erecta).

I -> K (in cv. Landsberg erecta).
 erecta).

C -> S (in cv. Di-17 and cv. Landsberg erecta).

T -> I (in cv. Di-17).

S -> R (in cv. Di-17).

S -> R (in cv. Di-17).

H -> Q (in cv. Di-17).

I -> L (in cv. Landsberg erecta).

KNXT -> RNAM (in cv. Di-17).

K -> N (in cv. Landsberg erecta).

R -> N (in cv. Landsberg erecta).
 /FTId=VSP 007171.
Missing (in isoform 2).
/FTId=VSP 007172.
/FTIG=VSP 007172.
G -> TORQI (in cv. Landsberg erecta)
G -> E (in cv. Di-17).
SGK -> RGE (in cv. Di-17).
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LER 2.
MAPLITERNITAL).
WATLITERNEGUGIH -> ELLWYIHEALFLIANS (in
 erecta)

P -> S (in cv. Di-17 and cv. Landsberg erecta).

W -> C (in cv. Di-17 and cv. Landsberg erecta).

C -> R (in cv. Di-17 and cv. Landsberg crecta).
 PRF -> SRFK (in cv. Di-17).
Y -> Y (in cv. Di-17).
C -> Y (in cv. Landsberg erecta).
C -> S (in cv. Di-17 and cv. Landsberg
 -> R (in cv. Di-17 and cv. Landsberg
InterPro; IPR001611; LRR.
InterPro; IPR002182; NB-ARC.
Pfam; PP00560; LRR; 2.
Pfam; PF00931; NB-ARC; 1.
Pfam; PF0094; DISBASERSIST.
Plant defense; ATP-binding; Repeat; Leucine-rich repeat;
Alternative splicing; Polymorphism.
In 45 LEUCINE-ZIPPER.
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Anablodopsis.;

Parablodopsis.;

Plant Cell 10:1861-1874(1998).

-I- FUNCTION: Disease resistance protein. Resistance proteins guard
the plant against pathogens that contain an appropriate avirulence
protein via an indirect interaction with this avirulence protein.

That triggers a defense system including the hypersensitive
response, which restricts the pathogen growth. In contrast to
RPB9, it does not specifically recognize the Emco5 avirulence
protein from Perchospora parasitica.

NISCELLANEOUS: In cv. Columbia and cv. Di-17 this protein is not
present due to an unequal rosssing over between the RPP8 and RPBHA

PRESENT SHORMENTY: Contains 1 the disease resistance NB-LRR family.

RPB9/RHT subfamily.

SIMILARITY: Contains 1 NB-ARC domain.

-I- SIMILARITY: Contains 1 NB-ARC domain.

NOTES-INCLIDANEOUS: NAME-NLB-LRRS;

NOTES-INCLIDANEOUS NAME-NLB-LRRS;
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 Holub E.B., Dangl J.L.,
"Intragenic recombination and diversifying selection contribute to the evolution of downy mildew resistance at the RPP8 locus of Arabidopsis.";
 Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TAXID=3702;
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 SEQUENCE FROM N.A., AND FUNCTION.
STRAINE-OV. Landsberg erects,
MEDLINE-99030193; Pubmed-9811794;
MCDowell J.M., Dhandaydham M., Long T.A., Aarts M.G.M., Goff S.,
 ö
 ö
 Score 34; DB 1; Length 910;
Pred. No. 55;
2; Mismatches 2; Indels
63.0%; Score 34; DB 1; Length 908; 60.0%; Pred. No. 54; ive 2; Mismatches 2; Indels
 10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last amotation update)
Disease resistance protein RPH8A (RPF8 homolog A).
 910 AA
 PRT;
 63.0%;
 Local Similarity 60.0
 Conservative
 STANDARD;
 |::|| | ||
885 EKLVPGGEDY 894
 |::|| |-||
883 EKLVPGGEDY 892
 BEVVPXGMDY 10
 1 EEVVPXGMDY 10
 Best Local Similarity
Matches 6; Conserv
 homologs;
 RP8H_ARATH
P59584;
 Query Match
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Matches 6
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RP8H_ARATH
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 STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDIATE=96337999; PubMed=8688087;

Bult C.U., White O. Olean G.U.; Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Raich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback F.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.W., Smith H.O., Woses C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
 Gaps
 .
0
 61.1%; Score 33; DB 1; Length 276;
45.5%; Pred. No. 26;
iive 4; Mismatches 2; Indels
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InterPro; IPR001163; snRNP Sm.
InterPro; IPR005358; UPF0153.
Pfam, PF03692; UPF0153; ...
Pfam, PF03692; UPF0153; ...
Rypothetical protein; Complete proteome.
SEQUENCE 276 AA; 33454 MW; 97BD69D392BC8FDF CRC64;
 Archaea, Euryarchaeota, Methanococci, Methanococcales, Methanocaldococcaceae, Methanocaldococcus.
 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ0939.
 276 AA
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 EMBL; U67537; AAB98946.1; -.
 Science 273:1058-1073(1996).
 5; Conservative
 STANDARD;
 Methanococcus jannaschii
 C64417; C64417.
 Query Match
Best Local Similarity
Matches 5; Conservi
 NCBI_TaxID=2190;
 Y939 METUA
Q58349;
 annaschii
RESULT 15
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Search completed: June 3, 2004, 11:49:52 Job time: 5.86667 secs

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 SEQUENCE FROM N.A.
 NCBI_TaxID=4932;
 STRAIN=FY1679;
 SEQUENCE FROM
STRAIN=FY1679
 YOR013W
 Q12479
 012479
 QBESY oceanobail

030260 archaeoglob

QBG106 surchaeoglob

QBG204 enterococcu

022081 citrus unsh

022096 citrus unsh

089568 arabidopsis

Q90947 arabidopsis

Q99130 arabidopsis

Q9130 oryza sativ

Q98064 oryza sativ

Q88064 oryza sativ
 Q12479 saccharomyc
 3, 2004, 11:35:06; Search time 29.8667 Seconds (without alignments) 116.206 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1017041 seqs, 315518202 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 Q8S064
Q9GQ04
Q8XPA8
O52367
 SPTREMBL 25:*

1: Sp archea:*
2: Sp bacteria:*
4: Sp hungi:*
5: Sp invertebrate:*
5: Sp invertebrate:*
5: Sp invertebrate:*
6: Sp organelle:*
7: Sp organelle:*
7: Sp Diage:*
 Q8ESV7
030260
Q8DIH0
Q82ZB4
022081
 Q8W568
Q9C9T7
P93782
 05N360
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 sp_unclassified: *
 sp_rodent:*
sp_virus:*
sp_vertebrate:*
 - rvirus:*
- bacteriap:*
- archeap:*
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seq length: 200000000
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54
1 EEVVPXGMDXS 11
 Query
Match Length DB
 Title:
Perfect score:
 Scoring table:
 Score
 Minimum DB
Maximum DB
 Searched:
 Sequence:
 Database
 Run on:
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|---------------------------------------------------------------------------------------------|---|---------------------------|--------|----------------------|--------|---------------|--------|----------|--------|-----------------|--------|--------|--------|------|-------|--------|----------|--------|--------|--------|----------|--------------------|--------|----------|--------|------------------|--------|----------|----|------|
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| <br>a<br>a w w w w w w w w w w w w w w w w w w                                              |   | 366                       | 357    | 344                  | 337    | 296           | 290    | 284      | 251    | 245             | 222    | 222    | 215    | 748  | 1828  | 1474   | 1420     | 1410   | 1150   | 1031   | 745      | 595                | 517    | 511      | 474    | 4                | m      | 470      | L  | 368  |
|                                                                                             |   |                           |        |                      |        |               | 63.0   | 63.0     | 63.0   | 63.0            | 63.0   | 63.0   | 63.0   | 63.9 | 64.8  | 64.8   | 64.8     |        |        |        |          | 4.                 | 4.     | 4.       | 4      | 4.               | 4.     | 4.       |    | 4    |
| 04 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -                                                    | , | 3.4                       | 34     | 34                   | 34     | 34            | 34     | 34       | 34     | 34              | 34     | 34     | 34     | 4.   | 35    | 35     | 35       | 35     | 35     | 35     | 35       | 35                 | 35     | 35       | 3      | 35               | 35     | 35       | יי | 400  |
|                                                                                             | 1 | 45                        | 44     | 43                   | 42     | 41            | 40     | 39       | 38     | 37              | 36     | 35     | 34     | 33   | 32    | 31     | 30       | 53     | 28     | 27     | 56       | 25                 | 24     | 23       | 22     | 21               | 20     | 13       | 81 | •    |

## ALIGNMENTS

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Siffanieria: PubMed=8413243;
MRDLINE=94019318; PubMed=8413243;
Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlendy G.,
 CYC2 encodes a factor involved in mitochondrial import of yeast
 Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 De haan M., Grivell L.A., Maarse A.C.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
 Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
 De haan M., Maarse A.C., Grivell L.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
 Last sequence update)
Last annotation update)
156 AA
 012479;
01-NOV-1996 (T-EMBLrel. 01, Created)
01-NOV-1996 (T-EMBLrel. 01, Last seq
01-JUN-2003 (T-EMBLrel. 24, Last ann
ORF YOR013W.
 cytochrome c.";
Mol. Cell. Biol. 13:6442-6451(1993)
 PRT;
 [5]
SEQUENCE FROM N.A.
STRAIN-FY1679;
MEDLINE-94169519; PubMed=7764548;
 PRELIMINARY;
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Multidrug efflux transporter.
TLL1618.
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Best Local Similarity 5%...
6; Conservative
 Local Similarity 63.6
 120 ENIVPYGIDES 130
 PRELIMINARY;
 843 EEVLPNGIGYS 853
 1 EEVVPXGMDYS 11
 1 EEVVPXGMDYS 11
 SEQUENCE FROM N.A.
 Complete proteome
SEQUENCE 1044 A
 FIGR; AF2411;
 Venter J.C.;
 Query Match
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Q8DIH0
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 SEQUENCE FROM N.A.
STRAIN=HTEB11 / DSM 14371 / JCM 11309;
MEDLINE=22220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments.";
Nucleic Acids Res. 30:3927-3935(2002).
 Gaps
 Gaps
Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
"Molecular cloning of a gene, DHS1, which complements a drug-
"Molecular cloning of a gene, DHS1, which complements a drug-
hypersensitive mutation of the yeast Saccharomyces cerevisiae.";
Biosci. Biotechnol. Biochem. 58:391-395 (1994).

EMBL, Z74920; CAA99201.1; -.

EMBL, X87331; CAA60762.1; -.

EMBL, S84619, S84619.

SGD, S0005539; YORQ13W.

SGD, S0005539; YORQ13W.
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 SEQUENCE FROM N.A.
STRAIN-VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 Bacteria, Firmicutes, Bacillales, Bacillaceae, Oceanobacillus.
NCBI_TaxID=182710;
 70.4%; Score 38; DB 16; Length 319; 60.0%; Pred. No. 18; ive 3; Mismatches 1; Indels
 Query Match

14.1%; Score 40; DB 3; Length 156;
Best Local Similarity 77.8%; Pred. No. 3;
Matches 7; Conservative 1; Mismatches 1; Indels
 EMBL; AP004594; BAC12465.1; -.
InterPro, IPR001279; Blactmase-like.
Pfam; PF00753; lactamase_B; L.
Hypothetical protein; Complete proteome.
SEQUENCE 319 AA; 35617 MW; 3BDAE4BF13E79E37 CRC64;
 Archaea; Buryarchaecta; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein AF2411.
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical conserved protein.
 363 AA
 319 AA
 PRT;
 PRT;
 60.08;
 Query Match
Best Local Similarity 60.vv,
 PRELIMINARY;
 PRELIMINARY;
 Archaeoglobus fulgidus.
 189 EQLVPHGIDY 198
 1 EEVVPXGMDY 10
 50 EVMPLGMDY 58
 2 EVVPXGMDY 10
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 RESULT 3
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 Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., A. Watamabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Atjokawa C., Kohara M., Matsumoch M., Matsumo A., Nakasaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., Thermosynechococcus albongatus BP-1.";
Thermosynechococcus albongatus BP-1.";
Thermosynechococcus albongatus BP-1.";
DNA Res S.123-130(2002).
REMBL; AP005374; BAC09170.1; -.
REMBL; AP005374; Extransporter activity; IEA.
RO; GO:0005215; F:transporter activity; IEA.
RO; GO:0005215; F:transporter activity; IEA.
RO; GO:0005315; F:transporte; IEA.
RO; GO:0005315; F:transporte; IEA.
RICEPPO; IPR001036; ACT[Vin.res.
Ketchum K.A., Dodson R.J., Gwinn M., Hickey B.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Octon M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 Gaps
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 "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364:370(1997).
EMBL, AEO01109; AAB91255.1; -.
PIR; D69551; D69551.
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 ;
 70.4%; Score 38; DB 16; Length 1044; 63.6%; Pred. No. 67; 2; Indels Cive 2; Mismatches 2; Indels C
 70.4%; Score 38; DB 17; Length 363; 54.5%; Pred. No. 20; tive 3; Mismatches 2; Indels
 1044 AA; 113205 MW; 00E9C13F0F636D2F CRC64;
 Synechococcus elongatus (Thermosynechococcus elongatus)
Bacteria; Cyanobacteria; Chrococcales; Synechococcus.
NCBI_TaxID=32046;
 Interpro; IPR002103; Bac_luciferase.
Pfam; PF00296; bac_luciferase; I.
Hypothetical protein; Complete proteome.
BSEQUENCE 363 AA; 41736 MW; 08976EAE788F4803 CRC64;
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 PRT; 1044 AA
 STRAIN=BP-1;
MEDLINE=22225144; PubMed=12240834;
 Pfam; PF00873; ACR tran; 1.
PRINTS; PR00702; ACRIFLAVINRP.
TIGRFAMS; TIGR00915; 2A0602; 1.
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Mol. Gen. Genet. 252:346-351(1996)
 O8W568;
01-MAR-2002 (TEMBLEEL. 20,
01-MAR-2002 (TEMBLEEL. 20,
01-OCT-2003 (TEMBLEEL. 25,
 Query Match
Best Local Similarity 6b.,
6; Conservative
 6; Conservative
 PRELIMINARY;
 PRELIMINARY;
 228 VIPPGMDFS 236
 234 VIPPGMDFS 242
 3 VVPXGMDYS 11
 3 VVPXGMDYS 11
 At1g73750/F25P22 17.
 Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Query Match
 022096
 Q8W568
 Matches
 RESULT 7
022096
 RESULT 8
Q8W568
ID Q8W5:
AC Q8W5:
DT 01-M
DT 01-M
DT 01-O
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 SEQUENCE FROM N.A.

STRAIR=V883 / ATCC 700802;

MEDLINE=2255087; PubMed=12663927;

Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R.,

Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,

Tettelin H., Dodson R.T., Umayam L., Brinkac L., Beanan M.,

Daugherty S., DeBoy R.T., Unikin S., Xolonay J., Madupu R., Nelson W.,

Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,

Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;

"Role of mobile DNA in the evolution of vancomycin-resistant
 Enterococcus faecalis (Streptococcus faecalis).
Bacteria, Firmicutes, Lactobacillales, Enterococcaceae, Enterococcus.
 Gabs
 Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Sapindales, Rutaceae, Citrus.
 STRAIN=CV. Miyagawa-Wase, TISSUB-Juice sacs and segment epidermis; MEDLINE=96439842; PubMed=8842155; Condten W., Takanchura Y., Omura M., Akihama T.; Conding and molecular analysis of cDNA encoding three sucrose phosphate synthase isoforms from a citrus fruit (Citrus unshiu
 ö
 Score 36; DB-16; Length 149;
Pred. No. 20;
0; Mismatches 3; Indels
 149 AA; 16127 MW; 555799BF1E47D34E CRC64;
 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Large conductance mechanosensitive channel protein.
MSCL OR EF3152.
 Last sequence update)
Last annotation update)
 GO; GO:0016020; C:membrane; IEA.
GO; GO:000216; F:ion channel activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro: IPR001185; MS_channel.
 149 AA
 341 AA
 од-оом-гооз (итымылет, 24, hast anno
Sucrose-phosphate synthase (Fragment)
 022081;
01-7AN-1998 (TrEMBLrel. 05, Created)
01-7AN-1998 (TrEMBLrel. 05, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
 Mol. Gen. Genet. 252:346-351(1996)
 Pfam; PF01741; MsCL; 1.—
PRINKY: PR01264; MECHCHANNEL.
ProDom; PD007253; MS Channel: 1
TICRFRAMS; TIGR00220; mscL; 1.
 Science 299:2071-2074(2003).
EMBL; AE016956; AAO82828.1; -.
 Citrus unshiu (Satsuma orange)
 66.7%;
70.0%;
 Local Similarity 70.0
nes 7; Conservative
 PRELIMINARY;
 PRELIMINARY;
 113 EEVVPTSEDY 122
 1 EEVVPXGMDY 10
 Complete proteome. SEQUENCE 149 AA;
 [2]
SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=1351;
 022081
 Best Loc
Matches
 RESULT 5
082ZB4
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 TISSUE-Juice and segment epidermis;
Konstea A., Takanokura Y., Moriguchi T., Omura M., Akihama T.;
Konstea A., Takanokura Y., Moriguchi T., Omura M., Akihama T.;
"Differential expression of three sucrose-phosphate synthase isoforms during sucrose accumulation in citrus fruits (Citrus unshiu Marc.).";
Plant Sci. 140:165-178[1999].
EMBL; AB006660; BAA22071.1; -.
FIR; S72650; S72650.
NON TER 348
SRQÜENCE 348 AA; 38556 MW; EBIC21EBA6FFSCSE CRC64;
STRAIN=cv. Miyagawa-Wase; TISSUE=Juice sacs and segment epidermis; Komatau A., Takanokura Y., Moriguchi T., Omura M., Akihama T.; Infiferential expression of three sucrose-phosphate synthase isoforms during sucrose accumulation in citrus fruits (Citrus unshiu Marc.)."; Plant Sci. 140:169-178 (1999).

PEMBL, AB006319; BAA2315-1; -.

PIR; S72649; S72649.

NOW TER 1 1

SEQÜENCE 341 AA; 38136 MW; 61417A69C4560777 CRC64;
 Citrus unshiu (Satsuma orange).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; rosids,
eurosids II, Sapindales, Rutaceae, Citrus.

NCBI_TaxID=55188;
 Gaps
 ö
 TISSUE-Juice sacs and segment epidermis;
MEDLINE-96438942; PubMed=8842155;
Komatsu A., Takanokura Y., Omura M., Akihama T.;
"Cloning and molecular analysis of cDNA encoding three sucrose phosphate synthase isoforms from a citrus fruit (Citrus unshiu
 ö
 Length 341;
 10; Length 348;
 Indels
 Indels
 341 341
341 AA; 38136 MW; 61417A69C4560777 CRC64;
 Created)
Last sequence update)
Last annotation update)
 Last sequence update)
Last annotation update)
 1,
 66.7%; Score 36; DB 10;
66.7%; Pred. No. 50;
 348 AA.
 66.7%; Score 36; DB 66.7%; Pred. No. 51; tive 2; Mismatches
 2; Mismatches
 Sucrose-phosphate synthase (Fragment)
 01-JAN-1998 (TrEMBLrel. 05, Created) 01-JAN-1998 (TrEMBLrel. 05, Last seq 01-JUN-2003 (TrEMBLrel. 24, Last ann
 PRT;
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414 VIPPGMDFS 422
 3 VVPXGMDYS 11
 thaliana.";
 Query Match
 P93782
 RESULT 11
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 Subjuster From M., Cheuk R., Shinn P., Banh J., Bowser L.,

A Kim C.J., Chen H., Cheuk R., Shinn P., Banh J., Bowser L.,

A Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,

Brida U., Jones T., Karlin-Neumann G., Kawai J., Lam B.,

Lee J.M., Lin J., Miranda M., Narusaka M., Supyen M., Onodera C.S.,

A Tang C.C., Toriudi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,

Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Arabidopsis ORF clones.",

I. Submitted (MAY-2502) to the EMBL/GenBank/DDBJ databases.

EMBL; AY113044; AAM47352.1; ...

R EMBL; AY113044; AAM47352.1; ...

GO; GO:0004281; F:caralytic activity; IEA.

GO; GO:0004281; P:proteolysis and peptidolysis; IEA.

R InterPro: IPRO00379; Sez_GetFe

R RROSTE; PS00708; PRO ENDODEP SER; 1.

R REGIER FE ASA, 49682 MW; A159955B21742C4A CRC64;
 Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carnincii P., Dale J.M., Goldsmith A.D., Hayashitzaki Y.,
Bowser L., Carnincii P., Dale J.M., Goldsmith A.D., Hayashitzaki Y.,
Kawai J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Phan P.K., Ouach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 STRAIN=CV. Columbia,
MEDLINE=210719; PubMed=11130712;
MEDLINE=2107719; PubMed=11130712;
Theologis A., Ecker U.R., Palm C.J., Federspiel N.A., Kaul S.,
White O., Alonso U., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Buchler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
Chung M.K., Con L., Conway A.B., Peng J.-D., Fong B., Fujii C.Y.,
Gill J.E., Goldamith A.D., Haasa B., Hansen N.F., Hughes B., Huizar L.,
Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Kwan A., Lam B.,
Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
 Gaps
 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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0
 Score 36; DB 10; Length 452;
Pred. No. 69;
0; Mismatches 3; Indels
 "Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
 Q9C9T7;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
 PRT; 460 AA
 66.78;
70.08;
 7; Conservative
 PRELIMINARY;
 210 EEDVPSAMDY 219
 1 EEVVPXGMDY 10
 Query Match
Best Local Similarity
Matches 7; Conserv
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 J.R.;
 Q9C9T7
 RESULT 9
Q9C9T7
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 TISSUB-Leaf,
Sugitarential Expression of T.;
Sugiyama T.;
Sugitarential Expression of Two Genes for Sucrose-Phosphate Synthase
in Sugarcane: Molecular Cloning of the cDNAs and Comparative Analysis
of Gene Expre ssion.";
Submitted (FEBL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB001337; BAA19241.1;
GO; GO:0046524; F:sucrose-phosphate synthase activity; IEA.
GO; GO:001675; F:transferase activity, transferring glycosyl. . .; IEA.
Interpro; IPR001296; Glyco_trans 1.
Fram; PR00344; Glycos_trans 1.
Glycosyltransferase.
 Gaps
 Gaps
Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P., Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A., Malitecher J., Miranda M., Nigruen M., Nierman W.C., Osborne B.I., Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M., Sun H., Tallon L.J., Tambunga G., Toriuml M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M., Sequence and analysis of chromosome 1 of the plant Arabidopsis
 ;
 ö
 66.7%; Score 36; DB 10; Length 1047; 66.7%; Pred. No. 1.8e+02; cive 2; Mismatches 1; Indels C
 Query Match
66.7%; Score 36; DB 10; Length 460;
Best Local Similarity 70.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 3; Indels
 SEQUENCE 1047 AA; 116379 MW; DOEDB34961E1D83D CRC64;
 Hypothetical protein.
SEOUENCE 460 AA, 50564 MM, E94B27B5C4B249EC CRC64;
 PRT; 1047 AA.
 Conservative
 PRELIMINARY;
 Nature 408:816-820(2000)
 218 EEDVPSAMDY 227
 1 EEVVPXGMDY 10
 Best Local Similarity
Matches 6; Conserv
 SEQUENCE FROM N.A.
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469 VIPPGMDFS 477
 |:| |||:|
453 VIPPGMDFS 461
 3 VVPXGMDYS 11
 3 VVPXGMDYS 11
 [1]
SEQUENCE FROM N.A.
TISSUE=G111;
 SEQUENCE FROM N.A
 NCBI_TaxID=39947;
 Query Match
 Q8S064
Q8S064;
 Q9GQ04
 Best Loc
Matches
 RESULT 14
 RESULT 13
 096004
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 SEQUENCE FROM N.A.

BU Arabidopsis sequencing project;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AL161516; CAB39764.1;

EMBL; AL161516; CAB78135.1;

PIR; 1704065; 1704062

GO; GO:0016757; F:transferase activity; IEA.

GO; GO:0016757; F:transferase activity, transferring glycosyl. ..; IEA.

GO; GO:0016757; F:transferases activity, transferring glycosyl. ..; IEA.

InterPro; IPR01296; Glyco_trans 1.

Fram; PF00354; Glyco_trans 1.

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GO; GO:007076; Glyco_trans 1.

GO; GO:008076; Glyco_trans 1.

GO; GO:008076; Glyco_trans 1.

GO; GO:008076; Glyco_trans 1.

GO; GO:008076; Glyco_trans 2.

GO; GO:008076; Glyco_trans 2.

GO; GO:008076; Glyco_trans 3.

GO; GO:008076; Glyco_trans 4.

GO; GO:008
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Sakamoto M., Satozawa T., Kishimoto N., Higo K., Shimada H.,
Sakamoto M., Satozawa T., Kishimoto N., Higo K., Shimada H.,
Fujimura T.,
Satozawa T., Kishimoto N., Higo K., Shimada H.,
Structura and RFLP mapping of a rice sucrose phosphate synthase (SPS)
gene that is specifically expressed in the source organ.";
Plant Sci. 112:207-217(1995).
Plant, D45890; BAA00304-1; -.
PIR; T04103; T04103.
 Gaps
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 24, Last annotation update)
8ucrose-phosphate synthsse-like protein (EC 2.4.1.14).
F28M11.40 OR AT4G10120.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Purosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL TAXID=3702;
 Oryza sativa (Rice).
Wkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
 .;
0
 Score 36; DB 10; Length 1083; Pred. No. 1.8e+02; 2; Mismatches 1; Indels
 GO; GO:0009058; F:L-lactate dehydrogenase activity; IEA. GO; GO:0009058; P:biosynthesis; IEA.
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SEQUENCE FROM N.A.
BU Arabidopsis sequencing project;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
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 PRT; 1083 AA
 66.7%;
 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
 PRELIMINARY;
 |:| |||:|
483 VIPPGMDFS 491
 3 VVPXGMDYS 11
 SEQUENCE FROM N.A.
 NCBI_TaxID=4530;
 Q9SN30
Q9SN30,
 RESULT 12
Q43010
 SPS1.
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 Gaps
 Gaps
 Putative sucrose-phosphate synthase.
P0678F11.14.
Oorza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 STAINTENT MATSUMOTO T., Yamamoto K.;
STAINTENT MIPPONDATE;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
T. Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC clone: P0678F11.";
EDMI, AP003437; BAR86107.1;
R EMBI, AP003437; BAR86107.1;
R GO; GO:0004459; F:L-lactate dehydrogenase activity; IEA.
R GO; GO:000096; F:L-LDH: I.
R ROSITE; PS00064; L. LDH: 1.
R ROSITE; PS00064; L. LDH: 1.
R ROSITE; PS00064; L. LDH: 1.
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 66.7%; Score 36; DB 10; Length 1084; 66.7%; Pred. No. 1.8e+02; ive 2; Mismatches 1; Indels (
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
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Na+(K+/2Cl-cortansporter (Fragment).
Eriocheir sinensis (Chinese mitten crab).
Eriocheir sinensis (Chinese mitten crab).
Bukaryota, Metazaa, Arthropoda; Crustacea, Malacostraca;
Bunalacostraca; Bucarida; Decapoda; Plecyemata; Brachyura;
Bubrachyura; Grapsoidea; Varunidae; Eriocheir.
GO, GO:0006096; P:glycolysis; IEA.
InterPro; IPR001296; Glyco_trans_1.
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Last annotation update)
 219 AA.
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 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
 PRT;
 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
 Local Similarity 66.7
 PRELIMINARY;
 PRELIMINARY;
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 Gaps
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MEDUINE=21664373; PubMed=11792842;
Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
Weihrauch D., Towle D.W.;

"Na+/H+-exchanger and Na+/K+/2Cl- -cotransporter are expressed in gills of the euryhaline Chinese crab Eriocheir sinensis.";

Comp. Biochem. Physiol. 126:S158-S158 (2000).

EMBL; AF301160; AAG3938.1; -.

NON TER 21 1 1

NON TER 219 219

SEQÜENCE 219 AA; 24159 MW; 599442DA26F0D3F1 CRC64;
 Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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InterPro; IPR000594; ThIF_domain.
Pfam; PF00899; ThIF; J. Complete protecome.
SEQUENCE 253 AA; 27714 MW; 814DF79D3E0D7486 CRC64;
 QBXPAB;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein CPE0057.
 flesh-eater.",
Proc. Mall. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL, AP003185; BAB79763.1; -.
GO; GO:0003824; F.catalytic activity; IBA.
 253 A.A.
 PRT;
 PRELIMINARY;
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108 EEIIPDDVDY 117
 1 EEVVPXGMDY 10
 107 VPQGLDYS 114
 4 VPXGMDYS 11
 SEQUENCE FROM N.A.
 OBXPAB
 RESULT 15
Q8XPA8
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Search completed: June 3, 2004, 11:57:32 Job time: 30.8667 secs Hepatitis Hepatitis Hepatitis

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Abg03621 N Abg08173 N Abg05826 N Abb805826 N

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 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5.
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 /note= "C-terminal amide"
 'note= "D-form residue"
ABB 0544
ABB 0553
ABB 0553
ABB 0554
ABB 0554
ABB 0530
ABB 0543
ABB 0544
ABB 0547
ABB 0554
ABB
 Location/Qualifiers
 Brunck TK;
 ABB80525 standard; peptide; 11 AA
 Claim 17; Page 64; 69pp; English.
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169
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 (first entry)
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39.
 Misc-difference
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002
 Synthetic.
 4 4 4 4 6 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0
 protease.
 ABB80525;
 RESULT 1
 ABB80525
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Abb80522 Hepatitis
Abb80562 Hepatitis
Abb80563 Hepatitis
Abb80565 Hepatitis
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Abb80559 Hepatitis
Abb80559 Hepatitis
Abb80524 Hepatitis
Abb80524 Hepatitis
Abb80524 Hepatitis
Abb80529 Hepatitis
Abb80529 Hepatitis
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Abb80529 Hepatitis
Abb80569 Hepatitis
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 3, 2004, 11:31:01 ; Search time 45.9333 Seconds (without alignments) 67.664 Million cell updates/sec
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 1586107
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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 SUMMARIES
 Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
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ABB80565
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ABB80568
ABB80561
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ABB80526
 ABB80539
ABB80549
 ABB80525
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geneseqp2000s:*
geneseqp2000s:*
geneseqp2002s:*
geneseqp2002s:*
geneseqp2003bs:*
geneseqp2003bs:*
 A_Geneseq_29Jan04:*
 Winimum DB seq length: 0 Maximum DB seq length: 2000000000
 US-09-909-164-9
52
1 EEVVPXGMSYS 11
 В
 Length
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 765
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60
 Post-processing:
 Title:
Perfect score:
 Scoring table:
 Score
 Sequence:
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 Database
 Run on:
 Result
No.
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Gaps

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Indels

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Mismatches

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Matches

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invention are alpha-ketoamide peptide analogues. The peptides have virudide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV processe. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 The sequence represents a peptide compound of the invention having the hepatities C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-kecoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 'note= "Norvalyl carbonyl forming keto-amide linkage with
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1.
 ö
 96.2%; Score 50; DB 5; Length 11; 100.0%; Pred. No. 0.002; or Mismatches 0; Indels
 Length 11;
 96.2%; Score 50; DB 5; 100.0%; Pred. No. 0.002;
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 Location/Qualifiers
 ABB80521 standard; peptide; 11 AA.
 Brunck TK;
 Claim 17; Page 64; 69pp; English.
 19-JUL-2001; 2001WO-US023169.
 21-JUL-2000; 2000US-0220101P.
 residue 7"
 (first entry)
 Local Similarity 100.
 1 EEVVPXGMSYS 11
 Η
 (CORV-) CORVAS INT INC
 Lim-Wilby M, Levy OE,
 1 EEVVPXGMSYS
 WPI; 2002-361643/39
 Query Match
Best Local Similarity
 Sequence 11 AA;
 Sequence 11 AA;
 WO200208251-A2
 Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002
 Synthetic
 protease.
 Query Match
 Matches
88888888
 à
 g
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ö
 note= "Norvaly1 carbony1 forming keto-amide linkage with
 The sequence represents a peptide compound of the invention having hebatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha *ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2.
 96.2%; Score 50; DB 5; Length 11;
100.0%; Pred. No. 0.002;
ive 0; Mismatches 0; Indels
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 'note= "D-form residue"
 Location/Qualifiers
 ABB80522 standard; peptide; 11 AA.
 Lim-Wilby M, Levy OE, Brunck TK;
 Claim 17; Page 64; 69pp; English.
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169.
 08-OCT-2002 (first entry)
 residue 7'
11; Conservative
 11; Conservative
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 디
 1 EEVVPXGMSYS 11
 (CORV-) CORVAS INT INC
 1 EEVVPXGMSYS
 WPI; 2002-361643/39.
 Similarity
 Misc-difference 9
 Sequence 11 AA;
 WO200208251-A2
 Modified-site
 Novel peptide activity usefu
 Modified-site
 Modified-site
 31-JAN-2002.
 Synthetic
 ABB80522;
 protease.
 Query Match
 Matches
 ઠે
 g
 g
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RESULT 4

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 /note= "Valyl carbonyl forming keto-amide linkage with residue 7"
 /note= "Norleucyl carbonyl forming keto-amide linkage with residue 7"
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #45
 ô
 o. 0.002;
o. Indels
 96.2%; Score 50; DB 100.0%; Pred. No. 0.0 ive 0; Mismatches
 /note= "N-terminal acetyl"
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 Location/Qualifiers
 Location/Qualifiers
 Brunck TK;
 ABB80565 standard; peptide; 11 AA.
 Claim 17; Page 65; 69pp; English.
 19-JUL-2001; 2001WO-US023169.
 21-JUL-2000; 2000US-0220101P.
 (first entry)
 11; Conservative
 1 EEVVPXGMSYS 11
 H
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 EEVVPXGMSYS
 WPI; 2002-361643/39
 Local Similarity
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Key
Modified-site
 Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002
 Synthetic.
 Synthetic
 protease.
 virucide
 virucide
 Query Match
 Best Loca
Matches
 RESULT 6
 111111X8XXXXXXXXXXX
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 셤
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 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 carbonyl residue forming a keto e 7"
 virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #43.
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46
 ö
 DB 5; Lens
o. 0.002;
0; Indels
 /note= "2-aminoisobutyryl ca
-amide linkage with residue
 0; Mismatches
 note= "N-terminal acetyl"
 /note= "C-terminal amide"
 96.2%; Score 50; 100.0%; Pred. No.
 Location/Qualifiers
ABB80566
ID ABB80566 standard; peptide; 11 AA.
 Brunck TK;
 ABB80563 standard; peptide; 11 AA.
 Claim 17; Page 65; 69pp; English.
 21-JUL-2000; 2000US-0220101P
 19-JUL-2001; 2001WO-US023169
 (first entry)
 (first entry
 Query Match
Best Local Similarity 100.
 1
 1 EEVVPXGMSYS 11
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC.
 1 EEVVPXGMSYS
 WPI; 2002-361643/39
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 08-OCT-2002
 31-JAN-2002
 Synthetic
 ABB80563
 ABB80566
 protease
 RESULT
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Modified-site

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "(s,s)allothreonyl carbonyl residue forming a keto-amide linkage with residue ?"
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #47.
 96.2%; Score 50; DB 5; Length 11; 100.0%; Pred. No. 0.002; 1ve 0; Mismatches 0; Indel8
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
11
/note= "C-terminal amide"
 Location/Qualifiers
 Brunck TK;
 ABB80567 standard; peptide; 11 AA
 Claim 17; Page 65; 69pp; English
 19-JUL-2001; 2001WO-US023169.
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
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 Conservative
 1 EEVVPXGMSYS 11
 11
 (CORV-) CORVAS INT INC
 Lim-Wilby M, Levy OE,
 BEVVPXGMSYS
 WPI; 2002-361643/39.
 Query Match
Best Local Similarity
Matches 11; Conserv
 Sequence 11 AA;
 WO200208251-A2
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002
 31-JAN-2002
 Synthetic
 ABB80567;
 protease.
 RESULT 7
 ABB8056
 g
 RXFXBXWXWXBXFFFFFFFFFFXBXWXWXWXRXRXRXRXRXRXRX
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ö
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have inventied activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C ^{\circ}
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #39.
 .
0
 Length 11;
 0; Indels
 96.2%; Score 50; DB 5;
100.0%; Pred. No. 0.002;
ive 0; Mismatches (
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 'note= "D-form residue"
 'note= "Oxymethionine"
 Location/Qualifiers
 Brunck TK;
 ABB80559 standard; peptide; 11 AA.
 Brunck TK;
 Claim 17; Page 65; 69pp; English.
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 Query Match
Best Local Similarity 100...
 (first entry)
 REVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 Levy OE,
 Levy OE,
 (CORV-) CORVAS INT INC
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39
 WPI; 2002-361643/39
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 Lim-Wilby M,
 31-JAN-2002.
 08-OCT-2002
 Synthetic.
 ABB80559
 protease
 RESULT 8
ABB80559
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Gaps

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English.

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The sequence represents a peptide compound of the invention having the peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Hepatitis C virus, HCV; serine protease, inhibitor, alpha-ketoamide, virucide.
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #6.
 ABB80526 standard; peptide; 11 AA.
 Claim 17; Page 64; 69pp; English
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 Claim 17; Page 65; 69pp;
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39.
 Query Match
Best Local Similarity
Matches 11; Conserv
 Misc-difference
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Novel peptide
activity usefu
 Novel peptide
activity usefu
 Key
Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 Synthetic
 ABB80526;
 protease
 protease
 RESULT 9
 ABB80526
 ਨੇ
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(first entry)

'note= "N-terminal acetyl"

Location/Qualifiers

/note= "C-terminal amide"

Brunck TK;

Levy OE,

notes "D-form residue" note= "D-form residue"

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 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have viruside activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hopatitis C virus
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "Leucyl carbonyl forming keto-amide linkage with
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #44.
 ö
 96.2%; Score 50; DB 5; Length 11;
100.0%; Pred. No. 0.002;
.ive 0; Mismatches 0; Indels
 /note= "N-terminal acetyl"
 /note= "C-terminal amide"
 Location/Qualifiers
 Ą.
 ŢĶ;
 Claim 17; Page 65; 69pp; English.
 11
 Brunck
 21-JUL-2000; 2000US-0220101P
 19-JUL-2001; 2001WO-US023169
 ABB80564 standard; peptide;
 (first entry)
 residue 7"
 Local Similarity 100.
 1 EEVVPXGMSYS 11
 H
 (CORV-) CORVAS INT INC
 Lim-Wilby M, Levy OE,
 1 EEVVPXGMSYS
 WPI; 2002-361643/39
 Sequence 11 AA;
 WO200208251-A2
 Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002
 Synthetic
 ABB80564;
 protease
 virucide
 Query Match
 Matches
 RESULT 10
 ABB80564

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 ö
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7^{\rm n}
 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
 virus
 Gaps
 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
```

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DB 5; here, 0.002; 0; Indels

Mismatches

Conservative

96.2%; Score 50; 100.0%; Pred. No. :ive 0; Mismatch

Sequence 11 AA;

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ABB80561 standard, peptide, 11 AA.
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Novel peptide
activity usefu
 Key
Modified-Bite
 Modified-site
 Lim-Wilby M,
 Modified-site
 Modified-site
 31-JAN-2002.
 08-OCT-2002
 Synthetic.
 Query Match
 protease
 ABB80561;
 virucide
 ð
 g
 ö
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV procease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 ö
 'note= "Alpha-propynyl-glycinyl-carbonyl residue forming i keto-amide linkage with residue 7"
 Virue
 Сарв
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #48
 ö
 .,
 Score 50; DB 5; Length 11;
Pred. No. 0.002;
0; Mismatches 0; Indels
 Length 11;
 'note= "N-terminal acetyl"
 11
/note= "C-terminal amide"
 Location/Qualifiers
 Brunck TK;
 ABB80568 standard, peptide, 11 AA.
96.2%; Scc.
100.0%; Pre
 Claim 17; Page 65; 69pp; English.
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 (first entry)
 Best Local Similarity 100.
Matches 11; Conservative
 Conservative
 1 EEVVPXGMSYS 11
 EEVVPXGMSYS 11
 (CORV-) CORVAS INT INC
 Levy OE,
 WPI; 2002-361643/39
 Similarity
 Sequence 11 AA;
 WO200208251-A2
 Modified-site
 Key
Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 11;
 Synthetic.
 protease.
 Query Match
 Query Match
Best Local S
Matches 11
 virucide.
 ABB80568;
 RESULT 11
ABB80568
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 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have furucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 'note= "Norvaly1 carbony1 forming keto-amide linkage with
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis \mathsf{C} .
Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
 ..
0
 Length 11;
 1; Indels
 Score 46; DB 5;
Pred. No. 0.013;
); Mismatches 1
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 'note= "D-form residue"
 note= "Oxymethionine"
 Location/Qualifiers
 ABB80524 standard; peptide; 11 AA.
 Brunck TK;
 Claim 17; Page 65; 69pp; English.
 88.5%;
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169
 residue 7"
 Best Local Similarity 90.8
Matches 10; Conservative
 11
 11
 Levy OE,
 (CORV-) CORVAS INT INC
 1 EEVVPXGMSYS
 EEVVPXGMDYS
 WPI; 2002-361643/39.
 ABB80524;
 RESULT 13
 ABB80524
ID ABBI
XX
AC ABBI
XX
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(first entry)

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 note= "Norvalyl carbonyl forming keto-amide linkage with
 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
 Length 11;
 1; Indels
 Score 46; DB 5;
Pred. No. 0.013;
); Mismatches
 note= "N-terminal acetyl"
 /note= "C-terminal amide"
 note= "D-form residue"
 Location/Qualifiers
 Ą
 Brunck TK;
 Claim 17; Page 64; 69pp; English.
 ABB80529 standard; peptide; 11
 88.5%;
90.9%;
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169
 residue 7"
 Best Local Similarity 90.9
Matches 10; Conservative
 1 EEVVPXGMSYS 11
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 Levy OE,
 EEVVPXGMDYS
 WPI; 2002-361643/39.
 (CORV-) CORVAS INT
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Novel peptide
activity usefu
 Key
Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 Synthetic
 Synthetic
 ABB80529
 virucide
 protease.
 Query Match
 RESULT 14
 ABB8052
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Gaps

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ô
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have artucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "Norvalyl carbonyl forming keto-amide linkage with
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C ^\circ
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8
 ;
0
 Score 46; DB 5; Length 11;
Pred. No. 0.013;
0; Mismatches 1; Indels
 'note= "N-terminal acetyl"
 'notes "N-terminal acetyl"
 /note= "C-terminal amide"
 note= "D-form residue"
 'note= "D-form residue"
 Location/Qualifiers
 Location/Qualifiers
 Brunck TK;
 ABB80528 standard; peptide; 11 AA
 Claim 17; Page 64; 69pp; English.
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 88.5%;
 (first entry)
 Ouery Match
Best Local Similarity 90.5
 11
 11
 Levy OE,
 (CORV-) CORVAS INT INC
 EEVVPXGMSYS
 EEVVPXGMDYS
 WPI; 2002-361643/39.
 Misc-difference
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Key
Modified-site
 Modified-site
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 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 Synthetic
 virucide.
 protease
 ABB80528
 ABB80528
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
 Query Match 88.5%; Score 46; DB 5; Length 11; Best Local Similarity 90.9%; Pred. No. 0.013; Matches 10; Conservative 0; Mismatches 1; Indels
 /note= "C-terminal amide"
 'note= "D-form residue"
 Lim-Wilby M, Levy OE, Brunck TK;
 Claim 17; Page 64; 69pp; English.
 19-JUL-2001; 2001WO-US023169.
 21-JUL-2000; 2000US-0220101P.
residue 7"
 (CORV-) CORVAS INT INC.
 WPI; 2002-361643/39.
 Misc-difference 8
 Sequence 11 AA;
 WO200208251-A2.
 Modified-site
 31-JAN-2002.
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1 EEVVPXGMSYS 11

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Gaps ö

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TYPE: PRT
ORGANISM: Enterococcus faecalis
 1 EEVVPXGMSYS 11
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 RESULT 2
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 Sequence 4, Appli
Sequence 3738, Appl
Sequence 73, Appl
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Sequence 2, Appli
Sequence 236, Ap
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Sequence 4, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 21, Appl
Sequence 22, Appl
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Match Length DB

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 Score
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Perfect score:
 Minimum DB
Maximum DB
 Database :
 Sequence:
 Searched:
 Run on:
 20224221098465442109846
 Result
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Sequence 3738, Application US/09134000C

Sequence 3738, Application US/09134000C

Patent No. 6617156

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: ENTEROCOCCUS FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ENTEROCOCCUS FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ENTEROCOCCUS FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: 1998-08-13

CURRENT APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR PILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SEQ ID NO 3738

LENGTH: 382
 US-09-408-020-4
US-09-408-020-4
US-09-408-020-4
Sequence 4, Application US/09408020
Sequence 4, Application US/09408020
Sequence 4, Application US/09408020
Sequence 4, Application US-080301
SERNEAL INFORMATION:
APPLICANT: Sendeman, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: UUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP. UOLA
CURRENT PELING DATE: 1999-09-29
FROM APPLICATION NUMBER: 60/102,294
PRIOR FILING DATE: 1998-09-29
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 123
SOGTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 3472
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 Score 38; DB 4; Length 3472;
Pred, No. 1.1e+02;
4; Mismatches 1; Indels
 US-08-465-772-6
US-08-246-772-6
US-08-246-361A-4
PCT-US93-05000-4
US-08-444-517-23
US-08-246-361A-5
US-08-246-361A-2
US-08-463-772-23
PCT-US9-05000-23
US-08-463-772-23
US-08-463-772-893A-8
 US-08-246-361A-19
 US-08-464-517-19
US-08-464-517-20
 ALIGNMENTS
 ; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-09-408-020-4
 Query Match 73.1%;
Best Local Similarity 54.5%;
Matches 6; Conservative
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2294 EDVIPRGISFS 2304
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```
Sequence 7885, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRESENCE: GTO99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7885
LENGTH: 1407
 us-uy-'bu-yeo.

j Sequence 2, Application US/09760946

j Sequence 2, Application US/09760946

j Patent No. 6608027

i GENBEAL INFORMATION:

APPLICANT: Cameron, Dale R.

APPLICANT: Generon, Dale R.

APPLICANT: Goldreau, Nathalie

APPLICANT: Halmos, Teddy

APPLICANT: Halmos, Teddy

APPLICANT: Halmos, Teddy

APPLICANT: Holmos, Teddy

APPLICANT: Holmos, Teddy

APPLICANT: Alines Procyclic Peptides Active Against the Hepatitis C Virus

TILE OF INVENTION: NUMBER: US/09/760,946

CURRENT FILING DATE: 2001-08-23

PRIOR PILING DATE: 2001-08-23

PRIOR PILING DATE: 1999-04-06

NUMBER OF SEQ ID NOS: 5

SEQ ID NO 2

LEASTHREE PATENTION OF SEQ ID NOS: 5

SEQ ID NO 2

LEASTHREE PATENTION OF SEQ ID NOS: 5

LEASTHREE PATENTE TERMET OF SEQ ID N
 ; OTHER INFORMATION: Substrate for recombinant HCV NS3 protease radiometric assay US-09-760-946-2
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 Gaps
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 Score 34; DB 4; Length 1407;
Pred. No. 2.5e+02;
2; Mismatches 1; Indels
 Score 33; DB 4; Length 12;
Pred. No. 1.7;
 2; Indels
 4; Mismatches
 Sequence 3, Application US/09760946
Patent No. 6608027
GENERAL INFORMATION:
APPLICANT: Fgantrizos, Youla S.
) ORGANISM: Acinetobacter baumannii
US-09-328-352-7885
 APPLICANT: Cameron, Dale R. APPLICANT: Faucher, Anne-Marie APPLICANT: Ghiro, Elise
 TYPE: PRT
ORGANISM: Artificial Sequence
 63.5%;
 Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
 Query Match
Best Local Similarity 45.5
Matches 5, Conservative
 1 DDIVPCSMSYT 11
 1 EEVVPXGMSYS 11
 596 EVVPEGLSF 604
 2 EVVPXGMSY 10
 RESULT 7
US-09-760-946-3
 US-09-760-946-2
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 GENERAL INFORMATION:
APPLICANT: GARY L. BRECON et al.
TITLE DE INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE DE INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
SEQ ID NOS: 3840
SEQ ID NOS: 3840
LENGTH: 1191
 APPLICANT: Strabala, Timothy
APPLICANT: Strabala,
APPLICANT: Strabala,
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: Compositions in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT PILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PSELSEQ for Windows Version 3.0
SEQ ID NO 73
LENGTH: 947
 ; FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (327)...(328)

COTHER INFORMATION: Amino acids 327 & 328 are Xaa wherein Xaa = any amino acid.
US-09-134-000C-3738
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 Score 34; DB 4; Length 1191;
Pred. No. 2e+02;
3; Mismatches 1; Indel8
 Length 947;
 Query Match 69.2%; Score 36; DB 4; Length 382; Best Local Similarity 66.7%; Pred. No. 22; Matches 5; Conservative 2; Mismatches 1; Indels
 1; Indels
 Score 34; DB 4; 1
Pred. No. 1.6e+02;
2; Mismatches 1;
 US-09-540-236-2902
; Sequence 2902, Application US/09540236
; Patent No. 6673910
 Sequence 73, Application US/09228986 Patent No. 6359198
 65.4%;
55.6%;
 Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
 Query Match
Best Local Similarity 55.6
Matches 5; Conservative
 ; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2902
 |::| ||:|
783 EILPVGMAY 791
 , TYPE: PRT
, ORGANISM: Pinus radiata
US-09-228-986-73
 332 LIPEGMSYS 340
 686 VMPSGISYS 694
 2 EVVPXGMSY 10
 3 VVPXGMSYS 11
 3 VVPXGMSYS 11
 GENERAL INFORMATION:
 RESULT 5
US-09-328-352-7885
 US-09-228-986-73
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Gaps

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63.5%; Score 33; DB 3; Length 45; 60.0%; Pred. No. 7.8; tive 1; Mismatches 3; Indels
 Query Match 63.5%; Score 33; DB 2; Length 45; Best Local Similarity 60.0%; Pred. No. 7.8; Matches 6; Conservative 1; Mismatches 3; Indels
 US-08-811-355A-236

18-08-811-355A-236

Sequence 236, Application US/08871355A

Patent No. 6015669

Patent No. 6015669

TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501

CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabat

STREET: 2000 One Atlantic Center
STREET: 30309-3450

CONTRY: USA

ITLE 30309-3450

CONTRY: USA

SOFTWARE: PRADALLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEADALLE FORM:
MEDIUM TYPE: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/871,355A

FILING DATE: 09-JUN-1997

CLASSIFICATION NUMBER: BCT/GB95/02875

FILING DATE: 1.1-DEC-1995

CLASSIFICATION NUMBER: 31.284

REFERENCE/DOCKET NUMBER: RPMS 101 CON
TELEROMONICATION INFORMATION:
 TELEPAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
 LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
 45 amino acids
 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
SEQUENCE CHARACTERISTICS
 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-637-759B-236
 single
 1 EEVVPXGMSY 10
 1 EEVVPXGMSY 10
 1 EEISPLGWSY 10
 1 EEISPLGWSY 10
 TYPE: amino acid
STRANDEDNESS: si
 linear
 ; TOPOLOGY: li:
; MOLECULE TYPE:
; HYPOTHETICAL: luS-08-871-355A-236
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 APPLICANT: Halmos, Teddy
APPLICANT: Linas-Brunet, Montse
APPLICANT: Linas-Brunet, Montse
TILLE OF INVENTION: Macroyclic Peptides Active Against the Hepatitis C Virus
FILE REFERENCE: 13/076-1-C1
CURRENT APPLICATION NUMBER: US/09/760,946
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US 09/542,675
PRIOR FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PARENTIN Version 3.1
SEQ ID NO S: 5
LENGTH: 12
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 Gaps
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 CHER INFORMATION: Tracer for NS3 protease assay
NAME/KEY: MOD_RES
LOCATION: (1)
COTHER INFORMATION: Asp at position 1 is biotinylated
NAME/KEY: MOD_RES
LOCATION: (10)
COTHER INFORMATION: Tyr at position 10 is iodinated with I-125
US-09-760-946-3
 Score 33, DB 4; Length 12;
Pred. No. 1.7;
4; Mismatches 2; Indels
 STATE: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
CONTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIDE
COMPUTER: BM PC COMPATION
SUSTING SYSTEM: 03-MAY-1996
CLASSITICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSITICATION: 435
FILING DATE: 11-DEC-1995
FILING DATE: 11-DEC-1995
CLASSITICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabet, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ 1D NO: 236:
 Sequence 236, Application US/08637759B
Patent No. 5876931
GENERAL INFORMATION:
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
 63.5%;
 TYPE: PRT
ORGANISM: Artificial Sequence
Goudreau, Nathalie
 Query Match
Best Local Similarity 45.5
Matches 5; Conservative
 1 EEVVPXGMSYS 11
 1 DDIVPCSMSYT 11
 US-08-637-759B-236
 FEATURE:
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Gaps

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Sequence 66, Application US/09357952

Patent No. 6248904

GENERAL INFORMATION:

APPLICANT: Zhang, Han-Zhong

APPLICANT: Zhang, Han-Zhong

APPLICANT: Zhang, Han-Zhong

APPLICANT: Drewe, John A.

TITLE OF INVENTION: No. 6248904e1 Fluorescence Dyes and Their Applications for Whole

TITLE OF INVENTION: Pluorescence Screening Assays for Caspases, Peptidases,

TITLE OF INVENTION: Other Enzymes and the Use Thereof

FILE REFERENCE: 1735.0030001

CURRENT APPLICATION NUMBER: US/09/357,952

CURRENT FILING DATE: 1999-07-21

CURRENT APPLICATION NUMBER: US 60/093,642
 0; Gaps
 ö
 APPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA; ; WERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH, ; LENA; HELDIN, CARL-HENRIK

TITLE OF INVENTIONS: 150LATED NUCLEOTIDE SEQUENCE EXPRESSING ; HUMAN TRANSFORMING GROWTH PACTOR-BETA1-BINDING PROTEIN

NUMBER OF SEQUENCES: 53

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/487,343

FILING DATE: 27-FEE-1990
 JERNATE TANZAKI, TETSUTO,OLOFSSON, ANDERS;MOREN, ANITA;
;WERNSTEDT, CHRISTER;HELLMAN, ULF;MIYAZONO, KOHEI;CLAESSON-WELSH,
;LENA;HELDIN, CARL-HERNEN,
;TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
;HUMAN TRANSFORMING GROWTH PACTOR-BETA1-BINDING PROTEIN
;NUPHER OF SEQUENCES: 53
CURRENT APPLICATION DATA:
;APPLICATION NUBBER: US/07/487,343
FILING DATE: 27-FEB-1990
 63.5%; Score 33; DB 6; Length 1394; 45.5%; Pred. No. 3.9e+02; Anismatches 3; Indels
 63.5%; Score 33; DB 6; Length 410; 45.5%; Pred. No. 97;
 3; Indels
 3; Indels
 3; Mismatches
 3; Mismatches
 Query Match
Best Local Similarity 45.5
Matches 5; Conservative
 5; Conservative
 Local Similarity 45.5
 399 KEICPGGMGYT 409
 399 KEICPGGMGYT 409
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52 KEICPGGMGYT 62
 1 EEVVPXGMSYS 11
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 1 EEVVPXGMSYS 11
 Patent No. 5177197
 5177197
 LENGTH: 1394
 LENGTH: 410
 US-09-357-952-66
 SEQ ID NO:30:
 Query Match
 SEQ ID NO:1:
 RESULT 13
5177197-30
;Patent No.
 5177197-30
 Matches
 Matches
 5177197-1
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 APPLICANT: KANZAKI, TETSUTO, OLOFSSON, ANDERS, MOREN, ANITA;
;WERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH,
;LENA, HELDIN, CARL-HENRIK
; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
; HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
; NUMBER OF SEQUENCES: 53
; CURRENT APPLICATION DATA;
; APPLICATION NUMBER: US/07/487,343
; FILING DATE: 27-FEB-1990
 Query Match 63.5%; Score 33; DB 4; Length 45; Best Local Similarity 60.0%; Pred. No. 7.8; Matches 6; Conservative 1; Mismatches 3; Indels
 Score 33; DB 6; Length 65;
Pred. No. 12;
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,945
 Sequence 236, Application US/09201945
; Patent No. 6342215
; Patent No. 6342215
; Patent INPORMATION;
APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
ADDRESSER: Patrea 1. Pabst
; STREET: 1200 One Atlantic Center
; STREET: 1201 West Peachtree Street
 STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 RPMS 101
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/637,759
 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabet, Patrea L.
REGISTRATION NUMBER: 31,284
REPERFOR/POCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
 63.5%;
 LENGTH: 45 amino acids
 HYPOTHETICAL: NO
 single
 1 EEVVPXGMSY 10
 1 BEISPLGWSY 10
 TYPE: amino acid
STRANDEDNESS: si
 linear
 Query Match
Best Local Similarity
 FILING DATE:
CLASSIFICATION:
 CITY: Atlanta
STATE: Georgia
 MOLECULE TYPE:
 ;Patent No. 5177197
RESULT 10
US-09-201-945-236
 US-09-201-945-236
 LENGTH: 65
 SEQ ID NO:51:
 RESULT 11
5177197-51
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MENULI 159
Sequence 66, Application US/09521650
Sequence 66, Application US/09521650
GENERAL INFORMATION:
APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui Xiong
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Use Thereof
TITLE OF INVENTION: Use Thereof
TITLE OF INVENTION: Use Thereof
TITLE OF INVENTION WUMBER: US/09/521,650
CURRENT FILING DATE: 1998-10-09
EARLIER APPLICATION WUMBER: US 60/61,582
EARLIER APPLICATION WUMBER: US 60/61,582
EARLIER FILING DATE: 1997-10-10
EARLIER FILING DATE: 1998-10-09
EARLIER FILING DATE: 1998-10-03
NUMBER OF SEQ ID NOS: 142
SECTIARE PLANCE PATENTING VET. 2.0
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 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Synthetic
OTHER INFORMATION: Peptide
US-09-357-952-66
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 Query Match 61.5%; Score 32; DB 3; Length 10; Best Local Similarity 50.0%; Pred. No. 2.3; Matches 5; Conservative 3; Mismatches 2; Indels
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EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 66
LENGTH: 10
 TYPE: PRT
ORGANISM: Artificial Sequence
 Best Local Similarity 50.0
Matches 5; Conservative
 1 DDIVPCSMSY 10
 1 EEVVPXGMSY 10
 US-09-521-650-66
 Query Match
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2; Indels

3; Mismatches

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Search completed: June 3, 2004, 12:03:07 Job time: 11.8 secs

Page 1

us-09-909-164-9.rapb

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Query Match
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 June 3, 2004, 11:57:42; Search time 33.7333 Seconds (without alignments) 91.741 Million cell updates/sec
 Sequence 9, A
Sequence 10,
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Sequence 50,
 Sequence 11,
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 Sequence 1
Sequence 1
Sequence
 Sequence
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 US-09-909-164-5

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US-09-909-164-47

US-09-909-164-47

US-09-909-164-50

US-09-909-164-51

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US-09-909-164-51

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US-09-909-164-13
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 1155919 seqs, 281338677 residues
 SUMMARIES
 Published_Applications_AA:*
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

 protein search, using sw model

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Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 US-09-909-164-9
52
1 EEVVPXGMSYS 11
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Match Length DB
 Score
 Title:
Perfect score:
 Scoring table:
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 Database :
 Sequence:
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 Run on:
 Result
No.
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| Appl        | יקקא.         | Appi          | App1          | App]          | Appl          | Appl          | Appl          | Appl          | Appl         | Appl       | Appl      | Appl          | Appl         | Appl         | Appl         | Appl       | Appl         | Appl       | Appl         | Appl     | Appl         | Appl     | App1          | Appl          | Appl     | Appl         | Appl          | App1             | Appl          |
|-------------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|--------------|------------|-----------|---------------|--------------|--------------|--------------|------------|--------------|------------|--------------|----------|--------------|----------|---------------|---------------|----------|--------------|---------------|------------------|---------------|
| , ,         | 2 0           | 73,           | 24,           | 28,           | 29,           | 33,           | 36,           | 37,           | 43,          | 14,        | 22,       | 26,           | 27,          | 61,          | 62,          | 21,        | 22,          | 31,        | 32,          | 35,      | 40,          | 41,      | 45,           | 46,           | 30,      | 34,          | 38,           | 39,              | 42,           |
| Sequence    | Sednence      | Sednence      | Sequence       Sequence   | Seguence  | Sequence      | Sequence     | Sequence     | Sequence     | Sequence   | Seguence     | Seguence   | Seguence     | Sequence | Sequence     | Seguence | Seguence      | Sequence      | Seguence | Sequence     | Sequence      | Sequence         | Seguence      |
| 09-909-164- | -09-909-164-2 | -09-909-164-2 | -09-909-164-2 | -09-909-164-2 | -09-909-164-2 | -09-909-164-3 | -09-909-164-3 | -09-909-164-3 | -09-909-164- | -909-164-I | -09-909-1 | -09-909-164-2 | -09-909-164- | -09-909-164- | -09-909-164- | 9-909-164- | -09-909-164- | -09-909-16 | -09-909-164- | -164-    | -09-909-164- | -006-60- | -09-909-164-4 | -09-909-164-4 | -09-     | -09-909-164- | -09-909-164-3 | US-09-909-164-39 | -09-909-164-4 |
| 21          | 12            | 12            | 12            | 12            | 12            | 12            | 12            | 12            | 12           | 12         | 12        | 12            | 12           | 12           | 12           | 12         | 12           | 12         | 12           | 12       | 12           | 12       | 12            | 12            | 12       | 12           | 12            | 12               | 12            |
| r4 :        | H             | 급             | 11            | 11            | 11            | 11            | 11            | r<br>r        | 17           | 11         | 17        | 11            | ᅼ            | 텀            | 11           | 11         | 11           | 11         | 11           | Ħ        | 11           | 11       | 11            | 11            | 11       | 11           | 11            | 1                | 11            |
| 45 86.5     | 98.           | 5 86.         | . 986.        | 84.           | 4 84.         | 4 84.         | 84.           | 4 84.         | 4 84.        | 2 80.      | 1 78.     | 1 78.         | 1 78.        | 1 78.        | 1 78.        | 0 76.      | 0 76         | 7          | 0 76.        | 0 76.    | 0 76.        | 0 76.    | .97 0         | 0 76.         | 9 75.    | 9 75.        | 9 75.         | 9 75.            | 9 75.         |
| 16          | 17            | 18            | 19            | 20            | 21            | 22            | 23            | 2 4           | 25           | 56         | 27        | 28            | 29           | 30           | 31           | 32         | 33           | 34         | 35           | 36       | 37           | 38       | 39            | 40            | 41       | 42           | 43            | 44               | 45            |

## ALIGNMENTS

```
Sequence 5, Application US/0990164

Publication No. US20020068702A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPRENCE: INTO 1192-105
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT PILING DATE: 2003-03-25
FRIOR APPLICATION NUMBER: 60/220,101
FRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
IENGTH: 11
 FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOS_CEATURE
 LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
 TYPE: PRT ORGANISM: artificial sequence
 NAME/KEY: MOD RES
LOCATION: (11)...(11)
COTHER INFORMATION: AMIDATION
US-09-909-164-5
```

Length 11;

DB 12;

96.2%; Score 50;

```
APPLICANT: Corvae International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
URRENT FILING DATE: 2003-03-25
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SSQ ID NO 10
LENGTH: 11
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 OTHER INFORMATION: 11-mer synthesized according to example 1
 OTHER INFORMATION: 11-mer synthesized according to example 1 FEATURE:
 Length 11;
 th 96.2%; Score 50; DB 12; Similarity 100.0%; Pred. No. 0.0014; 11; Conservative 0; Mismatches 0.
 US-09-909-164-10
; Sequence 10, Application US/09909164
; Publication No. US/0020068702A1
; GENERAL INFORMATION:
 LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
 FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
 DOCATION: (8) (8) OTHER INFORMATION: D-amino acid
 NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OCHER INFORMATION: ACSTYLATION
PEATURE:
 SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 11
 TYPE: PRT
ORGANISM: artificial sequence
 TYPE: PRT
ORGANISM: artificial sequence
 NAME/KEY: MOD RES LOCATION: (11\overline{1})...(11) OTHER INFORMATION: AMIDATION
 LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 1 BEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
NUMBER OF SEQ ID NOS: 62
 NAME/KEY: MISC FEATURE LOCATION: (6). (6)
 NAME/KEY: MISC_FEATURE LOCATION: (8)...(9)
 NAME/KEY: MISC FEATURE
 Best Local Similarity
Matches 11; Conserva
 NAME/KEY: MOD RES
 Query Match
 g
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 Sequence 9, Application US/09909164

Publication No. US20020068702A1

GENERAL INPORMATION:
APPLICANT: Cim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERENCE: INDIA192-US
CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT FILING DATE: 2003-03-25
 APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
URRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 11
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 FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
 96.2%; Score 50; DB 12; Length 11; 100.0%; Pred. No. 0.0014; tive 0; Mismatches 0; Indels
Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 11; Conservative 0; Mismatches 0; Indels
 PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
 Sequence 6, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
 NAME/KEY: MISC FEATURE LOCATION: (6). (6) OTHER INFORMATION: norvaline-(CO)
 NAME/KEY: MISC FEATURE
LOCATION: (9). (9)
OTHER INFORMATION: D-amino acid
 NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
 TYPE: PRT
ORGANISM: artificial sequence
 NAME/KEY: MOD RES
LOCATION: (11)...(11)
CTHER INFORMATION: AMIDATION
US-09-909-164-6
 Query Match
Best Local Similarity 100.
Matches 11; Conservative
 1 BEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 1 EEVVEXGMSYS 11
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Sequence 10 Sequen
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 FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11)..(1)
OTHER INFORMATION: AMIDATION
 FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
 Query Match 96.2%; Score 50; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 11; Conservative 0; Mismatches 0; Indels
 Query Match 96.2%; Score 50; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 11; Conservative 0; Mismatches 0; Indels
 ; LOCATION: (6). (6); OTHER INFORMATION: norleacine-(CO)
 LOCATION: (6).7(6)
CIHER INFORMATION: leucine-(CO)
US-09-909-164-48
 NAME/KEY: MOD_RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 48
LENGTH: 11
 TYPE: PRT ORGANISM: artificial sequence
 TYPE: PRT ORGANISM: artificial sequence
 NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 1 REVVPXGMSYS 11
 NAME/KEY: MISC_FEATURE
 NAME/KEY: MISC_FEATURE
 Sequence 47, Application US/09909164

Sequence 47, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Corves International, Inc.

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: IN01192-US

CURRENT APPLICATION NUMBER: 05/9999,164

CURRENT FILING DATE: 2003-03-25

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR PLING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQ ID NO 47
 APPLICANT: Corvae International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Dayle E
APPLICANT: Brunck, DEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR PPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
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 OTHER INFORMATION: 11-mer synthesized according to example 1 FRATURE:
 96.2%; Score 50; DB 12; Length 11; 100.0%; Pred. No. 0.0014; tive 0; Mismatches 0; Indels
 Query Match 96.2%; Score 50; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 11; Conservative 0; Mismatches 0; Indels
 Sequence 48, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
 ; OTHER INFORMATION: D-amino acids US-09-909-164-10
 NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
PEATURE:
 NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: valine-(CO)
US-09-909-164-47
 TYPE: PRT
ORGANISM: artificial sequence
 NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 Query Match 96.2
Best Local Similarity 100.
Matches 11; Conservative
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 -09-909-164-48
 LENGTH: 11
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RESULT 11
US-05-909-164-8
Sequence 8, Application US/09909164
; Publication No. US20020068702A1
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 OTHER
FEATURE:
NAME/KEY: MOD RES
 RESULT 10
US-09-909-164-52
 g
 ઠે
 Sequence 51, Application US/09909164

| Publication No. US20020068702A1
| GENERAL INFORMATION:
| APPLICANT: Orves International, Inc.
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Levy, Odile B
| PUBLICANT: Levy, Odile B
| TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
| TITLE OF INVENTION NOVER: US/09/909,164
| CURRENT APPLICATION NUMBER: US/09/909,164
| CURRENT RILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 51
 Sequence 50, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEDATITIS C
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SERGID NOS: 50
LENGTH: 11
 TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
 OTHER INFORMATION: 11-mer synthesized according to example 1
 Query Match 96.2%; Score 50; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 11; Conservative 0; Mismatches 0; Indels
 NAME/KEY: MISC FEATURE LOCATION: (6).7(6)
OTHER INFORMATION: 2-amino-butyric acid-(CO)
 NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
 TYPE: PRT
ORGANISM: artificial sequence
 FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
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 US-09-909-164-50
 US-09-909-164-51
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 OTHER INFORMATION: 11-mer synthesized according to example 1
 Query Match 96.2%; Score 50; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 11; Conservative 0; Mismatches 0; Indels
 Query Match 96.2%; Score 50; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 11; Conservative 0; Mismatches 0; Indels
 NAME/KEY: MISC_FRATURE

// DCATION: (6)...(6)
// OTHER INFORMATION: (8,8)-allothreonine-(CO)
// OS-09-909-164-51
 FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (6)...(6)

OTHER INFORMATION: propynyl glycine-(CO)
US-09-909-164-52
NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 NAME/KEY: MOD RES
LOCATION: (1) (1)
OTHER INFORMATION: ACETYLATION
 TYPE: PRT
ORGANISM: artificial sequence
 NAME/KEY: MOD RES
LOCATION: (11)...(11)
OOTHER INFORMATION: AMIDATION
FEATURE:
 LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
```

```
Sequence 13, Application US/09009164

| Sequence 13, Application W. US20020068702A1
| Publication No. US20020068702A1
| Publication No. US20020068702A1
| Publication No. US20020068702A1
| APPLICANT: Lim-Wilby, Marguerita
| TILL OF INVENTION NUMBER: US/09/909,164
| CURRENT APPLICATION NUMBER: 60/220,101
| PRIOR FILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 13
| Lim-Grafia 11
| Lim-Grafia 11
| Lim-Grafia 11
| Lim-Grafia 11
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 0; Gaps
 Gaps
 OTHER INFORMATION: 11-mer synthesized according to example 1
 Score 46; DB 12; Length 11;
Pred. No. 0.0091;
0; Mismatches 1; Indels
 Score 46; DB 12; Length 11; Pred. No. 0.0091; 0; Mismatches 1; Indels
DOCATION: (11)
COCATION: (11)
COCATION: (11)
COTHER INFORMATION: AMIDATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
COTHER INFORMATION: norvaline-(CO)
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (8)...(8)
COTHER INFORMATION: 0-amino acid
US-09-909-164-12
 NAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
 LOCATION: (8).7(9)
CTHER INFORMATION: D-amino acids
US-09-909-164-13
 NAME/KEY: MOD RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)... (11)
OTHER INFORMATION: AMIDATION
 TYPE: PRT ORGANISM: artificial sequence
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
 1 EEVVPXGMSYS 11
 1 EEVVPXGMDYS 11
 1 EEVVPXGMSYS 11
 1 EEVVPXGMDYS 11
 NAME/KEY: MISC FEATURE
 FEATURE:
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APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Oddile E
APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR PRILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NOS: 82
LENGTH: 11
 US-09-909-164-12
US-09-909-164-12
Sequence 12, Application US/09909164
Publication No US20020068702A1
Sequence 12, Application No US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TILE REFERENCE: INO192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
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 TYPE: PRT ORGANISM: artificial sequence FEATURE: CONTINUE ORGANISM: OTHER INFORMATION: 11-mer synthesized according to example 1
 PEATURE:
11-mer synthesized according to example 1
PEATURE:
 Query Match

88.5%; Score 46; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 1; Indels
 LOCATION: (6). . . (6)
OTHER INFORMATION: norvaline-(CO)
 FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (9) .. (9)
OTHER INFORMATION: D-amino acid
 NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MISC.FEATURE
 NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
 NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 11
 TYPE: PRT
ORGANISM: artificial sequence
 , COLHER INFORMATION: AMIDATION US-09-909-164-8
 1 EEVVPXGMDYS 11
 FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)..(1
```

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;
 Query Match 86.5%; Score 45; DB 12; Length 11; Best Local Similarity 90.9%; Pred. No. 0.015; Matches 10; Conservative 0; Mismatches 1; Indels
 Search completed: June 3, 2004, 12:57:15
Job time: 33.7333 secs
 FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
 FRATURE:
NAME/KRY: MISC FEATURE
COCATION: (8). (8)
CTHER INFORMATION: D-amino acid
US-09-909-164-11
OTHER INFORMATION: ACETYLATION PEATURE:
 NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 1 EEVVPXGMSYS 11
 1 EEVVPXGMHYS 11
 ઠે
 셤
 Sequence 7, Application US/0990164

Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Levy, Odlie E

APPLICANT: Lovy, Odlie E

APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT FILING DATE: 2003-03-25

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin Version 3.1

SEQ ID NO 7

LENGTH: 11
 APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEFATITIS C
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEFATITIS C
CURRENT APPLICATION NUMBER: 05/220,101
PRIOR FILING DATE: 2003-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 11
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 TYPE: PRT
ONCANISM: artificial sequence
FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
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 TYPE: PRT ORGANISM: artificial sequence CREATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
 86.5%; Score 45; DB 12; Length 11; 90.9%; Pred. No. 0.015;
 1, Indels
 5.09-909-164-11
Sequence 11, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
 FEATURE:
NAME/KEXY: MISC_PEATURE
LOCATION: (9)..(9)
OTHER INFORMATION: D-amino acid
 NAME/KEY: MOD_RES

DOCATION: (11)...(11)

OTHER INFORMATION: AMIDATION

US-09-909-164-7
 Best Local Similarity 90.8
 1 EEVVPXGMSYS 11
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 Query Match
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 3, 2004, 11:35:47 ; Search time 9 Seconds (without alignments) 117.567 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 283366
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 283366 seqs, 96191526 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - protein search, using sw model
 T31308
T4391308
T4391106
T4391106
T4391110
T4391110
T4391110
T4391110
T4391110
T4476119
T4476110
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 US-09-909-164-9
52
1 EEVVPXGMSYS 11
 Query
Match Length DB
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1: Dir1:*
2: Dir2:*
3: Dir3:*
4: Dir4:*
 Title:
Perfect score:
 Scoring table:
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 Database :
 Sequence:
 Searched:
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 Result
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Length 3472;<br>1; Indels 0; Gaps                                       | (Schizosaccharomyces pombe) Dec-1999 #text_change 03-Dec-1999 andream, M.A.; Barrell, B.G. er 1999 EMBL/DDBJ d C869                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 2; Length 840;<br>1; Indels 0; Gaps            |
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--------------------------------------------------------------------------------------------|------------------------------------------------|
| A38977<br>A4882<br>B72481<br>B72481<br>B72481<br>B72481<br>B72481<br>A42822<br>B7222<br>B72925<br>B72925<br>B72925<br>B72925<br>B72925<br>B72925<br>B73925<br>B73925<br>B73925<br>B73925<br>B73977                                                                                                                                                             | chaeum symision 11-J<br>ision 11-J<br>ston, C.M.<br>8<br>chromosom<br>98422450;<br>from GB/E<br>; NID:9359<br>sum hypoth                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Score 38; DB<br>Pred. No. 60;<br>4; Mismatches                             | ast<br>103-:<br>Raj<br>vemb<br>1GB/:<br>ON:CA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Score 37; DB<br>Pred. No. 21;<br>1; Mismatches |
| 115<br>1418<br>1418<br>1418<br>152<br>162<br>163<br>163<br>163<br>163<br>163<br>163<br>163<br>163<br>163<br>163                                                                                                                                                                                                                                                | an in series of the series of  | 73.1%;<br>y 54.5%;<br>rvative<br>SYS 11<br> : <br>SFS 2304                 | RESULT 2 T39116 probable sulfate permease - fission year cipeties: Schizosaccharomyces pombe (jbate: 03-bec-1999 #sequence_revision C; Accession: T39116 A; Accession: T39116 A; Reference number: 221829 A; Reference number: 221829 A; Residues: preliminary; translated from A; Residues: 1-840 c-HUN>A; Residues: 1-840 c-HUN>A; Residues: 1-840 c-HUN>A; Reparimental source: strain 972h-; cc; Generics: SDB: SPAC869.05c A; Map position: 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 71.2%;<br>larity 77.8%;<br>Conservative        |
| 933<br>944<br>944<br>944<br>944<br>944<br>944<br>944<br>944<br>944                                                                                                                                                                                                                                                                                             | 367% protein narchaeum syn n-2000 #seguu 173108 173108 180, 5003-55 mic analysis number: 22099-13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 13108 1 | Similarity<br>6; Conservat<br>1 EEVVPXGMGYS<br> : :  : : <br>4 EDVIPRGISFS | te perme<br>lizosacch<br>1-1999 #8<br>33916<br>ee S. S.<br>he EMBL<br>mber: Z2<br>3916 mber: Z2<br>101ary;<br>e: DNA<br>e: DNA<br>source: EUNA<br>source: EUNA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | imi<br>i                                       |
|                                                                                                                                                                                                                                                                                                                                                                | RESULT 1 T31308 hypotherical 3 hypotherical 3 C, Date: 11-Jan C, Accession: T R, Schleper. C. R, Schleper. C. R, Satteriol. A, Fitle: Genom A, Reference nu A, Rocession: T A, Status: prel A, Rocession: C, A, Residues: 1-A, Residues: 1-A, Coss-refere C, Superfamily:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Query Match Best Local S Matches 6  7 1                                    | le sulfa<br>lies. Sch<br>lies. Sch<br>lies. 33-Dec<br>ssion: T<br>C.; Av<br>ted to t<br>rence nu<br>ssion: I<br>selon: I<br>dues: 1-<br>dues: 1-<br>serfere<br>rrimental<br>is-refere<br>rrimental<br>is-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-refere<br>ris-r | Query Match<br>Best Local S<br>Matches         |
| ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩                                                                                                                                                                                                                                                                                                                          | RESULT<br>131308<br>hygoco<br>Cyboco<br>Cyboco<br>Cyboco<br>Ryboco<br>Ryboco<br>Ayrefe<br>Ayrefe<br>Ayrefe<br>Ayrefe<br>Ayrefe<br>Ayrefe<br>Ayrefe<br>Ayrefe<br>Ayrefe<br>Ayrefe                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Quer<br>Best<br>Matc<br>Qy<br>Db                                           | RESULT<br>T39116<br>probab<br>C; Spec<br>C; Spec<br>C; Acce<br>R; Acce<br>A; Refe<br>A; Acce<br>A; Cros<br>A; Expe<br>C; Gene<br>A; Gene<br>A; Gene                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Quer<br>Best<br>Matc                           |

3 VVPXGMSYS 11

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Gaps

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residuee: 1.425 <WIL>
A;Residuee: 1.425 <WIL>
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A;Reperimental source: clone R10D12
C;Genetics:
 hypothetical protein R10D12.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Dates: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24111
R;Percy, C.
 zinc finger protein AT-BP2 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Species: 29-Jan-1998 #sequence_revision 06-Peb-1998 #text_change 20-Sep-1999
C;Accession: 225233; I78623; I78623; I78623; I78623; I78633; I786335;
 C;Species: Lycopersicon esculentum (tomato)
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
C;Accession: 557810
 Finiligan, S.B.; Gasser, C.S.
Plant Mol. Biol. 28, 691-711, 1995
A;Title: Mature and regulation of pistil-expressed genes in tomato.
A;Reference number: S57808; MUID:95375233; PMID:7647301
A;Accession: S57810
A;Accession: S57810
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residuae: 1-225 AMIL.
A;Cross-references: EMBL:U20592; NID:9924625; PIDN:AAA80497.1; PID:9924626
C;Superfamily: plant Kunitz-type proteinase inhibitor
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DB 2; Length 1498;
63;
 Length 225;
 Indels
 2; Indels
 hypothetical protein precursor (clone TPP11) - tomato
 Score 35; DB 2;
Pred. No. 13;
3; Mismatches 2
 Score 35; DB 2;
Pred. No. 26;
3; Mismatches
 submitted to the EMBL Data Library, October 1996
 Score 36;
Pred. No. 6
 A; Map position: 5
A; Introns: 23/3; 56/3; 113/3; 257/2
 67.3%;
 69.2%;
 Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
 Query Match
Best Local Similarity 50.0
Matches 5; Conservative
 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
 1276 EQKIPMGMSY 1285
 : | | | | :|:
32 DEVVPNGKTYA 42
 1 REVVPXGMSYS 11
 335 ÉQIVÈGGLOY 344
 1 EEVVPXGMSY 10
 1 EEVVPXGMSY 10
 A;Reference number: Z19842
A;Accession: T24111
 A, Gene: CESP:R10D12.10
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 VI protein - tobacco yellow dwarf virus (strain Australia)
C;Species: tobacco yellow dwarf virus
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Accession: A42422
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
Virology 187, 633-642, 1992
A;Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yellogy RACCESSION: A42452; MUID:92188538; PMID:1546458
 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo A;Reference number: A96900; MUID:21359325; PMID:21359325
 DNA segregation Arpase, FtsK/SpoiliB family, YUKA B. subtilis ortholog [imported] - Clos C;Species: Clostridium acetobutylicum C;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 sulfate permease - fission yeast (Schizosaccharomyces pombe)
G.Species: Schizosaccharomyces pombe
G.Species: Schizosaccharomyces pombe
C.Species: Schizosaccharomyces pombe
C.Space: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C.Accession: T40413
M.A.; Bajandream, M.A.; Barrall, B.G.; Jimenez Martinez, J.
A.Reference number: Z21926
A.Reference number: Z21926
A.Stactus: preliminary; translated from GB/EWBL/DDBJ
A.Molecule type: DNA
A.Molecule type: DNA
A.Residuas: 1-877 < ALYN.
A.Residu
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 A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Reaidues: 1-1498 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK81629.1; PID:g15026814; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
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 A; Cross-references: GB: M81103; NID: 9335283; PIDN: AAA47947.1; PID: 9335284
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 71.2%; Score 37; DB 2; Length 877; 77.8%; Pred. No. 22; tive 1; Mismatches 1; Indels
 Query Match

69.2%; Score 36; DB 2; Length 102;
Best Local Similarity 60.0%; Pred. No. 3.5;
Matches 6; Conservative 3; Mismatches 1; Indels
 Query Match
Best Local Similarity 77.00
7, Conservative
 2 EVVPXGMSYS 11
 :||| |::||
7 QVVPSGINYS 16
 148 VVPQGMSYA 156
 3 VVPXGMSYS 11
 A; Molecule type: DNA
A; Residues: 1-102 <MOR>
 C,Genetics:
A,Gene: SPDB:SPBC3H7.02
 Accession: B97355
 A, Map position: 2
 Gene: CAC3709
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Gaps

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Query Match 67.3 Best Local Similarity 66.7 Matches 6; Conservative

376 VVPAGLTYS 384

3 VVPXGMSYS 11

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Riklenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson Riklenk, H.P.; Clayton, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Ajstatus: preliminary
Ajmolecule type: mRNA
Ajmolecule type: mRNA
Ajrossidues: 1-2717 <FMN>
Ajrossidues: 1-2717 <FMN>
Ajrossidues: LeClair, K.P.; Singh, H.; Sharp, P.A.
Ribaldwin Jr., A.S.; LeClair, K.P.; Singh, H.; Sharp, P.A.
Mol. Cell. Biol. 10, 1406-1414, 1990
Ajritle: A large protein containing zinc finger domains binds to related sequence eleme:
Ajreference number: A34779; MUID:90205817; PMID:2108316
 A; Status: preliminary; nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 801-1072, N', 1074-1168, K', 1170-1225, V', 1227-1434, N', 1436-1607, 'I', 1609-14
A; Crosser references: GB:M32019
C; Superfamily: HIV-EP2 enhancer-binding protein
C; Keywords: DNA binding; transcription regulation; zinc finger
 A;Molecule type: DNA
A;Residues: 1-156 <DEW>
A;Cross-references: EMBL:Z74920; NID:g1420109; PIDN:CAA99201.1; PID:g1420111; MIPS:YORO
A;Experimental source: strain S288C
 ,Title: A DNA-binding protein containing two widely separated zinc finger motifs that ,Reference number: A34203; MUID:90169514; PMID:2106471 ,Accession: A34203
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 NiAlternate protein YOR013w - yeast (Saccharomyces cerevisiae)
NiAlternate names: hypothetical protein O2612; hypothetical protein YOL303.3
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C;Accession: S54619; S66879
R;de Haan, M.; Maares, A.C.; Grivell, L.A.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54617
A;Molecusion: S54619
 A.Molecule type: DNA
A.Residues: 1-156 <DEH;
A.Crose-references: EMBL:X87331; NID:g1041652; PIDN:CAA60762.1; PID:g829123
R.de Haan, M.; Grivell, L.A.; Maarse, A.C.
submitted to the Protein Sequence Database, July 1996
A.Reference number: 866877
 cell division inhibitor (minD-2) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 26-Aug-1999
 Gaps
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 Query Match 67.3%; Score 35; DB 2; Length 2717; Best Local Similarity 66.7%; Pred. No. 1.9e+02; Matches 6; Conservative 2; Mismatches 1; Indels
 Score 34; DB 2; Length 156,
Pred. No. 14;
 Indels
 1; Mismatches
 A,Cross-references: SGD:S0005539
A,Map position: 15R
C,Superfamily: hypothetical protein YOR013w
 66.78;
 6; Conservative
 ||| |::||
2405 VVPAGLTYS 2413
 28
 3 VVPXGMSYS 11
 2 EVVPXGMSY 10
 Query Match
Best Local Similarity
 A; Accession: A34779
 C, Accession: H69491
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 copposementars IV subunit Xriisis [imported] - Xylella fastidiosa (strain 985c)
C;Species: Xylella fastidiosa consortium of the Organization for Nucleotide Sequen
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: H82691
Nature 406, 151-157, 2000
A;Title: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A62515; MUID:20365717; PMID:10910347; PID:ABS Below
A;Recession: H82691
A;Residues: 1-749 <SIM>A;Residues: 1-749 <SIM
A;Residues: 1-7
A;Title: Isolation of two cDNAs encoding zinc finger proteins which bind to the alpha 1-A;Reference number: IS8280; MUID:91187610; PMID:1901405
 A;Gene: XF1353
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomerase
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 A34203
DNA-binding protein PRDII-BF1 - human
NyAlternate names: major histocompatibility complex enhancer-binding protein 1
CiSpecies: Homo sapiens (man)
CiDate: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Sep-1999
CiAccession: A34203, A34779
RiFan, C.M., Maniatis, T.
Genes Dev. 4, 29-42, 1990
 topoisomerase IV subunit XF1353 [imported] - Xylella fastidiosa (strain 9a5c)
 Gaps
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 A;Status: mucleic acid sequence not shown
A;Mceule type: mRMT
A;Mcendues: 1.670 «MIT»
A;Cross-references: EMBL:X54250; NID:g57519; PIDN:CAA38151.1; PID:g57520
A;Note: the authors did not translate the codon for residue 1
C;Superfamily: HIV-EP2 enhancer-binding protein
C;Keywords: DNA binding; transcription regulation; zinc finger
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 67.3%; Score 35; DB 2; Length 670; 66.7%; Pred. No. 43; ative 2; Mismatches 1; Indels
 Length 749;
 2; Indels
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DB 2; 48;

Score 35; DB 2 Pred. No. 48; 0; Mismatches

67.3%; 77.8%;

Query Match 67.3 Best Local Similarity 77.8 Matches 7; Conservative

Contents: annotation

EVDPSGMSY 534

2 EVVPXGMSY 10

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 C;Species: Campylobacter jejuni
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 08-Oct-1999
C;Accession: 140758; S47317
R;Hani, E.K.; Chan, V.L.
A;Hani, E.K.; Chan, V.L.
A;Hini, E.K.; Chan, V.L.
A;Title: Expression and characterization of Campylobacter jejuni benzoylglycine amidohyd
A;Reference number: 140758; MUID:95247673; PMID:7730270
Ajauthors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.K.; Venter, J.C.

Title: The Complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A; Reference number: A69280; MUID:98049343; PMID:9389475

A; Reference number: A69280; MUID:98049343; PMID:9389475

A; Returs: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA

A; Returs: preliminary; nucleic acid sequence not shown; translation not shown A; Returs: Dxellminary; nucleic acid sequence not shown; translation not shown A; Retures: Carcoss-references: GB:ARD00970; GB:ARD00782; NID:92689293; PIDN:AAB89318.1; PID:9264860 C; Superfamily: cell division inhibitor minD
 min
 A;Accession: C82900
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-544 - GLAA
A;Cross-references: GB:AE002133; GB:AF222894; NID:g6899339; PIDN:AAF30768.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
 probable ABC substrate-binding protein, iron UU359 [imported] - Ureaplasma urealyticum
 C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: C82900
R;Glass, J.1; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a 1
A;Reference number: A82870
 ö
 ö
 ö
 A;Cross-references: EMBL:Z36940; NID:g535805; PIDN:CAA65392.1; PID:g535806
 Gaps
 Gaps
 Gaps
 ô
 ö
 ö
 Match 65.4%; Score 34; DB 2; Length 252; Local Similarity 75.0%; Pred. No. 24; local Similarity 1; Mismatches 1; Indels nes 6; Conservative 1; Mismatches 1; Indels
 Length 544;
 Score 33; DB 2; Length 94;
Pred. No. 14;
2; Mismatches 2; Indels
 2; Indels
 lypothetical protein 1 - Campylobacter jejuni (fragment)
 Score 34; DB 2;
Pred. No. 55;
1; Mismatches 2
 Status: preliminary; translated from GB/EMBL/DDBJ:
Molecule type: DNA
Residues: 1-94 <RES>
 Query Match
Best Local Similarity 55.6%;
Matches 5; Conservative
 Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
 135 BEVVPHYLSY 144
 1 EEVVPXGMSY 10
 2 EVVPXGMSY 10
 :: | ||||
26 DIFPSGMSY 34
 ||:| ||
81 EVIPAGMS 88
 2 EVVPXGMS 9
 A;Gene: ABCsbp-5; UU359
A;Genetic code: SGC3
 Query Match
 C.Genetica:
 RESULT 14
140758
 Best Loc
Matches
 RESULT 13
 ð
```

```
C.Accession: E90544
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pul
A;Reference number: A99512; WUID:21267165; PMID:11353084
 ö
 A; Cross references: GB A1445566; PID: g14089674; PIDN: CAC1343.1; GSPDB: GN00153 A; Experimental source: strain UAB CTIP
508 ribosomal protein L20 [imported] - Mycoplasma pulmonis (strain UAB CTIP) C;Species: Mycoplasma pulmonis (strain L20 [imported] - My-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001 C;Accession: E05544 R3, Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.;
 Gaps
 ö
 63.5%; Score 33; DB 2; Length 116; 77.8%; Pred. No. 17;
 Indels
 A;Gene: MYPU 2610
A;Genetic code: SGC3
C;Superfamily: Escherichia coli ribosomal protein L20
 0; Mismatches
 Search completed: June 3, 2004, 12:00:00 Job time: 9 secs
 7; Conservative
 3 VVPXGMSYS 11
 68 VRPLGMSYS 76
 Query Match
Best Local Similarity
 A; Status: preliminary A; Molecule type: DNA
 Genetics:
 Matches
```

```
PRT; 1058 AA
 ALIGNMENTS
 EMBL; AE010554; AAL94625.1; ALT_INIT
 HAMAP, MF_01210; -; 1.
InterPro; IPR006275; CarA L_glu.
InterPro; IPR006487; CPase_L_D2.
InterPro; IPR005479; CPase_L_D2.
InterPro; IPR005480; CPase_L_D3.
InterPro; IPR005481; CPase_L_N.
InterPro; IPR004362; MGS_IIRe.
Pfam; PP002785; CPSase_L_D2.
Pfam; PP002787; CPSase_L_D2.
 STANDARD;
 Fusobacterium.
NCBI_TaxID=76856;
 CARB FUSIN
 DBRGB6;
 CARB_FUSIN
 mus musculu
rattus norv
 homo sapien
mus musculu
brachydanio
 archaeoglob
campylobact
 homo sapien
clostridium
 homo sapien
 homo sapien
mus musculu
 homo sapien
 schizosacch
 mus musculu
 homo gapien
 rattus norv
 xenopus lae
 xenopus lae
 homo sapien
 tobacco yel
clostridium
 homo sapien
neurospora
 rattus norv
 Q8rg86 fusobacteri
074377 schizosacch
 vibrio chol
 gallus gall
 mus musculu
vibrio chol
 gallus gal
 тусор]авта
 3, 2004, 11:32:06; Search time 4.86667 Seconds (Without alignments) 117:693 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 904351
P25822
P25822
O60312
O60312
P25439
P45439
P45439
P45439
P96339
O99740
O99740
O99740
O99739
O99739
O99739
P22064
P2
 P50755
 P30280
 090459
 P55169
 24385
 141681
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 141681 segs, 52070155 residues
 SUMMARIES
 RAT
MOUSE
RAT
HUMAN
 Y1A9_CLOAB
ZEP1_HUMAN
CY14_NEUCR
A10A_HUMAN
 ARCFU
CAMJE
MOUSE
VIBCH
SCHPO
 HUMAN
CLOPE
MOUSE
HUMAN
VIBCH
 MOUSE
BRARE
XENLA
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 XENLA
 HUMAN
 OM protein - protein search, using sw model
 FUSNIN
 Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 US-09-909-164-9
52
1 EEVVPXGMSYS 11
 Query
Match Length DB
 SwissProt_42:*
 1401
1595
1712
1713
289
289
289
289
 1389
 June
 Title:
Perfect score:
 Score
 Scoring table:
 Database :
 Sequence:
 Searched:
 Run on:
 Result
No.
```

K

| P44677 haemophilus<br>O75355 homo sapien<br>Q99616 homo sapien<br>P90518 crithidia E<br>P52384 human herpe<br>P52544 human herpe<br>P32784 saccharcomyc<br>Q62671 rattus norv<br>P28931 comato aspe<br>P16916 escherichia<br>P16916 escherichia |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| TOLE_HAEIN ENP3_HUMAN S216_HUMAN S216_HUMAN SPC_TEPA PRTP_HSV6Z SCTI_YEAST SCTI_YEAST SDD_RAT V1A_TAN RHSA_ECOLI RHSC_ECOLI                                                                                                                     |
| нананананан                                                                                                                                                                                                                                     |
| 427<br>6229<br>7289<br>726<br>726<br>726<br>759<br>759<br>1337                                                                                                                                                                                  |
| 601.55<br>601.55<br>601.55<br>601.55<br>601.55<br>601.55<br>601.55                                                                                                                                                                              |
|                                                                                                                                                                                                                                                 |
| \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$                                                                                                                                                                                        |

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 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=ATCC 25586;

X MEDIINE-21886394; PubMed=11889109;
X Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
Rapatral V., Anderson I., Ivanova N., Grechkin G., Zhu L.,
Rapatral V., Chaga O., Goltsman E., Bernal A.,
Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
Larsen N., D'Souza M., Walumas T., Pusch G., Haselkorn R.,
Ronstein M., Xyrpides N., Overbeek R.;
Ronstein M., Xyrpides N., Overbeek R.;
Tucleatum strain ATCC 25586.";
U. Bacteriol. 184:2005-2018(2002)
U. Bacteriol. 184:2005-2018(2002)
U. Bacteriol. 184:2005-2018(2002)
U. GATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +
Dhosphate + L-glutamate + carbamoyl phosphate.
U. COPACTOR: Binds amaganese ions per subunit (By similarity)
U. PATHWAY: Pyrimidine biosynthesis, first step.
U. PATHWAY: Pyrimidine biosynthesis, the small (or glutamine) chain
Dromotes the hydrolysis of glutamine to ammonia, which is used by
C. I STBUNIT: Composed Of two Chains, the small (or glutamine)
C. STBUNIT: Camposed of two chains, the small (or glutamine)
C. STBUNIT: Camposed of two chains, the small (or glutamine)
C. STBUNIT: Camposed of two chains, the small (or glutamine)
C. STBUNIT: Camposed of two chains, the small (or glutamine)
C. STBUNITY: Belongs to the carB family.
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation u
 Pusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
```

```
genome sequence of Schizosaccharomyces pombe.";
 Y11K TYDVA
P31619;
 DOMAIN
SEQUENCE
 TRANSMEM
TRANSMEM
 TRANSMEM
 TRANSMEM
TRANSMEM
 TRANSMEM
TRANSMEM
TRANSMEM
 Query Match
 FRANSMEM
 TRANSMEM
 RESULT 3
 Matches
 ò
 셤
 RETARKS OCCUPATION OF THE STANK OCCUPATION O
 STRAIN=2972,

MEDLINE=21848401; PubMed=11859360;

MEDLINE=21848401; MEDLINE=218, Medlen I., Ribbet I., Ribbet I., Miblet I., Mibl
 ö
 R PRINTS; PRO0098; CPSASE.

R TIGREAMS; TIGRO1369; CPSASE.

R PROSITE; PSO0866; CPSASE.

R PROSITE; PSO0866; CPSASE.

R PROSITE; PSO0866; CPSASE.

R Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

M ATP-binding; Manganese; Complete proceome.

T DOMAIN 402 546 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.

T DOMAIN 402 646 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

T DOMAIN 547 929 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

T REPEAT 1 1058 ALLOSTERIC DOMAIN.

T REPEAT 547 1058 ALLOSTERIC DOMAIN.

T REPEAT 547 1058 ALLOSTERIC DOMAIN.

T NP BIND 153 210 ATP (POTENTIAL).

T NP BIND 302 352 ATP (POTENTIAL).

T METAL 284 MANGANESE 1 (BY SYMILARITY).
 Gaps
 ATP (POTENTIAL).

ATP (POTENTIAL).

ATP (POTENTIAL).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

ANANGANESE 3 (BY SIMILARITY).

117451 MW; ED7037AF77CLE39F CRC64;
 ÷
 73.1%; Score 38; DB 1; Length 1058; 60.0%; Pred. No. 7; tive 3; Mismatches 1; Indels
 Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
 SULH SCHPO

SULH SCHPO

TD SULH SCHPO

STANDARD; PRT; 877 AA.

AC 074377;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 10-CCT-2003 (Rel. 38, Last sequence update)

DF 10-CCT-2003 (Rel. 42, Last annotation update)

DF 10-CCT-2003 (Rel. 42, Last annotation update)

BF Probable sulfate permease C3H7.02.
 Conservative
 190 EIVPNGLNYS 199
 2 EVVPXGMSYS 11
 Pfam; PF02142; MGS; 1
 547 105
153 21
1302 35
298 298
300 30
820 82
832 83
 Schizosaccharomyces.
NCBI_TaxID=4896;
 Local Similarity
nes 6; Conserv
 SEQUENCE FROM N.A.
 METAL
SEQUENCE
 Query Match
 METAL
 Matches
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 ö
 Gaps
 ö
 -i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-i- SIMILARITY: Belongs to the SLC26A/SulP transporter (TC 2.A.53)
 SECUENCE FROM N.A.

MEDINES-92188538, PubMed-1546458;

MCTIS B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;

MCTIS B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;

"The nucleotide sequence of the infectious cloned DNA component tobacoo yellow dwarf virus reveals features of geminiviruses infecting monococyledonous plants.";

Virology 187:633-642(1992).
Nature 415:871.880(2002).
-!- FUNCTION: HIGH AFFINITY UPTAKE OF SULFATE INTO THE CELL (BY SIMILARITY).
 ö
 71.2%; Score 37; DB 1; Length 877; 77.8%; Pred. No. 9.4;
 1; Indels
 56995A8493371E43 CRC64;
 Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
NCBI_TaxID=31599;
 Last sequence update)
Last annotation update)
 1; Mismatches
 POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
 POTENTIAL. POTENTIAL.
 -!- SIMILARITY: Contains 1 STAS domain.
 POTENTIAL
 POTENTIAL
 POTENTIAL
 GenebB Sponbe; SPBG3H7.02; -.
InterPro; IPR002645; STAS.
InterPro; IPR01902; Sulph_transpt.
FEam; PF001740; STAS; 1.
Pfam; PF00916; Sulfate_transp; 1.
TCGRAMS; TTGRROB15; Sulfate_transp; 1.
PROSITE; PS01130; SLC264; 1.
PROSITE; PS00101; STAS; 1.
 01-001-1993 (Rel. 26, Created) 01-001-1993 (Rel. 26, Last seq 01-0CT-1993 (Rel. 27, Last annotation) Hypothetical 11.2 kDa protein.
 EMBL; AL031261; CAA20298.1; -. PIR; T40413; T40413.
 96373 MW;
 Transport; Transmembrane.
TRANSMEM 133 153
 Local Similarity 77.8
les 7, Conservative
 STANDARD;
 148 VVPQGMSYA 156
 3 VVPXGMSYS 11
 161
186
222
222
222
329
3329
424
461
461
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 ö
 Sauer U., Duerre P.;
"Sequence and molecular characterization of a DNA region encoding a small heat shock protein of Clostridium acetobutylicum.";
J. Bacteriol. 175:3394-3400 (1993).
-!- SIMILARITY: Contains 2 FtsK domains.
-!- CAUTION: Ref. 2 sequence differs from that shown due to frameshifts in positions 76 and 106.
 Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin B.V., Smith D.R.; "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
 Gaps
 Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 ;
0
 Length 102;
 1; Indels
 ll protein. -
102 Aa; 11178 MW; A40ECF1E0AF55B67 CRC64;
 69.2%; Score 36; DB 1;
60.0%; Pred. No. 1.6;
ive 3; Mismatches 1
 (Rel. 28, Created)
(Rel. 40, Last sequence update)
(Rel. 42, Last annotation update)
 PRT; 1498 AA
 [2]
SEQUENCE OF 1-108 FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=93273706; PubMed=8501044;
 STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
 EMBL; X65276; CAA46379.1; ALT_FRAME. PIR; B97355; B97355.
 Interpropriate 100 mov. 1. Appothetical protein. Seguence 102 m.
 J. Bacteriol. 183:4823-4838(2001).
 PIR; B97355; B97355.
InterPro; IPR002543; FtaK_SpoIIIE.
 Hypothetical protein CAC3709.
CAC3709.
 EMBL; AE007866; AAK81629.1;
 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
 2 EVVPXGMSYS 11
 SEQUENCE FROM N.A.
 NCBI_TaxID=1488;
 01-FEB-1994
16-OCT-2001
 10-OCT-2003
 CLOAB
 YLA9_CLOAB
 DATE TO THE STATE OF THE STATE
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 ö
 01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Zinc finger protein 40 (Human immunodeficiency virus type I enhancer-
binding protein 1) (HIV-BP) (Major histocompatibility complex binding
protein 1) (MBP-1) (Positive regulatory domain II binding factor 1)
 "High-resolution solution structure of the double Cys2His2 zinc finger from the human enhancer binding protein MBP-1."; Blochemistry 31:3907-2917(1992).

1- ELOCATION: THIS PROTEIN SEBCIFICALLY BINDS TO THE DNA SEQUENCE of GGGACTTTCC-3. WHICH IS FOUND IN THE ENHANCER ELEBRNIS OF NUMBEROUS VIRAL FROMOTERS SUCH AS THOSE OF SV40, CMV, OR HIVI. IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEBRNIS OF A NUMBER OF CELLULAR PROWOTERS, INCLUDING THOSE OF THE CLASS I MAC. INTERLEUKIN-2 RECEPTOR, AND INTERFERON-BETA GENES. IT MAY ACTIVATION.

1- SUBSCELLULAR LOCATION: Nuclear.
 Gaps
 STRUCTURE BY NWR OF 2113-2142.
MEDLINE=91064333; PubMed=2248949;
OmichinE=91064333; PubMed=2248949;
Omichinski J.G., Clore G.M., Appella E., Sakaguchi K.,
Gronemborn A.M.;
"High-resolution three-dimensional structure of a single zinc finger
from a human enhancer binding protein in solution.";
Elcom a human enhancer binding protein in solution.";
 -1- SUBCELLULAR LOCATION: MULTIPLE STORES, WHICH ARE WIDELY -1- INDUCTION: By mitogens and phorbol ester.
-1- DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE.
 Fan C.M., Maniatis T.;
"A DNA-binding protein containing two widely separated zinc finger motifs that recognize the same DNA sequence.";
Genes Dev. 4:29-42(1990).
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
 MEDLINE-52232684, PubMcd=1567844,
Omichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella B.,
 ö
 Complete proteome; Repeat
 Score 36, DB 1; Length 1498; Pred. No. 27;
 Indels
 675 682 ATP (POTENTIAL).
1498 AA, 168968 MW; FF42037A335A9649
 2717 AA.
 2; Mismatches
 Pfam; PFULSOV; EDGE, PRSK; 2.
PROSITE; PSS901; PTSK; 2.
Hypothetical protein; ATP-binding; Cc
DOMAIN 655 857
FISK 1.
 ZINC-FINGER IN-BETWEEN.
-!- SIMILARITY: STRONG, TO HIVEP2.
 SEQUENCE FROM N.A.
MEDLINE=90169514; Pubmed=2106471;
Pfam; PF01580; FtsK_SpoIIIE; 2.
 01-APR-1990 (Rel. 14, Created)
 [3]
STRUCTURE BY NMR OF 2087-2142.
 69.2%;
 Query Match
Best Local Similarity 60.0.
 1276 EQKIPMGMSY 1285
 STANDARD;
 1 EEVVPXGMSY 10
 Homo sapiens (Human)
 Gronenborn A.M.;
 NCBI_TaxID=9606;
 HIVEP1 OR ZNF40.
 ZEP1 HUMAN
P15822;
 PRDII-BF1)
 DOMAIN
NP BIND
SEQUENCE
 STTTS
 셤
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 ö
 PDB; 42x.
PDB; 1BBG); 3.4
PDB; 1BBG); 3.4
PDB; 1BBG); 3.4
PDB; 1BBG); 3.4
RANKERG; 1DC699; -..
R Genew; HGNC: 4920; HIVEP...
R GO; 60000567; F:DNA binding; TAS...
DR InterPro; IPR007087; Znf C2H2.
DR Pfam; PP00096; Zinc C2H2; 5.4
DR PROSITE; PS00026; Zinc C7H2; 5.4
DR PROSITE; PS0026; Zinc C7H2; 7.4
DR PROSITE; PS0026; Zinc C7H2;
 Gaps
 MEDLINE=94188926; PubMed=8140616;
Sandal N.N., Marcker K.A.;
"Similarities between a soybean nodulin, Neurospora crassa sulphate
 SEQUENCE FROM N.A.
MEDLINE=91129256; PubMed=1825178;
MEDLINE=91129256; PubMed=1825178;
Mincleotide sequence, messenger RNA stability, and DNA recognition elements of cys-14, the structural gene for sulfate permease II in Neurospora crassa.";
 0
 Neurospora crassa.
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes;
Sordariomycetidae, Sordariales; Sordariaceae, Neurospora.
 67.3%; Score 35; DB 1; Length 2717; 66.7%; Pred. No. 80; 1; Indels ive 2; Mismatches 1; Indels
 2127 2135
2717 AA; 297217 MW; D45D3CA951FEA561 CRC64;
 01-NOV-1991 (Rel. 20, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Sulfate permease II.
 Biochemistry 30:1780-1787(1991)
 EMBL, X51435, CAA35798.1; -.
PIR, A34203, A34203.
PDB, 3ZNF, 15-JAN-92.
PDB, 4ZNF, 15-JAN-92.
PDB, 1BBO, 31-OCT-93.
 Query Match
Best Local Similarity 66.
 STANDARD;
 2405 VVPAGLTYS 2413
 3 VVPXGMSYS 11
 PROBABLE REVISIONS.
 NCBI_TaxID=5141;
 CY14 NEUCR
P23622;
 HELIX
SEQUENCE
 STRAND
 RESULT 6
CY14_NEUCR
 HERER REPRESENTED TO THE PROPERTY OF THE PROPE
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permease II and a putative human tumcour suppressor.";

Trands Biochem. Sci. 19:19-19(1994).

1- FUNCTION: UPTAKE OF SULFATE INTO THE CELL.

1- SUBCELLULAR LOCATION: Integral membrane protein.

1- INDUCTION: Highly expressed, but only in cells subject to sulfur limitation, and it is turned on by the positive-acting Cys.3 sulfur regulatory protein.

1- MISCELLANEOUS: SULFATE PERMEASE II IS MAINLY FOUND IN MYCELLA.

1- SIMILARITY: Belongs to the SLC26A/SulP transporter (TC 2.A.53)
 Gaps
 SEQUENCE FROM N.A.

BEDLINE-1225279; PubMed=11326269;
Meguro M., Kashiwagi A., Mitsuya K., Nakao M., Kondo I., Saitoh S., Oshimura M.;
Shimura M.;
"A novel maternally expressed gene, ATP10C, encodes a putative aminophospholipid translocase associated with Angelman syndrome.";
Nat. Genet. 28:19-20(2001).
 ALON HUMAN STANDARD; PRT; 1499 AA.

060312; 056514;
30-MAY-2000 (Rel. 39, Created)
28-FRB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Potential phospholipid-transporting ATPase VA (EC 3.6.3.1) (ATFVA)
(Aminophospholipid translocase VA).

ATP10A OR ATP10C OR ATPVC OR KIAA0566.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primatee; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
4FC604B6079BCB77 CRC64;
 65.4%; Score 34; DB 1; Length 788; 66.7%; Pred. No. 36; 1; Indels ive 2; Mismatches 1; Indels
 EMBL; M59167; AAA33615.1; ALT_SEQ.
PIR; A37956; A37956.
InterPro; IPR001902; Sulph_transpt.
Pfam; PR00916; Sulface transp; 1.
TIGRFAMS; TIGR00815; Sulface transp; 1.
TRANSMER; P801130; SLOS6A; 1.
Transmort; Transmembrane; Glycoprotein.
TRANSMEM
 POTENTIAL.
POTENTIAL.
POTENTIAL.
 POTENTIAL. POTENTIAL.
 POTENTIAL
 POTENTIAL
 87864 MW;
 Local Similarity 66.7
hes 6; Conservative
 3 VVPXGMSYS 11
 90 VVPQGMAYA 98
 Homo sapiens (Human)
 788 AA;
 [2]
SEQUENCE FROM N.A.
 family.
 TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
 FRANSMEM
 CARBOHYD
 SEQUENCE
 Query Match
 TRANSMEM
 A10A_HUMAN
 Matches
 RESULT 7
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 AAC
DDT TO DD TO D
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MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
A strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schemer C.F., Shat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marushima K., Farmer A.A., Rubin G.M., Hong L.,
B Diatchenko L., Marushima K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
B Raha S.S., Longuellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
B Bosak S.A., McDwan P.J., McKernan K.J., Malek J.A., Glubbs R.A.,
B Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
N. Halton D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
"Generation and initial analysis of more than 15,000 full-length
Human and mouse cDNA sequences",
"The Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
MEDLINE=21313119; PubMed=11353404;
Herzing L.B.K., Kim S.-J., Cook B.H. Jr., Ledbetter D.H.;
The human aminophospholipid-transporting ATPase gene ATP10C maps
adjacent to UBE3A and exhibits similar imprinted expression.";
Am. J. Hum. Genet. 68:1501-1505 (2001).
 SEQUENCE FROM N.A.
```

RC TISSUE\_BERIAL;

RA MEDLINE=9829545; PubMed=9628581;

RA MEDLINE=9829545; PubMed=9628581;

RA MEDLINE=9829545; PubMed=9628581;

RA MEDLINE=9829545; PubMed=962881;

RA Momura M., Ohara O.;

RA Nomura M., Ohara O.;

RA Nomura M., Ohara O.;

The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA Res. 5:31-39(1998)

C. - CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.

SUBMELLIOUAR LOCATION: Integral membrane protein (By similarity).

C. - SUBERLIOUAR LOCATION: Integral membrane protein (By similarity).

C. - TISSUE SPECIFICITY: Widely expressed, with highest levels in kidney, followed by lung, brain, prostate, testis, ovary and small intestine.

C. - SUBSELIA intestine.

C. - INTEGRAL DEfects in ATPLOA are a cause of Angelman syndrome (AS) (MIM:105830]; also known as 'happy puppet syndrome'. AS is characterized by features of severe encore and intellectual retardation, microcephaly, ataxia, frequent jerky limb movements and flapping of the arms and hands, hypotomia, hypotomia, hypotomia, hypotomia, hypotomia, a great propensity for protruding the tongue ('tongue characterized by macrostomia, a large mandible and open-mouthed characterized by macrostomia, a large mandible and open-mouthed characterized by macrostomia, a large mandible and open-mouthed characterized by macrostomia, protruding the tongue ('tongue thrusting'), and an occipial groove.

-- SIMILARITY: Belongs to the cation transport ATPases family (P-type characterized).

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EMBL, AY029504; AAK3310U.1; --
EMBL, AY029487; AAK33100.1; JOINED.
EMBL, AY029488; AAK33100.1; JOINED.
EMBL, AY029499; AAK33100.1; JOINED.
EMBL, AY029491; AAK33100.1; JOINED.
EMBL, AY029491; AAK33100.1; JOINED.
EMBL; AB051358; BAB47392.1; -.
```

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Gaps
 MIM, 105830; -C. integral to membrane; NAS.
GO; GO:0016021; F:phospholipid-translocating Arpase activity; NAS.
GO; GO:0004012; F:phospholipid-translocating Arpase activity; NAS.
GO; GO:0004360; F:phospholipid-translocating Arpase activity; NAS.
GO; GO:0004360; F:phospholipid-El-E2.
InterPro; IPR00539; Hydrolase.
FINTERPRO; PR00119; CATAPASE.
FRINTS; PR00119; CATAPASE.
TIGREAMS; TIGR01652; Arpase-Plipid; 1.
TIGREAMS; TIGR01652; Arpase-Plipid; 1.
FROSITE; PR00544; Arpase B-type; 6.
FROSITE; PR00
 ..
0
 PHOSPHORYLATION (BY SIMILARITY)
MAGNESIUM (BY SIMILARITY)
MAGNESIUM (BY SIMILARITY).
 Score 34; DB 1; Length 1499;
Pred. No. 70;
0; Mismatches 3; Indels
 388 Q -> R (IN REF. 4).
AA; 167687 MW; D4996A4D0635A68D CRC64;
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
 EXTRACELLULAR (POTENTIAL)
 EXTRACELLULAR (POTENTIAL)
 CYTOPLASMIC (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 CYTOPLASMIC (POTENTIAL) .
 CYTOPLASMIC (POTENTIAL).
 CYTOPLASMIC (POTENTIAL)
 (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
 POTENTIAL.
 POTENTIAL
 POTENTIAL
EMBL; AY029493; AAK33100.1; JOINED. EMBL; AY029494; AAK33100.1; JOINED. EMBL; AY029494; AAK33100.1; JOINED. EMBL; AY029496; AAK33100.1; JOINED. EMBL; AY029496; AAK33100.1; JOINED. EMBL; AY02949; AAK33100.1; JOINED. EMBL; AY029499; AAK33100.1; JOINED. EMBL; AY029500; AAK33100.1; JOINED. EMBL; AY029501; AAK33100.1; JOINED. EMBL; AY029502; AAK33100.1; JOINED. EMBL; AY029503; AAK33100.1; JOINED. EMBL; BOE52551; AAK33100.1; JOINED. EMBL; BOE52551; AAK33100.1; JOINED. EMBL; BOE52551; AAK33100.1; JOINED. EMBL; BOE52551; AAK33100.1; JOINED. EMBL; AS031138; EAAZ5492.1; MIN; 605855; AM1M, 1058810.
 65.4%;
 8; Conservative
 469 EEVVPRGGSVS 479
 STANDARD;
 1 EEVVPXGMSYS 11
 Query Match
Best Local Similarity
 Multigene family.
DOMAIN
 1499
 427
1031
1035
467
 RESULT 8
RL20 MYCPU
ID RL20 MYCPU
AC Q98QV0;
DT 28-FEB-2003 (
DT 28-FEB-2003 (
 DOMAIN
TRANSMEM
DOMAIN
 DOMAIN
TRANSMEM
 TRANSMEM
DOMAIN
 TRANSMEM
DOMAIN
TRANSMEM
 CONFLICT
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 RANSMEM
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 RANSMEM
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us-09-909-164-9.rsp

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POTENTIAL.
 J. Bacteriol. 177:2396-2402(1995).
 SEQUENCE OF 160-253 FROM N.A.
 6; Conservative
 Nature 403:665-668(2000)
 1 EEVVPXGMSY 10
 60 EESIPDGASÝ 69
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=197;
 Venter J.C.;
 SEQUENCE
 TRANSMEM
 TRANSMEM
 RESULT 10
 SO TTWANT TO THE SO THE
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 ö
 "The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis", Nuclea Res. 29:2145.2153 (2001).

Nucleat Acids Res. 29:2145.2153 (2001).

-i- FUNCTION: This protein binds directly to 23s ribosomal RNA and is necessary for the in vitro assembly process of the 50s ribosomal subunit. It is not involved in the protein synthesizing functions
 STRAIN=UAB CTIP;
MEDLINE=21267165; PubMed=11353084;
MEDLINE=21267165; PubMed=11353084;
Membaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha B.P.C.,
Blanchard A.;
 Gape
 of that subunit (By similarity).
-!- SIMILARITY: Belongs to the L20P family of ribosomal proteins.
 SEQUENCE FROM N.A.
STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Klenk H.-P., Clayton R.A., Gwinn M., Hickey E.K., Peterson J.D.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
50S ribosomal protein L20.
RPLT CR MYDL 2610.
Mycoplasma pulmonis.
Bacteria: Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2107;
 ;
 Mypulist; Mypu 2610; -.
RANAD; M 00382; -; 1.
InterPro; IPR005812; Ribosomal L20.
InterPro; IPR005812; Ribosomal L20b/o.
Refam; PR00062; Ribosomal L20; 1.
PRINTS; PR00062; RIBOSOMÄLL20.
PRODOM; PR00082; RIBOSOMÄLL20.
TIGRFAM; F1GR01032; rpl bact; 1.
Ribosomal procein; rRNA-binding; Complete proteome.
SEQUENCE 116 AA; 13565 MW; C59C748901B18F14 GRC64;
 63.5%; Score 33; DB 1; Length 116; 77.9%; Pred. No. 8.1;
 2; Indels
 Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
 0; Mismatches
 EMBL; AL445563; CAC13434.1; -. PIR; E90544; E90544.
 Hypothetical protein AF1949.
 Query Match
Best Local Similarity 77.8
Matches 7; Conservative
 STANDARD;
 Archaeoglobus fulgidus.
 3 VVPXGMSYS 11
 68 VRPLGMSYS 76
 FROM N.A.
 NCBI_TaxID=2234;
 YJ49_ARCFU
ID YJ49_ARCFU
AC O28330;
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., MoNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 Gape
 PERMINICATE 11166;
MEDLINE-20150912; PubMed=10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Mhitchead S., Barrell B.G.,
"The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.";
 Campylobacter jejuní.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
 "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
 STRAIN=ATCC 43431 / TGH 9011;
MEDLINE=95247673; PubMed=7730270;
Hani E.K., Chan V.L.;
"Expression and characterization of Campylobacter jejuni benzoylglycine amidohydrolase (Hippuricase) gene in Escherichia
 .;
0
 63.5%; Score 33; DB 1; Length 165; 60.0%; Pred. No. 12; ative 1; Mismatches 3; Indels
 EMBL; AE000968; AAB89307.1; -.
PIR; D5943; D69493.
HYPOTA AF1949; -.
HYPOThetical protein; Transmembrane; Complete proteome.
 141 161 POTENTIAL.
165 AA; 17588 MW; BBC17054810ADBF8 CRC64;
 Y990 CAMJE STANDARD; PRT; 253 AA. P85487; OSPAVO; OL-NOV-1995 (Rel. 32, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical protein C10990c.
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RESULENCE FROM N.A. (ISOFORMS 1 AND 2).

RC STRAIN-C57BL/G0; TISSUE-Embryonic head;

RX MAMAJ U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA RAWAJ T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Shoori T., Bono H., Rasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Puruno M., Anno H., Baldarelli R., Barsh G.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Dronn P., Marchionni L., Mashima J., Mazarelli J., Mombaetts P.,

RA Saski H., Sato K., Schoenbadh C., Seya T., Shibata Y., Storch K.-F.,

RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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 MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hoop L.,
Staplaton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarene P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Gaps
 C200RF103.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
 .;
0
 63 5%; Score 33; DB 1; Length 253; 55.6%; Pred. No. 18; tive 2; Mismatches 2; Indels
 EMBL, AL139076; CAB73246.1; -.
EMBL, Z36940; CAA85392.1; -.
PIR; C81374; C81374.
PIR; 140758; 140758; L40758.
PHYPOthetial protein; Complete proteome.
SEQUENCE 253 AA; 29783 MW; F9503FF3265F8A6A CRC64;
 CTX3 MOUSE STANDARD; PRT; 280 AA. Q9D387; Q9CXQ4; 28-FEB-2003 [Rel. 41, Last sequence update) 10-OCT-2003 [Rel. 42, Last annotation update) Procein C20orf103 homolog precursor.
 SEQUENCE FROM N.A. (ISOFORM 2).
 5; Conservative
 185 DIFPSGMSY 193
 2 EVVPXGMSY 10
 Local Similarity
 Hayashizaki Y.;
 Query Match
 CTX3 MOUSE
 Best Loc
Matches
 RESULT 11
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 Isold=09D387-2; Sequence=VSP 003820; CAUTION: Ref.1 sequence differs from that shown due to frameshifts in positions 174 and 239.
Gaps
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSP Synthase)
 35 N-LINKED (GLCNAC. .) (POTENTIAL).
53 N-LINKED (GLCNAC. .) (POTENTIAL).
102 N-LINKED (GLCNAC. .) (POTENTIAL).
127 N-LINKED (GLCNAC. .) (POTENTIAL).
118 Missing (in leoform 2).
7 FII degressing (in leoform 2).
7 FII degressing (in Ref. i, BAB31124).
230 Q -> P (IN REF. i, BAB31124).
230 P -> A (IN REF. i, BAB31124).
231 P -> A (IN REF. i, BAB31124).
232 P -> A (IN REF. i, BAB31124).
 0
 Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBI_TaxID=666;
 Score 33; DB 1; Length 280;
Pred. No. 20;
 2; Indels
 PROTEIN C20ORF103 HOMOLOG. EXTRACELLULAR (POTENTIAL).
 CYTOPLASMIC (POTENTIAL)
 Event=Alternative splicing; Named isoforms=2;
 EMBL, AK014127, BAB29169.1, -.
EMBL, AK018222, BAB31124.1, ALT_FRAME.
EMBL, BC004791, AAH04791.1, -.
MGI, MGI:1920368, 3110005N03Rik.
MGD, MGI:1923411, 6330527006Rik.
Transmembrane, Signal, Alternative splicing.
 426 AA.
 0; Mismatches
 Isold=29D387-1; Sequence=Displayed;
 PRT;
 63.5%;
75.0%;
 Local Similarity 75.0
 STANDARD;
 173 VTPAGMSY 180
 3 VVPXGMSY 10
 230 2
238 2
280 AA;
 Vibrio cholerae.
 AROA VIBCH
 Name=1;
 CONFLICT
CONFLICT
SEQUENCE
 CARBOHYD
 Query Match
 TRANSMEM
 CARBOHYD
 VARSPLIC
 CONFLICT
 CARBOHYD
 SIGNAL
CHAIN
DOMAIN
 RESULT 12
AROA VIBCH
ID AROA VIBCH
DT 28-FEB
D
 Matches
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REQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-EI TO'N KIGSON

RA

STRAIN-EI TO'N KIGSON

RA

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

RA

Bodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

RA

Gill S.R., Nelson K.B., Reverson J.D., Tettelin H., Richardson D.,

RA

Gill S.R., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

RA

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

RA

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

RA

Fraser C.M.;

RA

Fraser C.M.;
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 ö
 Gapa
 Nature 406:477-483(2000).

-I- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate.

-I- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-C77-2003 (Rel. 42, Last annotation update)
Hsp90 co-chaperone Cdc37 (Hsp90 chaperone protein kinase-targeting subunit) (Cell division control protein 37).
CDC37 OR SPBC9B6.10.
 TIGR; VC1732; -...
ILLAMAP, MF 00210; -; 1.
InterPro; IPR006264, ArcA.
InterPro; IPR001986; EPSP_Synth.
InterPro; IPR001986; EPSP_Synthase; 1.
Proport, PD010867; EPSP_Synthase; 1.
Proport, PD010867; EPSP_Synthase; 1.
TIGRFAMS; TIGR01366, ArcOA; 1.
PROSTIE; PS00104; EPSP_SYNTHASE_1; 1.
PROSTIE; PS00885; EPSP_SYNTHASE_2; 1.
Archaetic anion acid biosynthesis; Transferase; Complete protecome. SEQUENCE 426 AA; 46101 MW; 38852D6483BFELC3 CRC64;
 ö
 63.5%; Score 33; DB 1; Length 426; 60.0%; Pred. No. 31; ive 1; Mismatches 3; Indels
 Westwood P.K., Preston N.C., Fantes P.A.;
"Schizosaccharomyces pombe cdc37 gene.";
Submitted (WAR-1999) to the EMBL/GenBank/DDBJ databases.
 -1-SUBUNIT: Monomer (By similarity).
-1-SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-1-SIMILARITY: Belongs to the EPSP synthase family.
 Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
 EMBL; AE004251; AAF94882.1; -.
 Local Similarity 60.0 nes 6; Conservative
 STANDARD;
 223 EFVIPAGOSY 232
 1 EEVVPXGMSY 10
 Schizosaccharomyces.
NCBI_TaxID=4896;
 D82163; D82163.
 SEQUENCE FROM N.A.
 CC37 SCHPO
094740;
 Query Match
 RESULT 13
CC37_SCHPO
ID 204740,
DT 28-FEB-
DT 10-OCT-
DE HEDDI
ID CCC77
CCC7_SCHPO
ID CCC75
I
 Matches
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R. SEGUENCE FROM N. A.

SEGUENCE FROM N. A.

SEGUENCE FROM N. A.

SEGUENCE FROM N. A.

SEGUENCE FROM N. A.

MEDITYRE-2186601. FURDWed-11853860, A. Basham D., Bowman S.,

R. MODITYRE-2186601. FURDWed-11853860, A.

R. MODITYRE-2186601. FURDWed-11853860, A. Basham D., Bowman S.,

R. MODITYRE-2186601. FURDWed-11853860, A. Basham D., Bowman S.,

R. MODITYRE-2186601. FURDWed-118690. Manual B.,

R. MODITYRE-218601. FURDWed-118690. Manual B.,

R. MODITYRE K., O'NORES D., JOHNS M., PARKER B., A' BART S.,

R. MODITYRE K., O'NORES D., Barneon D., Quail M.A., Rabbinowitsch B.,

R. MODITYRE K., O'NORES D., Barneon D., Quail M.A., Rabbinowitsch B.,

R. MODITYRE K., O'NORES D., Barneon D., Quail M.A., Rabbinowitsch B.,

R. MODITYRE K., O'NORES D., MODITYRE S., Saunders D., Seeger K., Sharp S.,

R. MODITYRE S., Saunders D., Modity B., Waller B., Waller B.,

R. MODITYRE S., O'NORES D., APET R., Robben J., Grymonprez B.,

R. MODITYRE S., O'NORES D., APET R., Robben J., Grymonprez B.,

R. MODITYRE S., O'NORES D., APET R., ROBBEN S., SERVER W., MALLER T., WILLER S.,

R. MODITYRE S., O'NORES D., APET R., ROBBEN S., SERVER W., MODITYRE S.,

R. MODITYRE S., O'NORES D., DEATH R., RABBAN S., MARINE S., MARINE S.,

R. MODITYRE S., O'NORES D., DEATH R., RABBAN S., MARINE S., DEATH R., SHORE S., SERVER S., S
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1 EEVVPXGMSY 10 : : | | | | | 98 DSAIPGGMSY 107

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RESULT 14

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STANDARD;
 Clostridium perfringens.
 EVAPAGASYN 248
 9 9 191
 215
 235
 478
 2 EVVPXGMSYS 11
 Local Similarity
 SEQUENCE FROM N.A.
 FROM N.A.
 Bacteriocin BCN5.
 NCBI_TaxID=1502;
 4
9
146
 235
417
433
 434
 198
 STRAIN=CPN50;
 STRAIN=CPN50;
 Clostridium
 CLOPE
 239
 CONFLICT
 CONFLICT
 SEQUENCE
 SEQUENCE
 CONFLICT
 Query Match
 CONFLICT
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 CONFLICT
 BCN5 CI
P08696;
 Best Loca
Matches
 RESULT 15
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMB outstation the European Bioinformatics Institute. There are no restrictions on its
 MEDLINE=22388257; PubMed=12477932;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,
A Stapleron M.S., Soarea M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Willalon D.K., Muzny D.M., Sodergren E.J., Lu K., Gibbs R.A.,
A Willalon D.K., Muzny D.M., Sodergren E.J., Lu K., Gibbs R.A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
B Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
B Generation and initial analysis of more than 15,000 full-length
 SEQUENCE OF 9-478 FROM N.A., AND SUBCELLUIAR LOCATION.
MEDILINE-99214118; PubMed=10196275;
BLUMI R., Fineschi B., OGLE W.O., Roizman B.;
"A novel cellular protein, p60, interacting with both herpes simplex virus I regularory proteins ICP2 and ICP0 is modified in a cell-type-specific manner and is recruited to the nucleus after infection.";
 SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE-20175430; PubMed=10708517;
MEDLINE-20175430; PubMed=10708517;
MEDLINE-20175430; PubMed=10708517;
Portier B.P., Tanchibana I., Pohl U., Lee H.K., Thanarajasingam U.,
Portier B.P., Welk K., Billings S., Ramaswamy S., Mohrenweiser H.W.,
Scheithauer B.W., Louds D.N., Jenkins R.B.;
"A transcript map of the chromosome 19q-Arm glioma tumor suppressor
 Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
GSR2 HUMAN STANDARD; PRT; 478 AA.
Q9NZM5; Q9BTC6; Q9HAX6; QNPP1; Q9NFR4; Q9UFI2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2003 (Rel. 40, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
Glioma tumor suppressor candidate region gene 2 protein (p60).
GLIOMS CREE.
 Andreu N., Estivill X., Escarceller M., Sumoy L.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
 human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 Virol. 73:3810-3817(1999).
 SEQUENCE OF 218-477 FROM N.A.
 SEQUENCE OF 12-478 FROM N.A.
 Genomics 64:44-50(2000)
 Homo sapiens (Human)
 SEQUENCE FROM N.A.
 region.'
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use by non-profit institutions as long as its content is in no way and its statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 (IN REF. 3).
A -> S (IN REF. 2; AAH04229).
D -> H (IN REF. 3).
PEGNILINDERESPORTAMIEPREAKFURKYKKIVELVERRAF
REIQ -> VLTVSCRQAPCPVWTPSLLPVPPRGYGRHHGCP
WAGPVGPWRG (IN REF. 5).
EGNILINDERESPORTAMIEPRERAFFRKKYKLVEKAFR
EGNILADAFWESFORTAMIEPRERAFFRGAT
ELQL -> RGCHSFETGSRAFRGGI (IN REF. 3).
W#, 7F18922B348CB52B CRC64;
 R -> Q.
Grida-Var 011486.
Grida-Var 011486.
G -> R (IN REF. 3).
THREOFUNEVILLNESATRAKFORDD
TVERP -> SGSYGRSWFSRASABLLNESATRAKFORDD
TVERP -> SGSYGRSWFSRASASBGGAQGPSFVARPEN
KGPNPAPGHRIAA (IN REF. 3).
 Gaps
 SDNPLDRPLVGQDEFFLE -> LNNPDKPVVWPGCLFPG
 "Complete nucleotide sequence and genetic organization of the bacteriocinogenic plasmid, pIP404, from Clostridium perfringens."; Plasmid 19:134-150(1988).
 MEDINE-8705/020; PubMed=2877971;
Garnier T., Cole S.T.;
"Characterization of a bacteriocinogenic plasmid from Clostridium
 Plasmid pIP404.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 ..
0
 63.5%; Score 33; DB 1; Length 478; 60.0%; Pred. No. 35; ive 1; Mismatches 3; Indels
 01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
 GO:0005622; C:intracellular; NAS.
 MEDLINE=88336297; PubMed=2901768;
Garnier T., Cole S.T.;
 EMBL; AF182076; AAF62873.1; --
EMBL; BC064229; AAH04229.1; --
EMBL; BC010095; AAH06311.1; --
EMBL; BC010095; AAH10095.1; --
EMBL; AC296124; AAG30413.1; --
EMBL; AL359335; CAB94786.1; --
EMBL; AL359336; CAB94787.1; --
EMBL; AL32063; CAB5242.1; --
EMBL; AL32063; CAB5478.1; --
EMBL; AL35063; CAB5478.1; --
EM
 Nuclear protein; Polymorphism.
VARIANT 389 389 R
 478 AA; 54417 MW;
 6; Conservative
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 MEDLINE=89039249; PubMed=2460717;
MEDLINE=89039249; PubMed=2460717;
MEDLINE=8000 S.T.;
"Studies of UV-inducible promoters from Clostridium perfringens in vivo and in vitro.";
vivo and in vitro.";
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vi
 Query Match 63.5%; Score 33; DB 1; Length 890; Best Local Similarity 66.7%; Pred. No. 67; Matches 6; Conservative 1; Mismatches 2; Indels
 EMBL; M14481; AAA98248.1; -.
EMBL; M32882; AAA98249.1; -.
PIR; A30481; A30481.
InterPro; IPR000834; Peptidase_M14.
InterPro; IPR00346; SH3 bac.
Pfam; PF00246; Zn carbOpept; 1.
SMART; SM0287; SH3b; 3.
Antibiotic; Bacteriocin; Plasmid.
DOMAIN 815 869 HYDROPHOBIC.
SEQUENCE 890 AA; 96699 MW; F4ESE8971C31C6C6 CRC64;
perfringens and molecular genetic analysis of the bacteriocin-encoding gene."; J. Bacteriol. 168:1189-1196 (1986).
 SEQUENCE OF 1-14 FROM N.A.
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Search completed: June 3, 2004, 11:49:53 Job time: 5.86667 secs

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tran; 1.
 PRELIMINARY;
 Pfam; PF00873; ACR
 [1]
SEQUENCE FROM N.A.
 Complete proteome
SEQUENCE 1044 A
 OBDIHO
 RESULT 1
 Q8dih0 synechococc
Q815a7 bacillus ce
Q98fx1 rhizobium 1
O74056 cenarchaeum
Q9ury8 schizosacch
Q8ewd4 mycoplasma
Q8r126 mus musculu
Q8bx126 mus musculu
Q8bx35 mus musculu
Q8bx35 mus musculu
Q8bx37 pseudomonas
Q40129 lycopersico
Q8yv44 caenorhabdi
Q8cud7 mus musculu
Q83yt prechloroco
 June 3, 2004, 11:35:06; Search time 29.8667 Seconds (without alignments) 116.206 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1017041 segs, 315518202 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
. Maximum Match 100%
. Listing first 45 summaries
 - protein search, using sw model
 Q8DIHO
Q815A7
Q98EX1
Q74056
Q9URY8
Q8EMD4
Q8EMD4
Q8UD18
Q8BTX4
Q8BTX4
Q8BTX4
Q8BTX4
Q8BTX4
Q8BTX4
 040129
07V604
09XVK4
08C1D7
 sp_virus:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 sp_archea.*
sp_bacteria.*
sp_tungi.*
sp_tungi.*
sp_human.*
sp_invertebrate.*
sp_mammal.*
sp_mammal.*
sp_organelle.*
 rvirus: *
bacteriap: *
 seq length: 0
seq length: 200000000
 sp_archeap:
 sp_plant:*
sp_rodent:*
 1 EEVVPXGMSYS 11
 Query
Match Length DB
 US-09-909-164-9
52
 SPIREMBL 25:*
 Score
 Title:
Perfect score:
 Scoring table:
 Minimum DB
Maximum DB
 OM protein
 Database :
 Sequence:
 Searched:
 Run on:
 Result
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| 0      | Osph83 plasmodium | Osphas plasmodium |        |        | Q8pmi6 xanthomonas | Q8pat2 xanthomona | Q9pdm6 xylella fa | Q14122 homo sapien | Q12479 saccharomyc | Q971s2 sulfolobus | O28342 archaeoglob | Q96mu1 homo sapien | Q92md6 rhizobium m | Q8iym3 homo sapien | Q98bp5 rhizobium | Q9pqd2 ureaplasma | Oluwu7 rhodopirel | Q9urr4 penicillium | Q8g4i5 bifidobacte | Q8xt05 ralstonia s | Q87kq5 vibrio para |        | ம      |        | O      | ın     | Q7sy67 xenopus lae |        |  |
|--------|-------------------|-------------------|--------|--------|--------------------|-------------------|-------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|--------|--------|--------------------|--------|--|
| Q7Z6R0 | Q9BH83            | Q9BHA5            | 081587 | 001487 | Q8PMI6             | Q8PAT2            | 9M0460            | 014122             | 012479             | 097152            | 028342             | Q96MU1             | Q92MD6             | QBIYM3             | Q98BPS           | Q9 PQD2           | Q7UWU7            | Q9URR4             | Q8G415             | QBXT05             | Q87KQ5             | Q8TX62 | Q8PPP5 | Q8VUA8 | Q8KTQ4 | QBRES6 | Q7SY67             | Q70552 |  |
| 4      | ທ                 | w                 | ហ      | 11     | 16                 | 16                | 16                | 4                  | m                  | 17                | 17                 | 4                  | 16                 | 4,                 | 16               | 16                | 16                | m                  | 16                 | 16                 | 16                 | 17     | 16     | 7      | N      | 16     | 13                 | 16     |  |
| 555    | 583               | 583               | 583    | 670    | 747                | 747               | 749               | 1902               | 156                | 219               | 252                | 290                | 387                | 489                | 541              | 544               | 731               | 842                |                    |                    | 1400               | 143    | 166    | 193    | 208    | 209    | 251                | 282    |  |
| 67.3   | 67.3              | 67.3              | 67.3   | 67.3   | 67.3               | 67.3              | 67.3              | 67.3               | 65.4               | 65.4              | 65.4               | 65.4               | 65.4               | 65.4               | 65.4             | 65,4              | 65.4              | 65.4               | 65.4               | 65.4               | 65.4               | 63.5   | 63.5   | 63.5   | 63.5   | 63.5   | 63.5               | 63.5   |  |
| 32     | 35                |                   |        |        |                    |                   |                   |                    |                    |                   |                    |                    |                    |                    |                  | 34                |                   |                    |                    |                    |                    |        |        |        |        |        | 33                 |        |  |
| 17     | 18                | 19                | 20     | 21     | 22                 | 23                | 24                | 25                 | 26                 | 27                | 28                 | 29                 | 30                 | 31                 | 32               | 33                | 34                | 35                 | 36                 | 37                 | 38                 | 39     | 40     | 41     | 42     | 43     | 44                 | 45     |  |

## AL I GNMENTS

Gaps : : A MAKAMURE-2222144; PubMed=12240834;
A MAKAMURE-2222144; PubMed=12240834;
A Watanabe A., Iriquchi M., Kavashima K., Kimura T., Xishida Y.,
A Watanabe A., Iriquchi M., Kawashima K., Kimura T., Xishida Y.,
Kiyokawa C., Xohara M., Mateumoto M., Matsuno A., Nakazaki N.,
Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
I "Complete genome structure of the thermophilic cyanobacterium
I Thermosynechococus elongatus BP-1.";
I Thermosynechococus elongatus BP-1.";
B EMBJ, AP005374; BAC09170.1, -.
R GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:0006310; P:transporter activity; IEA.
R GO; GO:006310; P:transporter activity; IEA.
R InterPro; IPR001036; Acrilvin\_res. ô Length 1044; Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBL\_TaxID=32046; Indels 1044 AA; 113205 MW; 00E9C13F0F636D2F CRC64; 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Multidrug efflux transporter. ; ; Query Match 75.0%; Score 39; DB 16; Best Local Similarity 63.6%; Pred. No. 28; Matches 7; Conservative 2; Mismatches 2 PRT; 1044 AA PRINTS; PR00702; ACRIFLAVINRP. TIGRFAMS; TIGR00915; 2A0602; 1.

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 Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Namoplete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti "."

DNA Res. 7:331-338(2000)
 MEDLINE=22608415; PubMed=12721630; Ivanova N., Candelon B., Rapatval V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A., Rapatval V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T., Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D., Overbeek R., Kyrpides N.; Grechkin S. D., Grechkin Bacillus archaecis."; Bacillus anthracis."; Mature 423:87-91(2003).
 Gape
 ö
 Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Phyllobacteriaceae, Mesorhizobium.
 Query Match 73.1%; Score 38; DB 16; Length 344; Best Local Similarity 60.0%; Pred. No. 13; Matches 6; Conservative 2; Mismatches 2; Indels
 Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=226900;
 344 AA; 38539 MW; C5526BACB7225995 CRC64;
 EMBL; AP0013002; BABSO445.1; -.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0005237; F:metallopeptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR002933; Peptidase M20.
 Q815A7 PRELIMINARY; PRT; 344 AA.
Q815A7;
Q1-UUN-2003 (TrEMBLrel. 24, Created)
O1-UUN-2003 (TrEMBLrel. 24, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 387 AA.
 ABC transporter substrate-binding protein.
BC5259.
 EMBL; AE017015; AAP12123.1; ...
InterPro, IPR000437; Prok lipoprot S.
PROSITE; PS00013; PROXAR LIPOPROTEIN; 1.
Complete proteome 344 AA; 38539 MW; C5526BACB
 Rhizobium loti (Mesorhizobium loti).
 PRT;
 STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
 PRELIMINARY;
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843 EEVLPNGIGYS 853
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152 EEIAPLGLSY 161
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 1 EEVVPXGMSY 10
 Hippurate hydrolase.
MLR3583.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Q98FX1;
 Q98FX1
 RESULT 3
 RESULT 2
 Q815A7
 Q98FX1
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 "Genomic analysis reveals chromosomal variation in natural populations of the uncultured psychrophilic archaeon Cenarchaeum symbiosum.";
J. Bacteriol. 180:5003-5009(1998).
BMBL; AF083072; AAC62699.1;
PIR; T31308; T31308.
GO; GO:0016020; Cimembrane; IEA.
GO; GO:00160215; F:transport; IEA.
GO; GO:0005215; F:transport; IEA.
InterPro; IPR001580; WD40.
SMART; SM00320; WD40! 2.
 Gaps
 Gaps
 074056 PRELIMINARY; PRT; 3472 AA.
074056;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Genarchaeum symbiosum.
Archaea; Crenarchaeota; Thermoprotei; Cenarchaeales; Cenarchaeaceae;
 SECUENCE FROM N.A.
STRAIN=972h-;
Hunt C., Aves S., McDougall R.C., Rajandream M.A., Barrell B.G.;
 ;
 ..
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 STRAIN=B;
MEDINE=99422450; PubMed=9748430;
Schlepper C. DeLong B.F., Preston C.M., Feldman R.A., Wu K.Y.,
Swanson R.V.;
 Score 38; DB 16; Length 387;
Pred. No. 15;
2; Mismatches 2; Indels
 Length 3472;
 PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; 1.
Hypothetical protein.
SEQUENCE 3472 AA; 367058 MW; 37F80707030F9355 CRC64;
 1; Indels
Pfam, PF01546, Peptidase M20, 1.
Hydrolase, Complete proteome.
SEQUENCE 387 AA, 41180 MW, 131BFF8E64306829 CRC64;
 Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 24, Last annotation update)
Probable sulfate permease.
 Score 38; DB 1; I
Pred. No. 1.7e+02;
4; Mismatches 1;
 840 AA
 PRT;
 73.1%;
 73.1%;
54.5%;
 Query Match
Best Local Similarity 54.00.
Best Local 6; Conservative
 Query Match
Best Local Similarity 60...
6; Conservative
 2294 EDVIPRGISFS 2304
 PRELIMINARY;
 1 EEVVPXGMSYS 11
 367 DEAIPHGMSY 376
 1 EEVVPXGMSY 10
 Schizosaccharomyces.
NCBI_TaxID=4896;
 SEQUENCE FROM N.A.
 NCBI_TaxID=46770;
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Gaps

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MEDLINE=22354683; PubMed=12466851;
MEDLINE=22354683; PubMed=12466851;
The FANTON Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
 Score 36; DB 11; Length 484;
Pred. No. 53;
 Score 36; DB 11; Length 471; Pred. No. 51; 2; Indels 2; Indels
 Ol-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
1-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to glidma tumor suppressor candidate region gene 2.
GLTSCR2 OR AW536411.
 OBBTX4;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to glioma tumor suppressor CANDIDATE region gene 2
 Strausberg R.; Strausberg R.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC055810; AAH58810.1; -. MGD; MGI:2154441; Gltscr2. Hypothetical protein. Strategues 471 AA; 54506 MW; E0DA685C374A9760 CRC64;
 Straubberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017637, AAH17637.1;
MGD; MGI:2154441; Gliecri.
SEQUENCE 484 AA; 55835 MW; BBB45F3B4BE02A36 CRC64;
 484 AA
 484 AA
 2; Mismatches
 PRT;
 PRT;
 69.2%;
 69.2%;
 SEQUENCE FROM N.A.
STRAIN-NOD; TISSUE-Thymus;
 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
 6; Conservative
 PRELIMINARY;
 PRELIMINARY;
 226 EVIPAGASYN 235
 239 EVIPAGASYN 248
 SEQUENCE FROM N.A.
TISSUE=Salivary gland;
 2 EVVPXGMSYS 11
 2 EVVPXGMSYS 11
 Mus musculus (Mouse)
 Query Match
Best Local Similarity
Matches 6; Conserv
 SEQUENCE FROM N.A. TISSUE=Liver;
 NCBI_TaxID=10090;
 NCBI_TaxID=10090;
 28VD18
 Q8BTX4
 RESULT 8
Q8VD18
 RESULT 9
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 Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K., Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
"The complete gamonic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans.";
Nucleic Acids Res. 30:5293-5300(2002).
EMBL, APRO417; BAC44062.1;
InterPro; IPR009885; Cond. like lec.gl.
InterPro; IPR009885; LipoproteIn. 7.
Pram, PF04500; LipoproteIn. 7; 3.
 Gaps
 Gaps
 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
GLTSCR2.
GLMs musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
 Mycoplasma penetrans.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=28227;
 0,
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 71.2%; Score 37; DB 16; Length 1123; 70.0%; Pred. No. 81; avative 1; Mismatches 2; Indels C
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; ALI32779; CABG0015.1; -.

R GeneDB SPOWDe; SPAC869.05c; -.

GO; GO: 0016020; C: membrane; IEA.

GO; GO: 0008271; F: sulfate pricer activity; IEA.

R GO; GO: 0008271; F: sulfate transport; IEA.

R GO; GO: 0008275; P: sulfate transport; IEA.

R InterPro; IPR001902; Sulph_transpt.

R Pfam; PF01740; STAS; 1.

R Pfam; PF01740; STAS; 1.

R Pfam; PF01740; STAS; 1.

R Pfam; PF0175; Sulfate_transp; 1.

R TIGRAPMS; TIGR0015; Sulph_transp; 1.

R PROSITE; PS50801; STAS; 1.

R PROSITE; PS50801; STAS; 1.

R PROSITE; PS50801; STAS; 1.
 Score 37; DB 3; Length 840;
Pred. No. 59;
1; Mismatches 1; Indels
 1123 AA; 123636 MW; A4D707330E3DB4AC CRC64;
 Created)
Last sequence update)
Last annotation update)
 471 AA
 PRT; 1123 AA
 MEDLINE=22354719; PubMed=12466555;
 71.2%;
 01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-007-2003 (TrEMBLrel. 25,
MYPE 2560 paralog, 57%.
 Query Match
Best Local Similarity 77.8
Matches 7; Conservative
 Query Match
Best Local Similarity 70.0
Matches 7; Conservative
 PRELIMINARY;
 PRELIMINARY;
 658 EYVPMGLSYS 667
 2 EVVPXGMSYS 11
 135 VVPQGMSYA 143
 3 VVPXGMSYS 11
 SEQUENCE FROM N.A. STRAIN=HF-2;
 Complete proteome
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QBEWD4; Q8EWD4

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SEQUENCE

Q8R126 Q8R126;

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RESULT 7

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Gaps

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 RESULT 12
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 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C2354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research droup Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full.length cDNAs.";
Nature 420.563-573 (2002).
BMBL; AK077341; BAC36760.1; -.
BCMBL; MGI:2154441; GLEGCZ.
SEQUENCE 484 AA; 55792 MW; EB67349BCBE92D44 CRC64;
 SEQUENCE FROM N.A.
STRAIN=V683 / ATCC 700802;
MEDLINE=22550857; PubMed=12663927;
Read T.D., Fouts D.E., Bisen J.A., Gill S.R., Heidelberg J.F.,
Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beann M.,
Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
 Gaps
 Enterococcus faecalis (Streptococcus faecalis).
Bacteria, Firmicutes, Lactobacillales, Enterococcaceae, Enterococcus.
NCBL_TaxID=1351;
 Gaps
 protein.
GITSCR2.
Mus musculus (Mouse).
Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus.
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 / Match
Local Similarity 69.2%; Score 36; DB 11; Length 484;
Local Similarity 60.0%; Pred. No. 53;
les 6; Conservative 2; Mismatches 2; Indels
 69.2%; Score 36; DB 11; Length 484; 60.0%; Pred. No. 53; 2; Indels tive 2; Mismatches 2; Indels
 QBEK35;
01-WAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UDN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to glioma tumor suppressor CANDIDATE region gene 2
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL, AKO88461; BAC40367.1; -.
MGD; MGI:2154441; G1tscr2.
SEQUENCE 484 AA; 55806 MW; B3056425B5EBCAD8 CRC64;
 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 484 AA.
 PRT; 559 AA.
 PRT;
 Pheromone binding protein, putative
 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
 PRELIMINARY;
 PRELIMINARY;
 239 EVIPAGASÝN 248
 239 EVIPAGASYN 248
 2 EVVPXGMSYS 11
 2 EVVPXGMSYS 11
 Query Match
 Q839T9;
 Q839T9
 QBBK35
 EF0063
 RESULT 10
Q8BK35
ID Q8BK3
 RESULT 11
0839T9
0839T
AC 0839T
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JC
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GN BRICH
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OC BRCTE
OC BRCTE
OC RATE
RR SEQUE
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 SEQUENCE FROM N.A.

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RETY K. Uterback T., Van Aken S., Feldblyum T., Gwinn M.,

Berry K., Uterback T., Van Aken S., Feldblyum T., Gwinn M.,

Ra Brinkac I., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,

Rhite O., Fraser C., Collmer A., Rolonay J., Madupu R., Davidsen T.,

Rhite O., Fraser C., Collmer A., Selengut J., Nelson W., Davidsen T.,

Rhite O., Fraser C., Collmer A.,

Rhite O., Fraser C., Collmer A.,

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 Gaps
TROLE of mobile DNA in the evolution of vancomycin-resistant
Thereoccus facealis.";
Science 299-2071-2074[2003].
Thereoccus Facealis.";
There 299-2071-2074[2003].
There 299-2071-2074[2003].
There 299-2071-2074[2003].
There 299-2071-2074[2003].
There 299-2071-2074[2003].
There 299-2074[2003].
There 299-2074[
 01-UN-2003 (TrEMBLrel. 24, Created)
01-UN-2003 (TrEMBLrel. 24, Last sequence update)
01-CTT-2003 (TrEMBLrel. 25, Last annotation update)
01-CTT-2003 (TrEMBLrel. 25, Last annotation update)
DNA-directed RNA polymerase, beta' subunit.
RPOC OR PSPRO0620.
Pseudomonas syringae (pv. tomato).
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales;
 .
 .
0
 Query Match 69.2%; Score 36; DB 16; Length 1399; Best Local Similarity 66.7%; Pred. No. 1.7e+02; Matches 6; Conservative 2; Mismatches 1; Indels C
 69.2%; Score 36; DB 16; Length 559; 66.7%; Pred. No. 62; 1; Indels ative 2; Mismatches 1; Indels
 PRT; 1399 AA
 Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=323;
 Query Match
Best Local Similarity 66.77
6; Conservative
 PRELIMINARY;
 351 LIPEGMSYS 359
 :||| |:||
581 QWPAGLSY 589
 2 EVVPXGMSY 10
 3 VVPXGMSYS 11
 SEQUENCE FROM N.A.
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 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 25, Last annotation update)
10-CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypochetical procesin precursor.
Lycopersicon esculentum (Tomato).
Eukaryora, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
 Gaps
 MEDLINE-22055698; PubMed=12917642; Malfatti S., Chain P., MEDLINE-22055698; PubMed=12917642; Malfatti S., Chain P., Ahlgren M.A., Arellano A., Coleman M., Hauser L., Hess W.R., Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M., Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A., Webb B.A., Zinser B.R., Chisholm S.W.; Genome divergence in two Prochlorococcus ecotypes reflects oceanic
 01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Phospholipid and glycerol acyltransferase (From 'motifs_6.msf').
 ô
 Prochlorococcus marinus (strain MIT 9313).
Bacteria, Cyanobacteria, Prochlorophytes, Prochlorococcaceae,
Prochlorococcus.
 Query Match 67.3%; Score 35; DB 10; Length 225; Best Local Similarity 54.5%; Pred. No. 37; Matches 6; Conservative 3; Mismatches 2; Indels
 67.3%; Score 35; DB 16; Length 245;
 niche differentiation.";
Nature 424:1042-1047(2003).
EMBL: BXS72099; CAEZIG7.1; -.
ACYLransferase; Transferase; Complete proteome.
SEQUENCE 245 AA; 26907 MW; 106F7C4CBE2C6427 CRC64;
 225 AA.
 245 AA.
 PRT,
 PRT;
 PRELIMINARY;
 PRELIMINARY;
 1 EEVVPXGMSYS 11
 32 DEVVPNGKTYA 42
 NCBI_TaxID=74547;
 Query Match
 Q40129
Q40129;
 Q7V6Q4
RESULT 13
Q40129
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 Gaps
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
 Gaps
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 Genome sequence of the nematode C.elegans: A platform for
 WormPep; R10D12.10; CE12690.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004672; F:protein kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006648; F:protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Prot_kinase.
 67.3%; Score 35; DB 5; Length 425; 50.0%; Pred. No. 75; 2; Indels :ive 3; Mismatches 2; Indels
 Indels
 Percy C.M.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
 ProDom; PD000001; Prot_kinase; 1.
PROSITE; PSSO11; PROTEIN KINASE_DOM; 1.
ATP-binding; Transferase.
SEQUENCE 425 AA; 49410 MW; 5D96E29B08C8E9D6 CRC64;
 Last sequence update)
Last annotation update)
 425 AA.
 Pred. No. 41;
2; Mismatches
 Search completed: June 3, 2004, 11:57:32
Job time: 29.8667 secs
 Created)
 MEDLINE=99069613; PubMed=9851916;
60.08;
 investigating biology.";
Science 282:2012-2018(1998).
EMBL; 281109; CAB03241.1; --
PIK; T24111; T24111.
 01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-CCT-2003 (TrEMBLrel. 25,
RIDD12.10 protein.
 Best Local Similarity 60.0
Matches 6; Conservative
 Local Similarity 50.0
les 5, Conservative
 PRELIMINARY;
 Pfam; PF00069; pkinase;
 179 OVVPVGLGYS 188
 335 EQIVPGGLQY 344
 2 EVVPXGMSYS 11
 1 EEVVPXGMSY 10
 SEQUENCE FROM N.A.
 [2]
SEQUENCE FROM N.A.
 Query Match
 Q9XVK4
 RESULT 15
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Abb80554 Hepatitis
Abb80552 Hepatitis
Abb80552 Hepatitis
Abb80542 Hepatitis
Abb80540 Hepatitis
Abb80543 Hepatitis
Abb80543 Hepatitis
Abb80547 Hepatitis
Abb80554 Hepatitis
Abb80551 Hepatitis
Abb80541 Hepatitis
Abb80541 Hepatitis
Abb80540 Hepatitis
Abg03621 Novel hum
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
 Hepatitis C virus, HCV, serine protease, inhibitor, alpha-ketoamide, virucide.
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5.
 'note= "N-terminal acetyl"
 ALIGNMENTS
 /note= "C-terminal amide"
 'note= "D-form residue"
 ABB80544
ABB80553
ABB80552
 ABB80545
ABB80530
ABB80542
ABB80542
ABB80548
ABB80547
ABB80557
ABB80557
ABB80557
ABB80557
ABB80557
ABB80557
ABB80557
ABB80557
 AAU76810
ABG03621
ABG08173
ABG05826
ABB80546
 Location/Qualifiers
 Brunck TK;
 ABB80525 standard; peptide; 11 AA.
 Claim 17; Page 64; 69pp; English.
 19-JUL-2001; 2001WO-US023169.
 21-JUL-2000; 2000US-0220101P.
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 (first entry)
 444444444444
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39.
 Misc-difference
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002
 Synthetic.
 ABB80525;
 RESULT 1
ABB80525
 Abb80525 Hepatitis
Abb80521 Hepatitis
Abb80552 Hepatitis
Abb80565 Hepatitis
Abb80563 Hepatitis
Abb80567 Hepatitis
Abb80559 Hepatitis
Abb80559 Hepatitis
Abb80559 Hepatitis
Abb80564 Hepatitis
Abb80564 Hepatitis
Abb80564 Hepatitis
Abb80568 Hepatitis
 Hepatitis
Hepatitis
Hepatitis
 Hepatitis
Hepatitis
 Hepatitis
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 June 3, 2004, 11:31:01; Search time 45.9333 Seconds (without alignments) 67.664 Million cell updates/sec
 Description
 Abb80521
Abb80565
Abb80565
Abb80565
Abb80565
Abb80565
Abb80561
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1586107 segs, 282547505 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 ABB60521
ABB80566
ABB80566
ABB80567
ABB80567
ABB80556
ABB80566
ABB80566
ABB80529
ABB80529
ABB80529
ABB80529
ABB80529
ABB80529
ABB80528
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ABB80528
ABB80566
 Gapop 10.0 , Gapext 0.5
 genesequ1990s:*
genesequ2000s:*
genesequ2002s:*
genesequ2002s:*
genesequ2003bs:*
genesequ2003bs:*
 A_Geneseq_29Jan04:*
1: geneseqp1980s:*
 Winimum DB seq length: 0 Maximum DB seq length: 2000000000
 US-09-909-164-10
52
1 EEVVPXGMSYS 11
 B
 Query
Match Length
 BLOSUM62
 Score
 Perfect score:
 Scoring table:
 Sequence:
 Searched:
 Database
 Run on:
 Result
No.
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Gaps

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Indels

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Mismatches

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Conservative

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Matches
 RESULT 3
ABB80522
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 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 'note= "Norvaly1 carbony1 forming keto-amide linkage with
 virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1
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 Length 11;
 Length 11;
 Indels
 DB 5; Le:
0.002;
thes 0;
 DB 5;
0.002;
 Score 50; DB 5; Pred. No. 0.000; Mismatches
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 Score 50;
Pred. No.
 Location/Qualifiers
 Ä
 Brunck TK;
 96.2%; Scor.
100.0%; Pre
 Claim 17; Page 64; 69pp; English
 ABB80521 standard; peptide; 11
 96.2%; S
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 (first entry)
 residue 7'
 11; Conservative
 11
 1 EEVVPXGMSYS 11
 Levy OE,
 (CORV-) CORVAS INT INC
 EEVVPXGMSYS
 WPI; 2002-361643/39
 Query Match
Best Local Similarity
 Query Match
Best Local Similarity
 Sequence 11 AA;
 Sequence 11 AA;
 WO200208251-A2
 Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 Synthetic.
 ABB80521;
 virucide.
 protease.
 Matches
 RESULT 2
 ABB80521
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 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture a medicament to treat disorders associated with HCV protease. A
 Gарв
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C ^{\circ}
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2.
 ö
 Length 11;
 0; Indels
 Score 50; DB 5;
Pred. No. 0.002;
0; Mismatches
 /note= "N-terminal acetyl"
 /note= "C-terminal amide"
 note= "D-form residue"
 Location/Qualifiers
 Ą
 Brunck TK;
 Claim 17; Page 64; 69pp; English.
 96.2%; Scoi
100.0%; Pri
tive 0;
 ABB80522 standard; peptide; 11
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P.
 (first entry)
 Local Similarity 100.
 EEVVPXGMSYS 11
1 EEVVPXGMSYS 11
 Levy OE,
 (CORV-) CORVAS INT INC
 1 EEVVPXGMSYS
 WPI; 2002-361643/39.
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Novel peptide activity usefu
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 Synthetic.
 ABB80522;
 Query Match
 virucide
 protease
 Matches
```

EEVVPXGMSYS 11

RESULT

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 /note= "Valyl carbonyl forming keto-amide linkage with residue ?"
 /note= "Norleucyl carbonyl forming keto-amide linkage
with residue 7"
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #45.
 DB 5; Lens.
0. 0.002;
0; Indels
 Mismatches
 /note= "N-terminal acetyl"
 'note= "N-terminal acetyl"
 'note= "C-terminal amide"
 Score 50; I
Pred. No. C
 Location/Qualifiers
 Location/Qualifiers
 ABB80565 standard; peptide; 11 AA.
 Brunck IK;
 96.2%; Scor
100.0%; Pre
 Claim 17; Page 65; 69pp; English.
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169.
 (first entry)
 Query Match
Best Local Similarity 100.
Matches 11, Conservative
 1 EEVVPXGMSYS 11
 BEVVPXGMSYS 11
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002
 Synthetic
 Synthetic.
virucide.
 protease
 RESULT 6
 LILLERXSXEEXPXCX
셤
 ઠ
 ö
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "2-aminoisobutyryl carbonyl residue forming a keto-amide linkage with residue 7"
 virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C ^{\circ}
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #43.
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46.
 ö
 , DB 5; Le...
 Query Match 96.2%; Score 50; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 11; Conservative 0; Mismatches
 note= "N-terminal acetyl"
 /note= "C-terminal amide"
 Location/Qualifiers
 Brunck TK;
 Ä
 \BB80566
ID ABB80566 standard, peptide, 11 AA.
 Claim 17; Page 65; 69pp; English.
 standard; peptide; 11
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 (first entry)
 (first entry)
 1 EEVVPXGMSYS 11
 Levy OE,
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39
 Sequence 11 AA;
 WO200208251-A2
 Novel peptide
 Key
Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 08-OCT-2002
 31-JAN-2002
 Synthetic
 ABB80563
 ABB80563;
 ABB80566;
 protease.
```

RESULT 5

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Gaps

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g
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 ö
 The sequence represents a peptide compound of the invention having hebgaticis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-kercamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "(8,8)allothreonyl carbonyl residue forming a keto -amide linkage with residue 7"
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #47.
 ö
 96.2%; Score 50; DB 5; Length 11; 100.0%; Pred. No. 0.002; ive 0; Mismatches 0; Indels
 note= "N-terminal acetyl"
11
/note= "C-terminal amide"
 /note= "C-terminal amide
 Location/Qualifiers
 Brunck TK;
 ABB80567 standard; peptide; 11 AA.
 Claim 17; Page 65; 69pp; English
 21-JUL-2000; 2000US-0220101P.
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169
 19-JUL-2001; 2001WO-US023169.
 (first entry)
 Best Local Similarity 100.
Matches 11; Conservative
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39.
 Sequence 11 AA;
 WO200208251-A2
 WO200208251-A2
Modified-site
 Key
Modified-site
 Modified-site
 Modified-site
 31-JAN-2002
 08-OCT-2002
 31-JAN-2002
 Synthetic.
 ABB80567;
 protease.
 Query Match
 virucide.
 RESULT 7
ઠ
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The sequence represents a peptide compound of the invention having the peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with RTO procease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treat disorders associated with hepatitis C virus
 /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 0; Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #39
 96.2%; Score 50; DB 5; Length 11; 100.0%; Pred. No. 0.002; ive 0; Mismatches 0; Indels
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 'note= "D-form residue"
 'note= "Oxymethionine"
 Location/Qualifiers
 Brunck TK;
 ABB80559 standard; peptide; 11 AA.
 Lim-Wilby M, Levy OE, Brunck TK;
 Claim 17; Page 65; 69pp; English.
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 Ouery Match
Best Local Similarity 100.
Matches 11, Conservative
 (first entry)
 1 REVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 Lim-Wilby M, Levy OE,
(CORV-) CORVAS INT INC.
 (CORV-) CORVAS INT INC.
 WPI; 2002-361643/39.
 WPI; 2002-361643/39.
 Sequence 11 AA;
 Misc-difference
 WO200208251-A2
 Modified-site
 Novel peptide
 Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002
 Synthetic.
 protease.
 ABB80559,
 virucide.
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The sequence represents a peptide compound of the invention having the peptides of the invepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the pebtide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #6.
 ABB80526 standard; peptide; 11 AA.
 Claim 17; Page 64; 69pp; English
 65; 69pp; English.
 21-JUL-2000; 2000US-0220101P
 19-JUL-2001; 2001WO-US023169
 (first entry)
 Query Match
Best Local Similarity 100.
Matches 11, Conservative
 1 EEVVPXGMSYS 11
 EEVVPXGMSYS 11
 (CORV-) CORVAS INT INC
 Levy OE,
 WPI; 2002-361643/39.
 Misc-difference
 Misc-difference
 Sequence 11 AA;
 Claim 17; Page
 WO200208251-A2
 Key
Modified-site
 Modified-site
 peptide
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 Synthetic
 protease
 Novel per
activity
 protease
 RESULT 9
ABB80526
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'note= "Norvalyl carbonyl forming keto-amide linkage with

/note= "C-terminal amide"

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Brunck

note= "D-form residue" 'notes "D-form residue"

residue 7"

'note= "N-terminal acetyl"

Location/Qualifiers

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ö
 The sequence represents a peptide compound of the invention having the peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with IRV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treat disorders associated with hepatitis C virus
 ingredient
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "Leucyl carbonyl forming keto-amide linkage with
residue 7"
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #44
 ö
 DB 5; here,
 96.2%; Score 50; DB 100.0%; Pred. No. 0.0
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 Location/Qualifiers
 Brunck TK;
 Ą.
 Claim 17; Page 65; 69pp; English
 디
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 ABB80564 standard; peptide;
 (first entry)
 Query Match
Best Local Similarity 100.
 1 EEVVPXGMSYS 11
 EEVVPXGMSYS 11
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39
 Sequence 11 AA;
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002
 Synthetic
 ABB80564;
 protease
 virucide
 RESULT 10
 ABB80564

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Gaps

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96.2%; Score 50; DB 5; Length 11; 100.0%; Pred. No. 0.002; ive 0; Mismatches 0; Indels

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Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
 ABB80561 standard; peptide; 11 AA.
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002
 Synthetic
 ABB80561;
 ABB80561
 윱
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 ö
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 note= "Alpha-propynyl-glycinyl-carbonyl residue forming a keto-amide linkage with residue 7"
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #48.
 ö
; DB 5; Le...
(°. 0.002;
0; Indels
 96.2%; Score 50; DB 5; Length 11; llarity 100.0%; Pred. No. 0.002; Conservative 0; Mismatches 0; Indels
 Score 50; DB 5 Pred. No. 0.00 0; Mismatches
 'note= "N-terminal acetyl"
 11
/note= "C-terminal amide"
 Location/Qualifiers
 ABB80568 standard; peptide; 11 AA.
 Brunck TK;
 96.2%; Scc...
100.0%; Pre
 Claim 17; Page 65; 69pp; English.
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 11; Conservative
 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 (CORV-) CORVAS INT INC
 Levy OE,
 WPI; 2002-361643/39.
 Similarity
 Query Match
Best Local Similarity
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Lim-Wilby M,
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002.
 Query Match
Best Local Si
Matches 11,
 Synthetic.
 ABB80568;
 Matches
 ABB80568
```

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ö
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-Ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 'note= "Norvalyl carbonyl forming keto-amide linkage with
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
 Gaps
Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 ô
 Length 11;
 1; Indels
 88.5%; Score 46; DB 5;
90.9%; Pred. No. 0.013;
iive 0; Mismatches 1
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 'note= "D-form residue"
 note= "Oxymethionine"
 Location/Qualifiers
 ABB80524 standard; peptide; 11 AA.
 Brunck TK;
 Claim 17; Page 65; 69pp; English.
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169.
 residue 7"
 Ħ
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 1 REVVPXGMSYS
 REVVPXGMDYS
 WPI; 2002-361643/39.
 Misc-difference
 ABB80524;
 RESULT 13
ABB80524
ID ABB800
XX
AC ABB800
```

Gaps

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1 BEVVPXGMSYS 11

11;

11

EEVVPXGMSYS

Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4

(first entry)

08-OCT-2002

us-09-909-164-10.rag

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Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 Synthetic
 protease.
 н
 ABB80528
 ABB80528
 virucide
 RESULT 15
 셤
 LLLLEXSXEXEXEXEX
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 ö
 The sequence represents a peptide compound of the invention having invention or virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcomide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
 note= "Norvaly1 carbony1 forming keto-amide linkage with
 pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9.
 ö
 Score 46; DB 5; Length 11;
Pred. No. 0.013;
0; Mismatches 1; Indels
 note= "N-terminal acetyl"
 /note= "C-terminal amide"
 note= "D-form residue"
 Location/Qualifiers
 Brunck TK,
 Ä
 Claim 17; Page 64; 69pp; English.
 .;
 ABB80529 standard; peptide; 11
 88.5%;
90.9%;
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169
 residue 7"
 (first entry)
 Local Similarity 90.5
nes 10; Conservative
 1 EEVVPXGMSYS 11
 EEVVPXGMDYS 11
 Levy OE,
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39.
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 Synthetic
 Synthetic
 ABB80529
 protease
 Query Match
 virucide
 Best Loca
Matches
 RESULT 14
 ABB80529
 ઠે
 셤
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ö
 'note= "Norvalyl carbonyl forming keto-amide linkage with esidue 7"
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hopatitis C virus
 /note= "Norvaly1 carbony1 forming keto-amide linkage with
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 serine protease inhibitor peptide #8.
 .
 Score 46; DB 5; Length 11;
Pred. No. 0.013;
); Mismatches 1; Indels
 'note= "N-terminal acetyl"
 /note= "N-terminal acetyl"
 /note= "C-terminal amide"
 'note= "D-form residue"
 note= "D-form residue"
 Location/Qualifiers
 Location/Qualifiers
 Ţ,
 11 AA.
 Claim 17; Page 64; 69pp; English
 Brunck
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
 standard; peptide;
 Hepatitis C virus NS3/NS4a
 (first entry)
 residue
 EEVVPXGMSYS 11
 EEVVPXGMDYS 11
 Levy OE,
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39
 Misc-difference
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Key
Modified-site
 Modified-site
 Modified-site
 Modified-site
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Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 /note= "C-terminal amide"
 /note= "D-form residue"
 19-JUL-2001; 2001WO-US023169.
 21-JUL-2000; 2000US-0220101P
residue 7"
8
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC.
 WPI; 2002-361643/39.
 Misc-difference
 WO200208251-A2
 Modified-site
 31-JAN-2002.
 protease.
```

Brunck TK;

Claim 17; Page 64; 69pp; English.

The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoande peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus

Sequence 11 AA;

Gaps ; 0 Query Match 88.5%; Score 46; DB 5; Length 11; Best Local Similarity 90.9%; Pred. No. 0.013; Matches 10; Conservative 0; Mismatches 1; Indels

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Search completed: June 3, 2004, 11:48:23 Job time: 45.9333 secs

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US-US-134-UUC-3/38

Sequence 3738, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: NUMBER: US/09/134,000C

CURRENT APPLICATION NUMBER: US 60/055,778

FRIOR APPLICATION NUMBER: US 60/055,778

FRIOR APPLICATION NUMBER: US 60/055,778

FRIOR APPLICATION NUMBER: US 60/055,778

SEQ ID NOS: 6812

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3738
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5
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 |:|:| |:|:|
2294 EDVIPRGISFS 2304
 6; Conservative
 1 EEVVPXGMSYS 11
 RESULT 2
US-09-134-000C-3738
0
 Matches
 g
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 Sequence 4, Appli
Sequence 3738, Ap
Sequence 2902, Ap
Sequence 2902, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 336, Appli
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Patent No. 51
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 GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
 US-09-408-020-4
US-09-134-000C-7738
US-09-228-986-73
US-09-540-236-2902
US-09-760-946-2
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US-08-637-759B-236
US-08-871-355A-236
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 PCT-US93-05000-21
US-08-464-517-22
US-08-246-361A-22
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 US-09-909-164-10
52
 1 EEVVPXGMSYS 11
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 Score
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Perfect score:
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 equence:
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 Jatabase
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 Result
No.
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| sequence 22, Appl<br>Sequence 22, Appl<br>Sequence 6, Appli<br>Sequence 4, Appli<br>Sequence 6, Appli<br>Sequence 6, Appli<br>Sequence 6, Appli<br>Sequence 23, Appli<br>Sequence 23, Appli<br>Sequence 23, Appli<br>Sequence 23, Appli<br>Sequence 23, Appli<br>Sequence 24, Appli<br>Sequence 24, Appli<br>Sequence 26, Appli<br>Sequence 19, Appli<br>Sequence 19, Appli<br>Sequence 19, Appli<br>Sequence 19, Appli<br>Sequence 19, Appli<br>Sequence 19, Appli | M CENARCHAEUM SYMBIOSUM                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Length 3472;<br>; Indels 0; Gaps 0;                                 |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------|
| 236 3 US-08-463-772-22 280 2 US-08-464-776 280 2 US-08-464-776 289 2 US-08-246-772-6 289 5 PCT-US93-0500-4 289 5 PCT-US93-0500-4 289 5 PCT-US93-0500-4 289 2 US-08-246-361A-4 292 2 US-08-246-377-23 292 2 US-08-246-361A-23 292 3 US-08-246-361A-23 293 1 US-07-947-120-8 295 1 US-07-947-120-8 295 2 US-08-464-517-19 295 2 US-08-464-517-19 295 2 US-08-464-517-19 295 2 US-08-464-517-19                                                                        | ALIGNMENTS  on US/09408020  Ronald V. Robert A. Christa NUCLEIC ACIDS AND PROTEINS FROM 1990-09-29 1995-09-29 1123 r Windows Version 3.0                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 1%; Score 38; DB 4;<br>5%; Pred. No. 1.1e+02;<br>4; Mismatches 1    |
| 28<br>30<br>31<br>31<br>32<br>33<br>33<br>34<br>35<br>36<br>37<br>38<br>38<br>38<br>38<br>38<br>38<br>38<br>38<br>38<br>38                                                                                                                                                                                                                                                                                                                                          | RESULT 1 US-09-408-020-4   Sequence 4 Application US/09408020   Parent No. 6632937   GENERAL INFORMATION:   APPLICANT: Swanson, Rohart A. APPLICANT: Schleper, Christa TITLE OF INVENTION: NUCLEIC ACIDS AND PRO TITLE OF INVENTION: NUCLEIC ACIDS AND PRO URRENT FILING DATE: 1999-09-29   CURRENT PILING DATE: 1998-09-29   PRIOR PELICATION NUMBER: 60/102,294   PRIOR PELICATION NUMBER: 05/09/408,020   OURRENT FILING DATE: 1998-09-29   NUMBER OF SEQ ID NOS: 123   SEQ ID NO 4   IENGTH: 3472   TYPE: PRIOR PRIOR OF MINIONE VERSION 3.0   ORGANISM: Cenarchaeum symbiosum US-09-408-020-4 | Query Match<br>Best Local Similarity 54.<br>Matches 6; Conservative |

Gaps

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Sequence 7885, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE REFERENCE: GCC99-036-04
CURRENT PILLING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7885
LENGTH: 1407
 Sequence 2, Application US/09760946
; Sequence 2, Application US/09760946
; Patent No. 6608027
; GENERAL INFORMATION:
; APPLICANT: Tauntrios, Youla S.
; APPLICANT: Cameron, Dale R.
; APPLICANT: Generon, Else
; APPLICANT: Generon, Else
; APPLICANT: Halmos, Teddy
; APPLICANT: And Selvent Peptides Active Against the Hepatitis C Virus
; TITLE OF INVENTION: MAGRET: US 09/760,946
; TITLE OF INVENTION NUMBER: US 09/542,675
; PRIOR PILING DATE: 2001-08-23
; PRIOR FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 2
; LENGTH: 12
 OTHER INFORMATION: Substrate for recombinant HCV NS3 protease radiometric assay
 ö
 ö
 Score 34; DB 4; Length 1407;
Pred. No. 2.5e+02;
2; Mismatches 1; Indels
 Query Match
Best Local Similarity 45.5%; Pred. No. 1.7;
Matches 5; Conservative 4; Mismatches 2; Indels
 Sequence 3, Application US/09760946
Patent No. 6608027
GENERAL INFORMATION:
APPLICANT: Teantrizes, Youla S.
APPLICANT: Camercn, Dale R.
APPLICANT: Faucht, Anne-Marie
APPLICANT: Ghizo, Rise
 ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7885
 65.4%;
 ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 66.
 1 REVVPXGMSYS 11
 1 DDIVPCSMSYT 11
 |||| |:|:
596 EVVPEGLSF 604
 2 EVVPXGMSY 10
 US-09-760-946-2
 Query Match
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 8
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 Sequence 2012, Application US/09540236

Patent No. 5673910

GENERAL INFORMATION:
PATENT GARY I.

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE REPERENCE: 2709.2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT PILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 2902

LENGTH: 1191
 Sequence 73, Application US/09228986
Sequence 73, Application US/09228986
Patent No. 635918
GENERAL INFORMATION:
GENERAL INFORMATION:
Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FASTSEQ for Windows Version 3.0
 ; FEATURE:
NAME/KEY: MISC FEATURE
1.0CATION: (327)..(328)
2.0CATION: Amino acids 327 & 328 are Xaa wherein Xaa = any amino acid.
US-09-134-000C-3738
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 Gaps
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 Score 34, DB 4, Length 1191;
Pred. No. 2e+02;
3, Mismatches 1; Indels
 Length 947;
 69.2%; Score 36; DB 4; Length 382; 66.7%; Pred. No. 22; 1; Indels tive 2; Mismatches 1; Indels
 1; Indels
 65.4%; Score 34; DB 4; 366.7%; Pred. No. 1.6e+02;
 2; Mismatches
 65.4%;
55.6%;
 Query Match
Best Local Similarity 66.'
Best Local Similarity 66.'
 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
 ; ORGANISM: M.catarrhalis
US-09-540-236-2902
 |::| ||:|
783 EILPVGMAY 791
 332 LIPEGMSYS 340
 ; ORGANISM: Pinus radiata
US-09-228-986-73
 686 VMPSGISYS 694
 2 EVVPXGMSY 10
 3 VVPXGMSYS 11
 3 VVPXGMSYS 11
 RESULT 4
US-09-540-236-2902
 RESULT 5
US-09-328-352-7885
 RESULT 3
US-09-228-986-73
 SEQ ID NO 73
LENGIH: 947
 TYPE: PRT
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Gaps

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Gaps
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0
 DB 3; Length 45;
 Length 45;
 3; Indels
 STREET: 1201 west reachier CITY: Atlanta
STATE: Georgia
SCOUNTRY: USA
ZIP: 30309-3450
COMPUTER: RELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Bam PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,355A
FILING DATE: 09-UN-1997
CLLASSIFICATION NUMBER: PCT/GB95/02875
FRICH APPLICATION NUMBER: PCT/GB95/02875
FRICH APPLICATION NUMBER: PCT/GB95/02875
FRICH APPLICATION NUMBER: PCT/GB95/02875
FRICH APPLICATION NUMBER: 11-DEC-1995
CLASSIFICATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101 CON
TELEBRATION NUMBER: 31,284
TELEBRATION SEQ ID NO: 236: SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acide
TVDE: amino acide
 Sequence 236, Application US/08871355A

Patent No. 6015669

GENERAL INFORMATION:
TITLE OF INVENTION: Jedentification of Genes
NUMBER OF SEQUENCES: 501

CORRESPONDENCE ADDRESS:
ADDRESSE: Patrea L. Pabet

STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
 Score 33; DB 3
Pred. No. 7.8;
1; Mismatches
 Score 33; DB Pred. No. 7.8;
 th 63.5%;
Similarity 60.0%;
6; Conservative
 Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
 45 amino acids
 single
 protein
 MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-871-355A-236
 1 EEVVPXGMSY 10
 1 EEISPLGWSY 10
 1 EEVVPXGMSY 10
 TYPE: amino acid
STRANDEDNESS: Bing
TOPOLOGY: linear
MOLECULE TYPE: prote
HYPOTHETICAL: NO-
US-08-637-7598-236
 Query Match
Best Local Similarity
Matches 6; Conserva
 1 EEISPLGWSY
 linear
 RESULT 9
US-08-871-355A-236
 ઠે
 셤
 g
 ઠ
APPLICANT: Goudreau, Nathalie
APPLICANT: Halmos, Teddy
APPLICANT: Halmos, Teddy
APPLICANT: Liliasa Brunet, Montse
APPLICANT: Liliasa Brunet, Montse
TITLE OF INVENTION: Macrocyclic Peptides Active Against the Hepatitis C Virus
FILE REFERENCE: 13/076-1-C1
CURRENT APPLICATION WUMBER: 08/99/760,946
CURRENT FILING DATE: 20010-04-03
PRIOR FILING DATE: 1099-04-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
ENGTHARE: Patentin version 3.1
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 Gaps
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 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Tracer for NS3 protease assay
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: Asp at position 1 is biotinylated
NAME/KEY: MOD_RES
LOCATION: (10)
LOCATION: (10)
CTHER INFORMATION: Tyr at position 10 is iodinated with I-125
US-09-760-946-3
 Score 33; DB 4; Length 12;
Pred. No. 1.7;
 2; Indels
 Sequence 236 Application US/08637759B
Sequence 236 Application US/08637759B
Patent No. 587631
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INTERTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COMPTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 11-DEC-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 4335
ATTORNEY/AGENT INFORMATION
 ATTORNEY AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101
TELECOMMUNICATION INFORMATION:
 TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236
 Query Match 63.5%;
Best Local Similarity 45.5%;
Matches 5; Conservative
 1 EEVVPXGMSYS 11
 1 DDIVPCSMSYT 11
 RESULT 8
US-08-637-759B-236
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Gaps

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Indels
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 3; Mismatches
 63.5%;
 Query Match
Best Local Similarity 45.5
Matches 5; Conservative
 Query Match 63.5
Best Local Similarity 45.5
Matches 5; Conservative
 5; Conservative
 399 KEICPGGMGYT 409
 399 KEICPGGMGYT 409
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 :|: | || |:
52 KEICPGGMGYT 62
 1 EEVVPXGMSYS 11
 SEQ ID NO:30:
 5177197-30
 Matches
 5177197-1
 셤
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 셤
 셤
 ö
 Gaps
 RESULT 11
517197-51
; PAGEDI NO. 5177197
; PAGEDI NO. 5177197
; PAGEDI NO. 5177197
; MERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH, LENN; HELDIN, CARL-HENRIK
; LENN; HELDIN, CARL-HENRIK
; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
; HUMAN TRANSFORMING GROWHT FACTOR-BETAL-BINDING PROTEIN
NUMBER OF SEQUENCES: 53
; CURRENT APPLICATION DATE: 18/07/487,343
; APPLICATION NUMBER: US/07/487,343
; FILING DATE: 27-FEB-1990
 ö
 Score 33; DB 6; Length 65; Pred. No. 12;
 Score 33; DB 4; Length 45; Pred. No. 7.8;
 3; Indels
 CORRESPONDENCE ADDRESS:
ADDRESSE:
Patrea L. Pabst
STREET: 2800 One Atlanta Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIF: 30309-3450
COMPUTER: ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PENDABLE FORM:
MEDIUM TYPE: PAPENTIN Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURPUTER: PAPENTICATION DATA:
APPLICATION NUMBER: US/09/201,945
FILING DATE:
CLASSIFICATION
PRIOR APPLICATION NUMBER: 08/637,759
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
MAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REBERRICE/DOCKET NUMBER: 31,284
REGISTRATION NUMBER: 31,284
TELEPHONE: (404) 873-8795
INFORMATION FOR SEO ID NO: 236:
SEQUENCE CHARACTERISTICS:
LEMGTH: 45 amino acids
TYPE: Amino acids
 Sequence 236, Application US/09201945
Patent No. 6344215
GARBAL INFORMATION:
GAPPLICANT: David William Holden
TITLE OF INFORTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
 Mismatches
 63.5%;
 63.5%;
 Best Local Similarity 60.0
Matches 6; Conservative
 MOLECULE TYPE: protein HYPOTHETICAL: NO
 1 EEVVPXGMSY 10
 1 EEISPLGWSY 10
 linear
 Query Match
Best Local Similarity
 US-09-201-945-236
 LENGIH: 65
 RESULT 10
US-09-201-945-236
 Query Match
 5177197-51
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RESULT 14
US-09-157-92-66
| Sequence 66, Application US/09357952
| Sequence 66, Application US/09357952
| Patent No. 6248904
| GENERAL INFORMATION:
| APPLICANT: Chai, Sui Xiong
| APPLICANT: Chai, Sui Xiong
| APPLICANT: Chare, John A.
| TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole TITLE OF INVENTION: Pluorescence Screening Assays for Caspases, Peptidases, Protease; TITLE OF INVENTION: Cher Enzymes and the Use Thereof
| TITLE OF INVENTION: Cher Enzymes and the Use Thereof
| FILE REFERENCE: 1735.0030001
| CURRENT FILING DATE: 1999-07-21
| CURRENT FILING DATE: 1999-07-21
| EARLIER APPLICATION NUMBER: US 60/093,642
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 Gaps
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FACTOR NO. 5177197

PATENT NO. 5177197

PAPLICANI: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;

PAPLICANI: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;

WERNSTEDT, CHRISTER, HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH,

IENN; HELDIN, CARL-HENRIK

TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING

HUMAN TRANSFORMING GROWIT FACTOR-BETAL-BINDING PROTEIN

NUMBER OF SEQUENCES: 53

CURRENT APPLICATION DATA;

FILING DATE: 27-FEB-1990
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 RESULT 13
5177197.
† PATENT NO. 5177197
† PATENT NO. 5177197
† PAPLICANT: KANZAKI, TETSUTO;OLOFSSON, ANDERS;MOREN, ANITA;
† PAPLICANT: KANZAKI, TETSUTO;OLOFSSON, KOHEI;CLAESSON-WELSH,
† LENA;HELDIN, CARL-HENRIK
† TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
† HUMAN TRANSPORMING GROWTH FACTOR-BETA1-BINDING PROTEIN
† CURRENT APPLICATION DATA:
† APPLICATION NUMBER: US/07/487,343
† FILING DATE: 27-FEB-1990
 Score 33; DB 6; Length 1394;
Pred. No. 3.9e+02;
3; Mismatches 3; Indels
 63.5%; Score 33; DB 6; Length 410; 45.5%; Pred. No. 97; tive 3; Mismatches 3; Indels
```

```
APPLICANT: Weber, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Came, John R.M.
APPLICANT: Change, Hau-Zhong
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: 1735.029002
CURRENT APPLICATION NUMBER: 09/168,888
EARLIER APPLICATION NUMBER: 09/168,888
EARLIER FILING DATE: 1998-10-10
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
SEQ ID NO 66
EBRIER FILING DATE: 1998-03-03
LENGTH: 10
ENGTH: 10
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 Gaps
 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Synthetic
OTHER INFORMATION: Peptide
JS-09-357-952-66
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 ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic ; OTHER INFORMATION: Peptide US-09-521-650-66
 Query Match 61.5%; Score 32; DB 3; Length 10; Best Local Similarity 50.0%; Pred. No. 2.3; Matches 5; Conservative 3; Mismatches 2; Indels
 61.5%; Score 32; DB 4; Length 10;
50.0%; Pred. No. 2.3;
tive 3; Mismatches 2; Indels
 JS-09-521-650-66; Sequence 66, Application US/09521650; Parent No. 6335429; GENERAL INFORMATION:
EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 66
LENGTH: 10
 TYPE: PRT
ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 50.0
Matches 5; Conservative
 1 EEVVPXGMSY 10
 1 DDIVPCSMSY 10
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Gaps ö

Search completed: June 3, 2004, 12:03:07 Job time: 11.8 secs

1 EEVVPXGMSY 10

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1 DDIVPCSMSY 10

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 June 3, 2004, 11:57:42; Search time 33.7333 Seconds (without alignments) 91.741 Million cell updates/sec
 Sequence 9, 7
Sequence 10,
 Sequence 47,
Sequence 48,
Sequence 49,
 Sequence 5,
 Sequence 1
Sequence 1
Sequence 3
 Sequence Sequence
 Description
 Sequence
 Sequence
 / cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/DEOGE_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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/ cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
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/ cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
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/ cgn2_6/ptodata/1/pubpaa/USO0B_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 US-09-909-164-5
US-09-909-164-6
US-09-909-164-19
US-09-909-164-19
US-09-909-164-44
US-09-909-164-48
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US-09-909-164-51
US-09-909-164-51
US-09-909-164-13
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US-09-909-164-13
US-09-909-164-13
US-09-909-164-13
 Total number of hits satisfying chosen parameters:
 1155919 segs, 281338677 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 Published_Applications_
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 finimum DB seq length: 0
 US-09-909-164-10
52
1 EEVVPXGMSYS 11
 Query
Match Length
 44444444
 Title:
Perfect score:
Sequence:
 Score
 Scoring table:
 Searched:
 Database
 489699979848
 Run on:
 Result
 ه الرسطين
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|                                                                                                                      | equence 29,<br>equence 33,<br>equence 36,<br>equence 37,<br>equence 43,<br>equence 14,                             | equence 22,<br>equence 26,<br>equence 27,<br>equence 61,<br>equence 22,<br>equence 21,<br>equence 31,                                                         | Sequence 32, Appl<br>Sequence 40, Appl<br>Sequence 41, Appl<br>Sequence 41, Appl<br>Sequence 45, Appl<br>Sequence 30, Appl<br>Sequence 30, Appl<br>Sequence 38, Appl<br>Sequence 38, Appl<br>Sequence 38, Appl<br>Sequence 38, Appl<br>Sequence 42, Appl                                                                                     |
|----------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1 12 US-09-908-164-2<br>1 12 US-09-909-164-2<br>1 12 US-09-909-164-2<br>1 12 US-09-909-164-2<br>1 12 US-09-909-164-2 | 12 US-09-909-164-2<br>1 12 US-09-909-164-3<br>1 12 US-09-909-164-3<br>1 12 US-09-909-164-3<br>1 12 US-09-909-164-4 | 1 12 US-09-909-164-<br>1 12 US-09-909-164-<br>1 12 US-09-909-164-<br>1 12 US-09-909-164-<br>1 12 US-09-909-164-<br>1 12 US-09-909-164-<br>1 12 US-09-909-164- | 0.09 - 900 - 164 - 3<br>0.09 - 900 - 164 - 4<br>0.09 - 900 - 164 - 4<br>0.09 - 900 - 164 - 4<br>0.09 - 900 - 164 - 3<br>0.09 - 900 - 164 - 3 |
| 44444<br>755<br>754<br>755<br>756<br>756<br>756<br>756<br>756<br>756<br>756<br>756<br>756                            |                                                                                                                    | 4 4 4 4 1 1 7 8 1 1 4 4 4 4 4 1 1 1 7 8 1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                                                                 | 99 75 99 76 99 76 99 76 99 76 99 76 99 76 99 76 99 76 99 76 99 76 99 99 76 99 99 99 99 99 99 99 99 99 99 99 99 99                                                                                                                                                                                                                            |

## ALIGNMENTS

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REBULT 1

19-909-164-5

19-909-164-5

19-909-164-5

19-909-164-5

19-909-164-5

19-909-164-5

19-909-164-5

19-909-164-5

19-909-164-5

19-909-164-5

19-909-164-5

19-909-164-5

19-909-164-7

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19-909-104-11

19-909-104-12

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19-909-104-12
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Sequence 10, Application US/09909164

Sequence 10, Application US/09909164

Sequence 10, Application No. US2002068702A1

GENERAL INFORMATION:
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile B
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lovy, Odile B
APPLICANT: Limbar: Limb
 FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
 PRATURE:
OTHER INFORMATION: 11-mer synthesized according to example sparture:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
FRATURE:
NOTHER INFORMATION: ACETYLATION
FRATURE:
NAME/KEY: MOD_RES
LOCATION: (11)..(11)
 Query Match

96.2%; Score 50; DB 12; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.0014;

Matches 11; Conservative 0; Mismatches 0; Indels
 NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
 LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
 FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
FEATURE:
 LOCATION: (8). (8)

OTHER INFORMATION: D-amino acid
US-09-909-164-9
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 11
 TYPE: PRT ORGANISM: artificial sequence
 TYPE: PRT ORGANISM: artificial sequence
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 NAME/KEY: MISC FEATURE
 NAME/KEY: MISC FEATURE
 LOCATION:
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 US-09-909-164-6

US-09-909-164-6

Sequence 6, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Odile E
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQ ID NO 6

LENGTH: 11

TAVER: DOT
 Sequence 9, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim.Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
APPLICANT: Brunck, Terence K
TILLE OF INVENTION: NOVE PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR FILING DATE: 2000-07-21
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 FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6) ... (6)
OTHER INFORMATION: norvaline-(CO)
 Query Match
96.2%; Score 50; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels
 Pred. No. 0.0014; ; Mismatches 0; Indels
 .
 LOCATION: (9).7(9)
OTHER INFORMATION: D-amino acid
FEATURE:
 100.08;
 TYPE: PRT
ORGANISM: artificial sequence
 NAME/KEY: MOD RES

LOCATION: (11)...(11)

CTHER INFORMATION: AMIDATION

US-09-909-164-6
 Best Local Similarity 100.
Matches 11; Conservative
 1 EEVVPXGMSYS 11
 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 FEATURE:
NAME/KEY: MISC_FEATURE
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US-09-909-164-49

Sequence 49, Application US/09909164

Sequence 49, Application US/09909164

Sequence 49, Application No. US2002068702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Error K

TITLE OF INVENTION: NOVEL PEPPIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: INO1192-US

CURRENT PILING DATE: 2000-07-21

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PATENTIN VERSION 3.1

LENGTH: 11
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 OTHER INFORMATION: 11-mer synthesized according to example 1
 Query Match 96.2%; Score 50; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 11; Conservative 0; Mismatches 0; Indels
 96.2%; Score 50; DB 12; Length 11; 100.0%; Pred. No. 0.0014; tive 0; Mismatches 0; Indels
 OTHER INFORMATION: 11-mer synthesized according to example FRATURE:
NOMEN KEY: MOD_RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
 NAME/KEY: MISC_FEATURE
| LOCATION: (6)...(6)
| OTHER INFORMATION: norleucine-(CO)
US-09-909-164-49
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 48
LENGTH: 11
TYPE: PRT
ORGANISM: artificial sequence
FRATURE:
 FEATURE:
NAMEKEY: MISC FEATURE
LOCATION: (6). (6). (6)
OTHER INFORMATION: leucine-(CO)
US-09-909-164-48
 LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 ORGANISM: artificial sequence
 LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 Query Match
Best Local Similarity 100.
Matches 11, Conservative
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 FEATURE:
NAME/KEY: MOD_RES
 à
 Sequence 47. Application US/09909164

Sequence 47. Application US/09909164

Sequence 47. Application No. US20020068702A1

GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: NUMBER: US/09/909,164
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEQ ID NOS: 62
SEQ ID NO 47
LENGTH: 11
LENGTH: 11
 Sequence 48, Application US/0990164
Sequence 48, Application US/0990164
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim.Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
APPLICANT: Brunck, Terence K
APPLICANT: Brunck, Serince K
APPLICANT: NOVE PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERENCE: IN01192-US
CURRENT APPLICATION NUMBER: 2003-03-25
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
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 OTHER INFORMATION: 11-mer synthesized according to example 1 PEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
 96.2%; Score 50; DB 12; Length 11; 100.0%; Pred. No. 0.0014; Live 0; Mismatches 0; Indels
 Length 11;
 0; Indels
 DB 12;
0.0014;
 Query Match 96.2%; Score 50; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 11; Conservative 0; Mismatches
 ; OTHER INFORMATION: D-amino acids JS-09-909-164-10
 LOCATION: (6). (6)
CTHER INFORMATION: valine-(CO)
US-09-909-164-47
 TYPE: PRT
ORGANISM: artificial sequence
 FEATURE: NAME/KEY: MOD RES LOCATION: (11\overline{1}, ..., (11) OCHER INFORMATION: AMIDATION FEATURE:
 11; Conservative
 1 REVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 NAME/KEY: MISC_FEATURE
 Query Match
Best Local Similarity
Matches 11; Conserva
 RESULT 6
US-09-909-164-48
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Sequence 52, Application US/09909164
Sequence 52, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas international, Inc.
APPLICANT: Lim Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 52
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 FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
 Length 11;
 Length 11;
 96.2%; Score 50; DB 12; Length 11 100.0%; Pred. No. 0.0014; cive 0; Mismatches 0; Indels
 Indels
 96.2%; Score 50; DB 12;
100.0%; Pred. No. 0.0014;
tive 0; Mismatches 0.
 ; NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
; OTHER INFORMATION: (8,8)-allothreonine-(CO)
US-09-909-164-51
 ; LOCATION: (6)...(6)
; OTHER INFORMATION: propynyl glycine-(CO)
US-09-909-164-52
 ; Sequence 8, Application US/09909164
; Publication No. US20020068702A1
 FEATURE:
NAME/KEY:
NOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
 NAMB/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 TYPE: PRT
ORGANISM: artificial sequence
 FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OCTHER INFORMATION: AMIDATION
FEATURE:
 Query Match
Best Local Similarity 100.
Matches 11, Conservative
 11; Conservative
 1 EEVVPXGMSYS 11
 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 NAME/KEY: MISC FEATURE
 Query Match
Best Local Similarity
Matches 11; Conserva
 US-09-909-164-52
 RESULT 11
US-09-909-164-8
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 US-09-909-164-50

US-09-909-164-50

US-09-909-164-50

Sequence 50, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: STUNCE, Terence K
FILE REPERENCE: IN01193-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 06/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
LENGTH: LIM-WILD APPLICATION NUMBER: DELEMBER DEBUGANT: Corves International, Inc.
APPLICANT: Corves International, Inc.
APPLICANT: Lim Wilby, Marguerita
APPLICANT: Lim Wilby, Marguerita
APPLICANT: Lim Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: 209-03-25
PRIOR RILING DATE: 2000-03-25
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SUPPRARE: PATEURIN Version 3.1
SEQ ID NO 51
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 TYPE: PRT
ORGANIEM: artificial sequence
PERATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
 OTHER INFORMATION: 11-mer synthesized according to example 1 FRATURE:
NAME/KAY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
 Query Match 96.2%; Score 50; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 11; Conservative 0; Mismatches 0; Indels
 NAME/KEY: MISC_FEATURE

LOCATION: (6)...(6)

CHER INFORMATION: 2-amino-butyric acid-(CO)
US-09-909-164-50
 Sequence 51, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: artificial sequence
 FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
COTHER INFORMATION: AMIDATION
 1 EEVVPXGMSYS 11
||||||||||||||||
EEVVPXGMSYS 11
 RESULT 9
JS-09-909-164-51
 요
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Sequence 13, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION

APPLICANT: Corvas International, Inc.

APPLICANT: Lewy, Odile E.

APPLICANT: Lewy, Odile E.

APPLICANT: Lewy, Odile E.

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C.

FILE REPERENCE: IND1192-US

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT FILING DATE: 2003-03-25

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR APPLICATION NUMBER: 60/220,101

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PATENT OF SEQ ID NOS: 62

SEQ ID NO 13

LEMSTH: 11

FENDER OF SEQ ID NOS: 62

SEQ ID NO 13

FENDER OF SEQ ID NOS: 62

SEQ ID NO 13
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 FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
NAME/KEY: MOD_RES
IOCATION: (1)...(1)
FEATURE:
LOCATION: (1)...(1)
OTHER INFORMATION: AMIDATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
 0
 ô
 Score 46; DB 12; Length 11;
Pred. No. 0.0091;
0; Mismatches 1; Indels
 Query Match

88.5%; Score 46; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 1; Indels
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11)...(11)
LOCATION: (11)...(11)
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATIOR: (6)...(6)
COTHER INFORMATION: norvaline-(CO)
FEATURE:
FEATURE:
COTHER INFORMATION: norvaline-(CO)
FEATURE:
COTHER INFORMATION: norvaline-(CO)
FEATURE:
COTHER INFORMATION: Damino acid
US-09-909-164-12

88.5$; SCOT
 FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (8)...(9)
CTHER INFORMATION: D-amino acids
US-09-909-164-13
 TYPE: PRT ORGANISM: artificial sequence
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
 1 EEVVPXGMDYS 11
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 1 EEVVEXGMDYS 11
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 Sequence 12, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Levy, Odile E
APPLICANT: Levy NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 1.2
LENGTH: 11
TYPE: PRIT
 APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerica
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
SUPTARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 11
 ö
 Gaps
 PEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
 FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
 DB 12; Length 11;
 1; Indels
 Score 46; DB 12;
Pred. No. 0.0091;
0; Mismatches
 NAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
 LOCATION: (9). . (9)
OTHER INFORMATION: D-amino acid
 NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
 NAME/KBY: MOD RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
 ORGANISM: artificial sequence
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
 OTHER INFORMATION: AMIDATION

S-09-909-164-8
 1 EEVVPXGMSYS 11
 1 EEVVPXGMDYS 11
 NAME/KEY: MISC_FEATURE LOCATION: (9)...(9)
 SENERAL INFORMATION:
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0
 Query Match 86.5%; Score 45; DB 12; Length 11; Best Local Similarity 90.9%; Pred. No. 0.015; Matches 10; Conservative 0; Mismatches 1; Indels
 Search completed: June 3, 2004, 12:57:15 Job time : 33.7333 secs
 NAME/KEY: MISC FEATURE
LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
 NAME/KEY: MISC_FEATURE
LOCATION: (8)..(8)
CTHER INFORMATION: D-amino acid
US-09-909-164-11
NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 FEATURE:
NAME/KEY: MOD RES
LOCATION: (11\overline{\text{11}}\).(11)
OCTHER INFORWATION: AMIDATION
FEATURE:
 1 REVVPXGMSYS 11
 1 EEVVPXGMHYS 11
 à
 Sequence 7, Application US/09909164

Publication No. US2002068702A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: November 100192-US

CURRENT APPLICANTON NUMBER: 1003-09-21

PRIOR FILING DATE: 2003-09-21

NUMBER OF SEQ ID NOS: 62

SEQ ID NO 7

LENGTH: Lim-Wilby, Marguerita

SEQ ID NO 7

LENGTH: Lim-Wilby, Marguerita

SEQ ID NO 7
 Sequence 11, Application US/0909164

Publication No. US20020068702A1

Genemce 11, Application No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lerence K

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: 1001192-105

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT FILING DATE: 2003-03-25

PRIOR PLING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQ ID NO 11

LENGTH: 11
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0
 TYPE: PRT
ORGANISM: artificial sequence
PEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
 TYPE: PRT
PERATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
 Score 45; DB 12; Length 11; Pred. No. 0.015;
 1; Indels
 0; Mismatches
 NAME/KEY: MISC FEATURE
LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
 FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (9)...(9)
OTHER INFORMATION: D-amino acid
FEATURE:
 FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1) - (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
 NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
US-09-909-164-7
 EEVVPXGMHYS 11
 1 EEVVPXGMSYS 11
 RESULT 15
US-09-909-164-11
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 VI protein tobac DNA segregation AT hypothetical protein finger protein topoisomerase IV s DNA-binding proteins proteins and proteins a
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iron(III) ABC tran
bacteriocin BENS -
ATP-dependent DNA
conserved hypothet
transforming growt
DNA-directed RNA p
 hypothetical 367K probable sulfate psulfate psulfate -
 June 3, 2004, 11:35:47 ; Search time 9 Seconds (without alignments) 117.567 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 283366
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Potal number of hits satisfying chosen parameters:
 283366 segs, 96191526 residues
 SUMMARIES
 Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 NM protein - protein search, using sw model
 T31308
T439116
742451
742451
742451
754111
754111
754111
754111
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 finimum DB seq length: 0
 US-09-909-164-10
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1 EEVVPXGMSYS 11
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2: pir2:*
3: pir3:*
4: pir4:*
 Query
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 Post-processing:
 Pitle:
Perfect score:
Sequence:
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| 30 33 63.5 1548 2 T04456 hypothetical prote masking protein profession of the control of the con | ALIGNMENTS | archaeum symbiosum archaeum symbiosum archaeum symbiosum 31308 31000 #sequence_revision 11-Jan-2000 #text_chan 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 31308 313 | Query Match 71.2%; Score 37; DB 2; Length 840;  Best Local Similarity 77.8%; Pred. No. 21;  Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  Qy 3 VVPQGMSYS 11  Db 135 VVPQGMSYA 143 |
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A;cross-references: EMBL:281109; PIDN:CAB03241.1; GSPDB:GN00023; CESP:R10D12.10
A;Experimental source: clone R10D12
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C;Date: 28-Oct.1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
C;Date: 28-Oct.1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
C;Accession: S5781
A;Milligan, S.B.; Gasser, C.S.
Plant Mol. Biol. 28, 691-711, 1995
A;Title: Nature and regulation of pistil-expressed genes in tomato.
A;Reference number: S57808; MUID:95375233; PMID:7647301
A;Accession: S57810
A;Accession: S57810
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C;Bacession: T24111
R;Percy, C
submitted to the EMBL Data Library, October 1996
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Sep-1999
C;Accession: S22293; I788 #sequence revision C;Richanore, C; Traboni, C; Cortese, R.
Nucleic Acids Res. 19, 141-147, 1991
 A,Cross-references: EMBL:U20592, NID:9924625; PIDN:AAA80497.1; PID:9924626
C,Superfamily: plant Kunitz-type proteinase inhibitor
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 Score 35; DB 2; Length 225;
Pred. No. 13;
3; Mismatches 2; Indels
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A;Residues: 1-425 <WIL>
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50.0%; Pred. No. 26;
rative 3; Mismatches
 hypothetical protein precursor (clone TPP11)
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A,Introns: 23/3; 56/3; 113/3; 257/2
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54.5%;
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 335 EQIVPGGLQY 344
 32 DEVVPNGKTYA 42
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSY 10
 1 EEVVPXGMSY 10
 A,Gene: CESP:R10D12.10
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 RESULT 4

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V1 242452

V2 242452

V2 242452

C; Species: tobacco yellow dwarf virus
C; Species: tobacco yellow dwarf virus
C; Accession: A42452

R; Accession: A42452

R; Accession: A42452

R; Aurich B. A.M.; Fichardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
VIrology 187, 633-642, 1992

A; Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yello
 C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: B97355
R;Nolling, U; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
U, Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Reference number: A96900; MUID:21359325; PMID:21359325
 DNA segregation ATPase, FtsK/SpolIIE family, YUXA B. subtilis ortholog [imported] - Clos
 A, Accession: T40413
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-877.
A, Cross-references: EMBL: AL031261; PIDN: CAA20298.1; GSPDB: GN00067; SPDB: SPBC3H7.02
A, Experimental source: strain 972h-; cosmid c3H7
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 A; Status: preliminary
A; Modecule type: DNA
 C;Species: Schizosaccharomyčes pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40413.
S;Lyne, M:; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
submitted to the EMBL Data Library, August 1998
A;Reference number: 221926
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 A;Molecule type: DNA
A;Residues: 1-102 <MOR>
A;Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
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3; Mismatches 1; Indels
 Length 877;
 1; Indels

 fission yeast (Schizosaccharomyces pombe)
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Query Match
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|||| |::|| 7 QVVPSGINYS 16

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2 EVVPXGMSYS 11

Score 37; DB 2; Pred. No. 22; 1; Mismatches

71.2%;

Query Match
Best Local Similarity 77.8
Matches 7; Conservative

C; Genetica: A; Gene: SPDB: SPBC3H7.02 A; Map position: 2 148 VVPQGMSYA 156

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3 VVPXGMSYS 11

Gaps

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A,Title: A DNA-binding protein containing two widely separated zinc finger motifs that z A,Reference number: A34203; MUID:90169514; PMID:2106471
A,Rocession: A34203
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: L-2717 < FAN>
A,References: BMEL.X51455, NID:938017; PIDN:CAA35798.1; PID:938018
A,Reference number: A34779; MUID:90205817; PMID:2108316
A,Accession: A34779
A,Reference number: BNA A779
A,Reference number: A779
A,Reference number: BNA A779
A,Reference number:
 Nythernate names: hypothetical protein 02612; hypothetical protein Yol303.3
C; Species: Saccharomyces cerevisiae
C; Species: Saccharomyces cerevisiae
C; Species: Saccharomyces cerevisiae
C; Accession: S54619; S66879
R; de Haan, M.; Maarse, A.C.; Grivell, L.A.
submitted to the EMBL Data Library, May 1995
A; Reference number: S54619
A; Molecule type: DNA
A; Residues: L156 cDEH>
A; Cross-references: EMBL:X87331; NID:g1041652; PIDN:CAA60762.1; PID:g829123
A; Cross-references: EMBL:X87331; NID:g1041652; PIDN:CAA60762.1; PID:g829123
A; Cross-references: S6877
A; Reference number: S66879
A; Accession: S66879
A; Residues: 1-156 cDEM>
A; Cross-references: EMBL:Z74920; NID:g1420109; PIDN:CAA99201.1; PID:g1420111; MIPS:YOR01
A; Experimental source: Etrain S288C
 hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein O2612; hypothetical protein YOL303.3
 67.3%; Score 35; DB 2; Length 2717; 66.7%; Pred. No. 1.9e+02; tive 2; Mismatches 1; Indels
 2; Length 156;
 2; Indels
 Score 34; DB 2; Pred. No. 14; 1; Mismatches
 65.4%; Score 34;
Local Similarity 66.7%; Pred. No. 1
Les 6; Conservative 1; Mismatch
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C, Superfamily: hypothetical protein YOR013w
 A;Cross-references: SGD:S0005539
 Query Match
Best Local Similarity 66.7.
Then 6; Conservative
 2405 VVPAGLTYS 2413
 3 VVPXGMSYS 11
 2 EVVPXGMSY 10
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 4,Title: Isolation of two cDNAs encoding zinc finger proteins which bind to the alpha 1-Xeference number: IS8280; MUID:91187610; PMID:1901405
4,Accession: 822293
4,Status: nucleic acid sequence not shown
4,Modecule type: mRNA
4,Modecule type: mRNA
4,Residues: 1-670 cMIT>
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5,Superfamily: HIV-EP2 enhancer-binding protein
5;Superfamily: HIV-EP2 enhancer-binding protein
5;Keywords: DNA binding; transcription regulation; zinc finger
 A; Experimental source: Strain 9a5c
A; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A strones, M.R.P.; Decena, C.; Bleno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H as-Neto, E.; Docena, C.; Bl-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000
J.A.; Arabora, S.C.; Franca, S.C.; Franco, M.C.; Frohm J. M. M. Macheira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, B.E.; Laigh J. Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Marino, C.L.; Marques, M.V.; Martins, E.R.; Andeira, A.M.B.N.; Madeira, A.Y.; Menck, C.F.N.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, A.Y.; Menck, C.F.N.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D. A; Odrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa. R.G.; Santelli, R.V.; Sawasak, J. Huthors and Silva, A.M.; Salva, A.M.; Salva, A.M.; Salva, A.M.; Veriore, A.M.; Sawasak, M.; Vallada, H.; Vallada, F.R.; Veriovski-Almeida, S.; Vettore, A.L.; Z. A.R.; Z. A.J.; Z.
 ; Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomerase
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 DNA-binding protein PRDII-BF1 - human
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2;Species: Homo sapiens (man)
2;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Sep-1999
2;Accession: A34403; A34779
3;Fan, C.M.; Maniatis, T.
3enes Dev. 4, 29-42, 1990
 opoisomerase IV subunit XF1353 [imported] - Xylella fastidiosa (strain 9a5c)
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67.3%; Score 35; DB 2; Length 749;
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 526 EVDPSGMSY 534
 3 VVPXGMSYS 11
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 A; Contents: annotation
 4, Gene: XF1353
 Genetics:
 RESULT 10
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R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson R;Klenk, H.P.; Clayton, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
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 cell division inhibitor (minD-2) homolog - Archaeoglobus fulgidus
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 probable ABC substrate-binding protein, iron UU359 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Species: Us-aug-2000 #text_change 02-Sep-2000 C;Daccession: US-2000 #text_change 02-Sep-2000 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, B.Y.; Cassell, G.H. submitted to GenBank, February 2000 fureaplasma urealyticum: Alternate views of a min A;Reference number: A82870
 hypothetical protein 1 - Campylobacter jejuni (fragment)
C:Species: Campylobacter jejuni
C:Species: Campylobacter jejuni
C:Accession: 140758, 847317
C:Accession: 140758, 847317
R:Hani, E.K.; Chan, V.L.
R:Hani, E.K.; Chan, V.L.
A:Title: Expression and characterization of Campylobacter jejuni benzoylglycine amidohyd
A:Reference number: 140758, MUID:95247673; PMID:7730270
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Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Wesse, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: H69491
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;Cross-references: GB:AE002133; GB:AF222894; NID:g6899339; PIDN:AAF30768.1; GSPDB:GN001
;Experimental source: serovar 3; biovar 1
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 135 EEVVPHYLSY 144
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 2 EVVPXGMSY 10
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 2 EVVPXGMS 9
 A;Gene: ABCsbp-5; UU359
A;Genetic code: SGC3
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Molecule type: DNA
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50S ribosomal protein L20 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2011 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accesion: B90544
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmoris complete genome sequence of the murine respiratory pathogen Mycoplasma pulmy. A;Recence number: A99512; MUD:21267165; PMID:11353084
A;Recence number: A99512; MUD:21267165; PMID:11353084
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A;Recence B0054
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A;Recence S0054
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 xenopus lae
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vibrio chol
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 P23622 neurospora
O60312 homo sapien
Q98qv0 mycoplasma
O28330 archaeoglob
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 Q8rg86 fusobacteri
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O94740
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P22064
Q9kv29
 Q14766
Q00918
Q004827
P30279
P30280
Q90459
P50755
 Q9nzm5
P08696
 24385
 P31619
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
 otal number of hits satisfying chosen parameters:
 141681 segs, 52070155 residues
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| P44577 haemophilus O75355 homo sapien Q9y016 homo sapien P50518 crithidia f P52384 human herpe P52544 human herpe P52544 human herpe P525431 tattus norv P28931 tomato aspe P16916 escherichia P16919 escherichia |
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| 427<br>529<br>691<br>719<br>726<br>726<br>729<br>920<br>13377<br>13377                                                                                                                                            |
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## ALIGNMENTS

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BESTAT 2 (Treated)

BEST 3 (Treated)
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 Gaps
 OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
Pfam; PF02142; MGS; 1.
PRINTS; PR00098; CPSASE.
TIGREAMS; TIGR01369; CPSASE.1
FROSITE; PS00866; CPSASE.1; 2.
PROSITE; PS00867; CPSASE.2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat; Arginine biosynthesis; Complete proteome.
ATP-binding; Manganese; Complete SYNTHETIC DOMAIN.
CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
 ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
MANGANESE 1 ND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
 ö
 Score 38; DB 1; Length 1058;
Pred. No. 7;
3; Mismatches 1; Indels
 Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable sulfate permease C3H7.02.
 117451 MW;
 73.1%;
 6; Conservative
 STANDARD;
 190 EIVPNGLNYS 199
 2 EVVPXGMSYS 11
 546
929
1058
1058
1058
352
 Schizosaccharomyces.
 1058 AA;
 Query Match
Best Local Similarity
Matches 6; Conserv
 SEQUENCE FROM N.A.
 NCBI_TaxID=4896;
 SULH SCHPO
 SPBC3H7.02
 METAL
SEQUENCE
 REPEAT
NE BIND
NP BIND
MP BIND
 DOMAIN
DOMAIN
DOMAIN
 RESULT 2
SULH SCHPO
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 .
0
 Gaps
 MEDIJNE=92188538; PubMed=1546458;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
"The nucleotide sequence of the infectious cloned DNA component of
tobacco yellow dwarf virus reveals features of geminiviruses
infecting monocotyledonus plants.";
Virology 187:633-642(1992).
 -i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-i- SIMILARITY: Belongs to the SLC26A/SulP transporter (TC 2.A.53)
NATULE 415:871-880(2002).
-!- FUNCTION: HIGH AFFINITY UPTAKE OF SULFATE INTO THE CELL (BY
 ö
 71.2%; Score 37; DB 1; Length 877; 77.8%; Pred. No. 9.4; 1; Indels tive 1; Mismatches 1; Indels
 56995A8493371E43 CRC64;
 Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses, ssDNA viruses; Geminiviridae; Mastrevirus.
NCBI_TaxID=31599;
 POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
 POTENTIAL.
 -!- SIMILARITY: Contains 1 STAS domain.
 PIR; T40413; T40413.
GenebB Spombe; SPECTAT.02; -
InterPro; IPR0015045; STAS.
InterPro; IPR001902; Sulph_transpt.
Pfam; PF01740; STAS.
IGRFAMS; TIGR00815; Sulfate transp; 1.
PROSITE; PS01030; SLC26A; 1.
PROSITE; PS50801; STAS; 1.
Transport; Transmembrane.
 96373 MW;
 EMBL; AL031261; CAA20298.1; -.
 Local Similarity 77.8 nes 7; Conservative
 148 VVPQGMSYA 156
 3 VVPXGMSYS 11
 [1]
SEQUENCE FROM N.A.
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us-09-909-164-10.rsp

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 STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
 Gaps
 Clostridium acetobutylicum.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
 ö
 69.2%; Score 36; DB 1; Length 102; 60.0%; Pred. No. 1.6; ive 3; Mismatches 1; Indels
 102 AA; 11178 MW; A40ECF1E0AF55B67 CRC64;
 01-FEB-1994 (Rel. 28, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypotherical protein CAC3709.
 1498 AA
 EMBL; X65276; CAA46379.1; ALT_FRAME.
PIR; B97355; B97355.
InterPro; IPR002543; FteK_SpoillE.
 PIR; A42452; A42452.
InterFro; IPR002621; Gemini mov.
Fran; PF01708; Gemini mov; I.
Hypothetical protein.
SEQUENCE 102 AA; 11178 MW; A4
 EMBL; M81103; AAA47947.1; -.
 EMBL; AE007866; AAK81629.1;
 Local Similarity 60.0
Les 6; Conservative
 |||| |::||
7 QVVPSGINYS 16
 2 EVVPXGMSYS 11
 SEQUENCE FROM N.A.
 NCBI_TaxID=1488;
 Clostridium
 CLOAB
 Query Match
 (1A9_CLOAB
(D _Y1A9_CLO
(C _ 004351;
 Best Loc
Matches
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 "High-resolution solution structure of the double Cys2His2 zinc finger from the human enhancer binding protein MBP-1."; Blochemistry 31:3907-3917(1992).

19. GAGAGETTTCC-3. WHICH IS POUND IN THE ENHANCER ELEMENTS OF NUMERCUS VIRAL PROMOTERS SUCH AS THOSE OF SV40, CMV, OR HIV1. IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS OF A NUMBER OF CELLUTAR PROMOTERS, INCLUDING THOSE OF THE CLASS I MHC, INTERLEUKIN-2 RECEPTOR, AND INTERFERON-BETA GENES. IT MAY ACT
 01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 14, Last sequence update)
Zinc finger protein 40 (Human immunodeficiency virus type I enhancer-binding procein 1) (HIV-EP1) (Major histocompatibility complex binding protein 1) (MBP-1) (Positive regulatory domain II binding factor 1) (PRDII-BF1).
 Gaps
 "High-resolution three-dimensional structure of a single zinc finger from a human enhancer binding protein in solution."; Biochemistry 29:9324-9334(1990).
 IN T-CELL ACTIVATION.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- INDUCTION: By mitogens and phorbol ester.
-!- DOWAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY
-!- DOWAIN: CONTAINS THE SAME DNA SEQUENCE. THERE IS A FIFTH
 MEDIJUES=90169514; PubMed=2106471;
Fan C.M., Maniatis T.;
Fan C.M.,
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
 MEDLINE-92232684; PubMed=1567844;
Omichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E.,
Gronenborn A.M.;
 ö
Pfam; PF01580; FtsK_SpoiliE; 2.
PROSITE; PS50901; FTSK; 2.
Hypothetical protein; ATP-binding; Complete proteome; Repeat.
DOMAIN 655 857 FTSK 1.
DOMAIN 1001 1188 FTSK 2.
 Score 36; DB 1; Length 1498; Pred. No. 27;
 675 682 ATP (POTENTIAL).
1498 AA; 168968 MW; FF42037A335A9649 CRC64;
 STRUCTURE BY NWR OF 2113-2142.
MEDLINE=9106433; PubMed=2248949;
Omichinski J.G., Clore G.M., Appella E., Sakaguchi K.,
Gromenborn A.M.;
 PRT; 2717 AA.
 2; Mismatches
 ZINC-FINGER IN-BETWEEN.
-!- SIMILARITY: STRONG, TO HIVEP2.
 STRUCTURE BY NMR OF 2087-2142
 69.2%;
 Query Match
Best Local Similarity 60.0-
 STANDARD;
 1276 EQKIPMGMSY 1285
 1 EEVVPXGMSY 10
 Homo sapiens (Human)
 SEQUENCE FROM N.A.
 NCBI TaxID=9606;
 HIVEPI OR ZNF40.
 ZEP1 HUMAN
P15822;
 DOMAIN
NP BIND
SEQUENCE
 RESULT 5
ZEP1 HUMAN
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 TRANSMEM
TRANSMEM
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 TRANSMEM
 SEQUENCE
 Query Match
 TRANSMEM
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 CARBOHYD
 CARBOHYD
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 ALOA_HUMAN
 RESULT
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 Gaps
 MEDLINE-94188926; PubMed-8140616;
Sandal N.N., Marcker K.A.;
"Similarities between a soybean nodulin, Neurospora crassa sulphate
 [1]
SEQUENCE FROM N.A.
MEDLINE-91129256; PubMed=1825178;
Ketter J.S., Jarai G., Fu Y.-H., Marzluf G.A.;
Ketter J.S., Jarai G., Fu Y.-H., Marzluf G.A.;
"Nucleotide sequence, messenger RNA stability, and DNA recognition
"Nucleotide sequence, messenger RNA stability, and bla recognition
"Nucleotide sequence, messenger II in
elements of cys-14, the structural gene for sulfate permease II in
 ô
 Eukaryota; Fungi; Ascomycota; Perizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCPI_TaxID=5141;
 / Match 67.3%; Score 35; DB 1; Length 2717; Local Similarity 66.7%; Pred. No. 80; local Schervative 2; Mismatches 1; Indels
 297217 MW; D45D3CA951FEA561 CRC64;
 01-NOV-1991 (Rel. 20, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Sulfate permease II.
CYS-14.
 EMBL; X51435; CAA35798.1; -.
 PIR, A34203; A34203.
PDB, 32NF, 15-JAN-92.
PDB, 4ZNF, 15-JAN-92.
PDB, 18BO; 31-OCT-93.
TRANSPAC, T00497; --
Genew; HGNC,4920; HIVEPI.
 STANDARD;
 2405 VVPAGLTYS 2413
 3 VVPXGMSYS 11
 2717 AA;
 PROBABLE REVISIONS.
 Neurospora crassa
 2090
2095
2099
2109
2115
2123
 CY14 NEUCR
P23622;
 HELIX
SEQUENCE
 Query Match
 TURN
STRAND
HELIX
 STRAND
 RESULT 6
CY14 NEUCR
 Matches
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 ö
 Gaps
SEGUENCE FROM N.A.
MEDILINE-21225279; PubMed=11326269;
MEGURO M., Kashiwagi A., Mitsuya K., Nakao M., Kondo I., Saitoh S.,
Oshimura M.;
 "A novel maternally expressed gene, ATP10C, encodes a putative aminophospholipid translocase associated with Angelman syndrome."; Nat. Genet. 28:19-20(2001).
[2] SEQUENCE FROM N.A.
 30-MAY-2000 (Rel. 39, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Potential phospholipid transporting ATPase VA (EC 3.6.3.1) (ATPVA)
(Aminophospholipid translocase VA).
ATP10A OR ATP10C OR ATPVC OR KIAA0566.
ATP10A OR ATP10C OR ATPVC OR KIAA0566.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
 ö
 Length 788;
 1; Indels
 4FC604B60798CE77 CRC64;
 DB 1;
36;
 PRT; 1499 AA
 2; Mismatches
 EMBL; M59167; AAA33615.1; ALT_SEQ.
PIR; A37956; A37956.
InterPro; IPR001902; Sulph_transpt.
PERM; PF00916; Sulfate_transp; 1.
TIGRRAMS; TIGRR0815; Sulp; PROSITE; PS01130; SLC26A; 1.
Transport; Transmembrane; Glycoprotein.
 POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
 Score 34;
Pred. No.
 87864 MW;
 65.4%;
 6; Conservative
 STANDARD;
 23
578
 VVPXGMSYS 11
 VVPQGMAYA 98
 788 AA;
 Local Similarity
 NCBI_TaxID=9606;
 060312; 096914;
 family.
 A10A HUMAN
```

```
Supplement Figure 12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold B.A., Garnen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshlykis S., Carninci P., Scheetz T.E.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Rhohards S., Morley K.C., Hale S., Garcia A.M., Galy L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahas S., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Stalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Generation and initial analysis of more than 15,000 full-length

Numan and mouse CDNA sequences.
 Herzing L.B.K., Kim S.-J., Cook E.H. Jr., Ledbetter D.H.; "The human aminophospholipid-transporting ATRase gene AFP10C maps adjacent to UBE3A and exhibits similar imprinted expression."; Am. J. Hum. Genet. 68:1501-1505(2001).
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 EMBL; AR051358; BAB47392.1; -.
EMBL; AY029504; AAX33100.1; -.
EMBL; AY029487; AAX33100.1; JOINED.
EMBL; AY029488; AAX33100.1; JOINED.
EMBL; AY029499; AAX33100.1; JOINED.
EMBL; AY029491; AAX33100.1; JOINED.
EMBL; AY029491; AAX33100.1; JOINED.
MEDLINE=21313119; PubMed=11353404
 TISSUE=Brain;
MEDLINE=98290545; PubMed=9628581;
 SEQUENCE OF 337-1499 FROM N.A.
 SEQUENCE FROM N.A.
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R Genew, HGNC:13542; ATP10A.

R MIN; 105830; -

R MIN; 105830; -

R MIN; 105830; -

R GO; GO:0016021; C:integral to membrane; NAS.

R GO; GO:0004012; F:phospholipid-translocating ATPase activity; NAS.

R GO; GO:000830; F:phospholipid-translocating ATPase activity; NAS.

R GO; GO:000830; F:phospholipid-translocating ATPase activity; NAS.

R InterPro; IPR005839; F:lippase.

R InterPro; IPR005839; F:lippase.

R InterPro; IPR005839; F:lippase.

R TIGRPAMS; T:RG01652; ATPase-P:lipid; 1.

R TIGRPAMS; T:RG01652; ATPase-P:lipid; 1.

R TIGRPAMS; T:RG01652; ATPase-P:Lype; 6.

R PROSITE; PS00114; ATPASE EI E2; 1.

R Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
 Gaps
 ;
 PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
 Score 34; DB 1; Length 1499;
Pred. No. 70;
0; Mismatches 3; Indels
 388 388 Q -> R (IN REF. 4).
1499 AA; 167687 MW; D4996A4D0635A68D CRC64;
 CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
 POTENTIAL.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
 POTENTIAL.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
 EXTRACELLULAR (POTENTIAL)
 POTENTIAL.
EXTRACELLULAR (POTENTIAL)
 CYTOPLASMIC (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 CYTOPLASMIC (POTENTIAL)
 (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
 116 AA
 POTENTIAL
 POTENTIAL
 POLY-GLU
65.4%;
Local Similarity 72.7%;
tes 8; Conservative 0
 469 EEVVPRGGSVS 479
 STANDARD;
 1 EEVVPXGMSYS 11
 1249
1267
1292
 1499
 Multigene family.
DOMAIN
TRANSMEM 87
 11193
1200
1223
1229
1250
1268
1293
427
1031
 RL20 MYCPU
ID RL20 MYCPU
AC Q96070;
DT 28-FEB-2003 (
DT 28-FEB-2003 (
DT 28-FEB-2003 (
 DOMAIN
TRANSMEM
DOMAIN
TRANSMEM
 DOMAIN
TRANSMEM
DOMAIN
TRANSMEM
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TRANSMEM
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TRANSMEM
 DOMAIN
 SEQUENCE
 Query Match
 FRANSMEM
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Venter J.C.;
 TRANSMEM
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 Query Match
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 RESULT 10
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 ö
 Mycoplasma pulmonis.";

Nucleic Acids Res. 29:2145-2153(2001).

-I-FUNCTION: This protein binds directly to 23s ribosomal RNA and is necessary for the in vitro assembly process of the 50s ribosomal subunit. It is not involved in the protein synthesizing functions of that subunit (By similarity).

-I- SIMILARITY: Belongs to the L20P family of ribosomal proteins.
 Gaps
 STRAIN-UAB CTIF;
WEDLINE=21267165; PubMed=11353084;
Chambaud I., Feilig R., Ferris S., Barbe V., Samson D., Galisson
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha B.P.C.,
Blanchard A.;
 "The complete genome sequence of the murine respiratory pathogen
 STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.B., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 ö
 MYDLList; MYDC 2610; -.

**HANAP; MF 00382; -; 1.

**HANAP; MF 00382; -; 1.

**HANAP; MF 00382; -; 1.

**Thresto; IPR005812; Ribosomal_L20b/o.

**PRINTS; PR00062; RIBOSOMÄLL20; 1.

**PRINTS; PR00062; RIBOSOMÄLL20; 1.

**TIGREAMM; TIGR01032; **PIL bact; 1.

**TIGREAMM; TIGR01032; **PIL bact; 1.

**PROSITE; PS00937; RIBOSOMÄLL20; 1.

**Ribosomal protein; rRNA-binding; Complete proteome.

**SEQUENCE 116 AA; 13565 MM; C59C74890B1BF14 CRC64;
 63.5%; Score 33; DB 1; Length 116; 77.8%; Pred. No. 8.1;
 2; Indels
 Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
 0; Mismatches
 EMBL; AL445563; CAC13434.1; -.
 Hypothetical protein AF1949.
50S ribosomal protein L20. RPLT OR MYPU 2610. Mycoplasma pulmonis.
 Local Similarity 77.8
 STANDARD;
 3 VVPXGMSYS 11
 68 VRPLGMSYS 76
 PIR; E90544; E90544.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=2107;
 NCBI_TaxID=2234;
 YJ49 ARCFU
O28330;
 Query Match
 AF1949
 Matches
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Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayze J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 Gaps
 STRAIN=NCTC 11168;
MEDLINE=20150912; PubMed=10688204;
MEDLINE=20150912; PubMed=10688204;
Parkhill J., Wren B.W., Mingall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.";
 Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
 "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
 [2]
SEQUENCE OF 160-253 FROM N.A.
STRAIN-ATCC 43431 / TGH 9011;
STRAIN-SP2647673; PubWed=7730270;
Hani E.K., Chan V.L.; Aracterization of Campylobacter jejuni
"Expression and characterization of Campylobacter jejuni
berzoylglycine amidohydrolase (Hippuricase) gene in Escherichia
 ö
 63.5%; Score 33; DB 1; Length 165; 60.0%; Pred. No. 12; ive 1; Mismatches 3; Indels
 TIGR; AF1949; -.
Hypothetical protein; Transmembrane; Complete proteome.
 141 161 POTENTIAL.
165 AA; 17588 MW; BBC17054810ADBF8 CRC64;
 POTENTIAL.
 EMBL; AE000968; AAB89307.1; -. PIR; D69493; D69493.
 6; Conservative
 Nature 403:665-668(2000).
 1 EEVVPXGMSY 10
 60 EESIPDGASY 69
 Campylobacter jejuni
 Local Similarity
 SEQUENCE FROM N.A.
 TaxID=197;
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. 9
 CONFLICT
CONFLICT
CONFLICT
SEQUENCE
 TRANSMEM
 CARBOHYD
 CARBOHYD
 VARSPLIC
 CHAIN
 AROA_VIBCH
 Best Loc
Matches
 RESULT 12
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 SCOOR BENEFIC
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 ÷
 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

STRATN=CSTBL/6J; TISSUB=Embryonic head;

MEDLINE=2108560; PubMed=11217851.

Arakawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S., Arakawa T., Shibara K., Yoshino M., Arakawa T., Salto R., Kiyosawa H., Kondo S., Yamanaka I., Asito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Salto R., Kadota K., Matsuda H.A., Ashburner M., Bacalov S., Casavant T., Kachota K., Matsuda H.A., Ashburner M., Bacalov S., Cochiwa H., Salto R., Schim I., M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G., Bronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Bronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerte P., Nordone P., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Wanniaw-Bonish A., Wenter C., Whittaker C., Wilming L., Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohteuki S., B., Wanniaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohteuki S.,
 TISSUE=Mammary fibroblast;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Felngold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunararne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Murinae, Mus
 annotation of a full-length mouse cDNA collection.";
 ô
 Query Match 63.5%; Score 33; DB 1; Length 253; Best Local Similarity 55.6%; Pred. No. 18; Matches 5; Conservative 2; Mismatches 2; Indels
 EMBL; Z36940; CAA85392.1; -.
PIR; C81374; C81374
PIR; 140758; HOSE PIR; Complete proteome.

SEQUENCE 253 Aa; 29783 MW; F96D3FF3265F8A6A CRC64;
 CTX3_MOUSE STANDARD; PRT; 280 AA. 201387, 09CMQ4; Created) 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-CCT-2003 (Rel. 42, Last annotation update) C20chein C20orf103 homolog precursor.
 EMBL; AL139076; CAB73246.1; -.
 Nature 409:685-690(2001)
 185 DIFFSGMSY 193
 2 EVVPXGMSY 10
 Mus musculus (Mouse)
 NCBI_TaxID=10090;
 Hayashizaki Y.;
 CIX3 MOUSE
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 IsoId=Q9D387-2; Sequence=VSP_003820;
CAUTION: Ref.1 sequence differs from that shown due to frameshifts
in positions 174 and 239.
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbe R.A.,
Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SUBCELLULAR LOCATION: Type I membrane protein (Fotential).
 Gaps
 AROA VIBCH STANDARD; PRT; 426 AA.

Q9KRBG;
Q9FRBG;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
29-FEB-2003 (Rel. 41, Last annotation update)
29-FEB-2003 (Rel. 41, Last annotation update)
29-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 4
 POTENTIAL.

CYTOPLASNIC (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).

MASSING (In isoform 2).

/FIId=VSP 003820.

E -> V (IN REF. 1; BAB31124).

P -> A (IN REF. 1; BAB31124).

P -> A (IN REF. 1; BAB31124).

P -> A (IN REF. 1; BAB31124).
 ö
 Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBI_TaxID=666;
 63.5%; Score 33; DB 1; Length 280; llarity 75.0%; Pred. No. 20; Conservative 0; Mismatches 2; Indels
 POTENTIAL.
PROTEIN C200RF103 HOMOLOG.
EXTRACELLULAR (POTENTIAL).
 Event=Alternative splicing; Named isoforms=2;
 EMBL; AK014127; BAB29169.1; -.
EMBL; AK016222; BAB31124.1; ALT_FRAME.
EMBL; BC004791; AAH04791.1; -.
MGD; MGI:1920368; 3110035103Rik.
MGD; MGI:1923411; 6330527006Rik.
Transmembrane; Signal; Alternative splicing.
SIGNAL
 Name=1;
IsoId=09D387-1; Sequence=Displayed;
 230 230 Q
238 238 P
280 AA; 31721 MW;
 173 VTPAGMSY 180
 3 VVPXGMSY 10
 Query Match
Best Local Similarity
 Vibrio cholerae
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DSAIPGGMSY 107
 1 EEVVPXGMSY 10
 [2]
SEQUENCE FROM N.A.
 86
 Query Match
 RESULT 14
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[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=El Tor N16961 / Serotype Ol;
STRAIN=El Tor N16961 / Serotype Ol;
MEDLINE=20406833; PubMed=10952301;
Meddelberg J.F., Elsen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson R.B., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 Gapa
 CC37_SCHPO STANDARD; PRT; 466 AA.
094740;
294740;
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
110-OCT-2003 (Rel. 42, Last annotation update)
subunit) (Cell division control protein kinase-targeting cDC37 OR SPBC9B6:10.
 cholerae.";
Nature 406:477-483(2000).
-!- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate.
-!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
 TIGR, VC1732; -..
InterPro; IPR005264; ArcA.
InterPro; IPR005264; ArcA.
InterPro; IPR001966; EPSP_synth.
Pfam; PF00275; EPSP_synthase; 1.
Propon; Pp001867; EPSP_synthase; 1.
Prostre; PS00104; EPSP_SYNTHASE 1; 1.
PROSTRE; PS00104; EPSP_SYNTHASE 2; 1.
PROSTRE; PS00104; EPSP_SYNTHASE 2; 1.
Aromatic, amino acid Diosynthesis; Transferase; Complete protecome. SEQUENCE 426 AA; 46101 MW; 38852D6483BFELC3 CRC64;
 "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 ;
 63.5%; Score 33; DB 1; Length 426; 60.0%; Pred. No. 31; ive 1; Mismatches 3; Indels
 Westwood P.K., Preston N.C., Fantes P.A.;
"Schizosaccharomyces pombe cdc37 gene.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
 sixth step.
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: Belongs to the EPSP synthase family.
-!- SIMILARITY: Belongs to the EPSP synthase family.
 Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
 EMBL; AE004251; AAF94882.1; -. PIR; D82163; D82163.
 6; Conservative
 223 EFVIPAGOSY 232
 1 EEVVPXGMSY 10
 Schizosaccharomyces.
 Best Local Similarity
 SECUENCE FROM N.A.
 NCBI_TaxID=4896;
 RESULT 13
CC37_SCHPO
 Matches
 SOURCE STANTANT STANT
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 ö
 Gaps
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 DB 1; Length 466;
 Indels
 InterPro, IPR004918; Cdc37.

Pfam; PP03234; Cdc37, 1.

Chaperone; Cell division; Cell cycle; Nuclear protein.

SEQUENCE 466 AA; 52554 MW; 647238B34CABB3C5 CRC64;
 3,
 2; Mismatches
 63.5%; Score 33; DB 50.0%; Pred. No. 34;
STRAIN=972;
MEDLINE=21848401; PubMed=11859360;
 EMBL; AJ132377; CAB38758.1; -. EMBL; AJ132376; CAB38757.1; -.
 EMBL; AL049769; CAB42371.2;
PIR; T43653; T43653.
GeneDB_SPombe; SPBC9B6.10; -
 Conservative
 Local Similarity
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Clostridium
 CLOPE
 CONFLICT
CONFLICT
CONFLICT
 CONFLICT
 SEQUENCE
 CONFLICT
 CONFLICT
 CONFLICT
 CLOPE
BCNS CLC
P08696;
 RESULT 15
 BCN5_
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
 MEDLINE=22388257; PubMed=12477932;
Atlastaer R.D., Collins F.S., Wagner L.H., Derge J.G.,
Atlastaer R.D., Collins F.S., Wagner L., Schamer C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Butcow K.H., Schamer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marushia K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Gares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
As Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Ganaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Millalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Febey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.W.,
Milling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Generation and initial analysis of more than 15,000 full-length
Human and mouse CDNA sequences",
L. House S., 1000 full-length
 SEQUENCE OF 9-478 FROM N.A., AND SUBCELLULAR LOCATION.
MEDLINE=99214318; PubMed=10196275;
Bruni R., Fineschi B., Ogle W.O., Roizman B.;
"A novel cellular protein, p60, interacting with both herpes simplex virus 1 regulatory proteins ICP22 and ICP0 is modified in a cell-type-specific manner and is recruited to the nucleus after
 SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=20175430; PubMed=10708517;
Smith J.S., Tachibana I., Pohl U., Lee H.K., Thanarajasingam U.,
Portier B.P., Ucki K., Billings S., Ramaswamy S., Mohrenweiser H.W.,
Scheithauer B.W., Louis D.N., Jenkins R.B.;
"A transcript map of the chromosome 19q-Arm glioma tumor suppressor
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 GSR2_HUMAN STANDARD;
PRT; 478 AA.
Q9NZN5; Q9BTC6; Q9HAR6; Q9NPR4; Q9NFI2;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glioma tumor suppressor candidate region gene 2 protein (p60)
GLTSCR2.
 SEQUENCE OF 12-478 FROM N.A.
Andreu N., Estivill X., Escarceller M., Sumoy L.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
 SEQUENCE OF 218-477 FROM N.A.
 J. Virol. 73:3810-3817(1999)
 Genomics 64:44-50(2000)
 Homo sapiens (Human)
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 rissum=Testis;
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 R -> Q.
Fridavpa 011496.

G -> HEG (IN REF. 2; AAH04229).

G -> R (IN REF. 3).

FREKGUMBEKLAKGGELENEVREAQARLINPSATRAKFGFQD
TVERP -> SGSYGRSWPERASSASFGGAQGPGFCN
KOPNPAPGHRIAA (IN REF. 3).
 PEGNIIRDERKSFORRNMIEPRERAKFKRKYKVKLVEKRAF
REIQ -> VITVSCRGAPCPVMTPSILIPVPPRGYGRHHGCP
WAGPVGPMPRG (IN REF. 5).
 EGNILRDREKSFORRUMIEBEREAKFKKKKKVKLVENERFR
EIQL -> RCQHSFETGSRAFRGGI (IN REF. 3).
7F18923E348CB52B CRC64;
 SDNPLDRPLVGQDBFFLE -> LNNPDKPVVWPGCLFPG
 Gaps
 Garnier T., Cole S.T.; "Complete nucleotide sequence and genetic organization of the bacteriocinogenic plasmid, pIP404, from Clostridium perfringens."; Plasmid 19:134-150(1988).
 Garnier T., Cole S.T.; "Characterization of a bacteriocinogenic plasmid from Clostridium
 Plasmid pIP404.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 ö
 Score 33; DB 1; Length 478; Pred. No. 35; 1; Mismatches 3; Indels
 (IN REF. 3).
A -> S (IN REF. 2; AAH04229)
D -> H (IN REF. 3).
 01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
 GO; GO:0005622; C:intracellular; NAS.
Nuclear protein; Polymorphism.
VARIANT 389 389 R -> Q.
 PRT;
 STRAIN=CPN50;
MEDLINE=87057020; PubMed=2877971;
 MEDLINE=88336297; PubMed=2901768;
 EMBL; AF182076; AAF66873.1; EMBL; BC004229; AAH04229.1; EMBL; BC006311; AAH06311.1; EMBL; BC010095; AAH10095.1; EMBL; AF296124; AAG30413.1; EMBL; AL35935; CAB94786.1; EMBL; AL35935; CAB94787.1; EMBL; AL122063; CAB94787.1; EMBL; AL122063; CAB9478.1; GMLSS-2DPAGE; Q9NZMS; HUMAN. Genew; HGNC;4333; GLTSCR2.
 478 AA; 54417 MW;
 63.5%;
 Query Match 63.5
Best Local Similarity 60.0
Matches 6; Conservative
 STANDARD;
 Clostridium perfringens.
 239 EVAPAGASYN 248
 6
191
 478
 2 EVVPXGMSYS 11
 [1]
SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Bacteriocin BCN5
 NCBI_TaxID=1502;
 4 6 7
146
 417
 434
 605691; -
 STRAIN=CPN50
 THE REPORT OF THE PROPERTY OF
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Perfiningens and molecular genetic analysis of the RT Pacteriol. 168:1189-1196 (1986).

RY Accretion. According gene.";

RY SECTION. 168:1189-1196 (1986).

RY SECTION. 168:1189-1196 (1986).

RY SECTION. 168:1189-1196 (1986).

RY SECTION. 169:1189-1196 (1986).

RY SECTION. 169:1189-1196 (1986).

RY SECTION. 169:1189-1196 (1988).

RY STAINSER OF UV. Indiciple promoters from Clostridium perfringens in vivo and in vitro.";

RY STAINSER OF UV. 1720 (1988).

RY MOI. Microbiol. 2:607-614 (1988).

CC -1- FUNDION. BY UV. Intradiation.

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DR EMBL; M1481; AA308249.1; -.

DR EMBL; M32824; AA308249.1; -.

DR FRM, A30481; A30481.

FY DOWAIN BIS GENERAL PROPERTY.

RESET LOCAL Similarity 66:7%; Pacor 33; DB 1; Length 890; Best Local Similarity 66:7%; Pacor 33; DB 1; Length 890; Best Local Similarity 61:7%; Pacor 33; DB 1; Length 890; Best Local Similarity 61:7%; Pacor 33; DB 1; Length 890; Best Local Similarity 61:7%; Pacor 33; DB 1; Length 890; Best Local Similarity 61:7%; Pacor 33; DB 1; Length 890; Best Local Similarity 61:7%; Pacor 33; DB 1; Length 890; Best Local Similarity 61:7%; Pacor 33; DB 1; Leng
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Search completed: June 3, 2004, 11:49:53 Job time: 4.86667 secs

2 EVVPXGMSY 10 |||| :| 170 EVVPGGFTY 178

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08dih0 synechococc 0815a7 bacillus ce 098far Arizobium 1 074056 cenarchaeum 09ury8 schizosacch 08ed18 mus musculu 08vd18 mus musculu 08bk35 mus musculu 08bk35 mus pseudomonas 040129 lycopersico 07v6q4 prochloroco 07v6q4 prochloroco 07v6q4 cenorchabdi 08sv4 cenorchabdi 08sv4 cenorchabdi
 June 3, 2004, 11:35:06; Search time 29.8667 Seconds (without alignments) 116.206 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 otal number of hits satisfying chosen parameters:
 1017041 segs, 315518202 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 M protein - protein search, using sw model
 Q8DIHO
Q815A7
Q815A7
Q917X8
Q917X8
Q81126
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Q81718
Q81737
Q81779
Q81875
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Q8
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sp_plant:*
sp_plant:*
sp_vrodent:*
sp_vrodent:*
sp_vrrebrate:*
sp_unclassified:*
sp_vritus:*
sp_bacteriap:*
sp_bacteriap:*
 BLOSUM62
Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_human:*
sp_human:*
sp_nammal:*
 finimum DB seq length: 0 faximum DB seq length: 2000000000
 Query
Match Length DB
 US-09-909-164-10
52
 1 EEVVPXGMSYS 11
 SPTREMBL 25:*
 scoring table:
 berfect score:
 Score
 ;equence:
 searched:
 Jatabase
 ino un;
 Result
No.
 litle:
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| Q726FC homo sapien Q9bh83 plasmodium Q9bh85 plasmodium Q81587 plasmodium Q81587 plasmodium Q01487 rattus ratt Q8pm16 xarthomonas Q8pm16 xylella fas Q14122 homo sapien Q12479 saccharomyc Q97182 sulfolobus Q97182 sulfolobus Q97182 sulfolobus Q97182 rattasequelob Q96mul homo sapien Q97182 rilacobium m Q81787 rhomo sapien Q98mg rhizobium m Q81787 penicillium Q98ty penicillium Q8415 bifidobacte Q8xxfs raleconia s Q8xxfs raleconia s Q8xxfs raleconia s | Q8ppb xaturomonas<br>Q8vua8 lactococcus<br>Q8ktq4 candidatus<br>Q8re56 fusobacteri<br>Q7sy67 xenopus lae<br>Q7u552 synechococ |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------|
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Q8PPPS<br>Q8VUA8<br>Q8KTQ4<br>Q8RE56<br>Q7SY67                                                                                |
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| ါလ်တိတ်တိတ်တိတ်လိတ်လိတ်လိတ်လိတ်လိတ်လိတ်လိ                                                                                                                                                                                                                                                                                                                                                                                                                         | ουουου                                                                                                                        |
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## ALIGNMENTS

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|---------------------------------|----------------------------|--------------------|----------------------|---------------------------------------------------------|-------------------------------|--------------------------|--------------------|--------------|------------------------------------|----------|----------------------------------------------------------------|------------------------------------------------------------|------------------------------------------------------------|------------------------------------------------|---------------------------------------|---------------------------|-----------------------------|-------------------------------------|--------|-------------------|------------------------------------|--------|--------------------|-------------------------------|----------------------|--------------------|-------------------------|--------------|------------|---------------|
|                                 |                            |                    |                      |                                                         |                               |                          |                    |              |                                    | Sasamoto |                                                                | ,<br>N                                                     |                                                            | rıum                                           |                                       |                           |                             |                                     |        |                   |                                    |        |                    |                               |                      |                    |                         | 44;          |            | 0             |
|                                 |                            |                    |                      | . (sn:                                                  | 18.                           |                          |                    |              |                                    | Sa       | Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., | Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki | Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; | cyanobacterium                                 |                                       |                           |                             |                                     |        |                   |                                    |        |                    |                               |                      |                    | C64;                    | Length 1044; |            | Indels        |
|                                 | te)                        | date)              |                      | Synechococcus elongatus (Thermosynechococcus elongatus) | Chroococcales; Symechococcus. |                          |                    |              |                                    | atoh E   |                                                                | Ä.                                                         | , Tabe                                                     | cyan                                           |                                       |                           |                             |                                     |        |                   |                                    |        |                    |                               |                      |                    | 00E9Cl3F0F636D2F CRC64; | Leng         |            | 2; II         |
| AA.                             | upda                       | dn uo              |                      | cus e                                                   | ynech                         |                          |                    |              |                                    | M., X    | imura                                                          | Buno                                                       | da M                                                       | hilic                                          |                                       |                           |                             | IEA.                                | IEA.   |                   |                                    |        |                    |                               |                      |                    | 0F636                   | B 16;        |            |               |
| 1044 AA.                        | ed)<br>sequence update)    | annotation update) |                      | hococ                                                   | lea; S                        |                          |                    |              |                                    | uchi     | ж.,<br>ж                                                       | Mat                                                        | Yama                                                       | "Complete genome structure of the thermophilic | <u>.</u> .                            |                           |                             |                                     |        |                   |                                    |        |                    |                               |                      |                    | 39C13F                  | Score 39; DB | Io. 28;    | 2; Mismatches |
| PRT;                            | Created)<br>Last sec       |                    |                      | synec                                                   | coccal                        |                          |                    |              | 334;                               | ; ;      | ahima                                                          | oto M.                                                     | ر<br>ان                                                    | the th                                         | 3P-1.                                 |                           |                             | nembra                              | activi | Ä.                | res.                               |        |                    |                               |                      |                    |                         | core 3       | Pred. No.  | Misn          |
|                                 | 23, Creat<br>23, Last      | 24, Last           | cer.                 | Therm                                                   | Chroo                         |                          |                    |              | 122408                             | ato S    | Kawas                                                          | atsumo                                                     | akeuci                                                     | e Of                                           | atus I                                |                           | 1,                          | L to 1                              | rter   | rt.               | [V1n_1                             |        | .:                 | INRP.                         | 2A0602; 1.           |                    | 113205 MW;              |              |            |               |
| ARY;                            |                            | el. 2              | nspor                | tus (                                                   | ria;                          |                          |                    |              | pwed=                              | T., S    | i M.;                                                          | Σ.                                                         | Ξ.Σ                                                        | uctur                                          | elong                                 | 002).                     | 9170.                       | tegra                               | anspo  | P:transport; IEA. | Acrt                               | HAEL   | tran; 1.           |                               |                      |                    | 1132                    | 75.0%;       | 63.68;     | tive          |
| PRELIMINARY;                    | (TrEMBLrel.                | (TrEMBLrel.        | etilux transporter.  | longa                                                   | Bacteria, Cyanobacteria;      | 9                        | . A.               |              | MEDLINE=22225144; PubMed=12240834; | neko     | iguch                                                          | hara                                                       | moto                                                       | le str                                         | Thermosynechococcus elongatus BP-1."; | DNA Res. 9:123-130(2002). | EMBL; AP005374; BAC09170.1; | GO:0016021; C:integral to membrane; | F:tr   | P:tr              | InterPro; IPR001036; Acrtivin_res. |        | AGR T              | PRINTS; PR00702; ACRIFLAVINRP | TIGRFAMS; TIGR00915; | æ.                 | 1044 AA;                |              | tty        | Conservative  |
| PRE                             |                            | 3 (Tr              | etti                 | cus e                                                   | Cyano                         | NCBI_TaxID=32046;<br>[1] | SEQUENCE FROM N.A. | -1;          | 222514                             | ć., Ka   | A., IX                                                         | .;<br>8                                                    | Sugi                                                       | genou                                          | schooc                                | 9:123-                    | 05374;                      | 16021;                              | )5215; | GO; GO:0006810;   | IPROC                              | IPROC  | Pfam; PF00873; ACR | 300702                        | TIGRO                | Complete proteome. | 1044                    |              | imilar     | 7; Conser     |
| 10                              | 01-MAR-2003<br>01-MAR-2003 | 01-JUN-2003        | Multidrug<br>TLL1618 | chococ                                                  | eria;                         | _raxII                   | ENCE               | STRAIN-BP-1; | INE=22                             | nura 1   | abe 7                                                          | cawa (                                                     | , s od                                                     | plete                                          | nosyme                                | Rea.                      | , AP0(                      | 30:00                               | 30:00  | 30:00             | rPro;                              | rPro;  | , PF0(             | IS; PI                        | FAMs;                | lete 1             | ENCE                    | atch         | cal S      | 7             |
| LT 1<br>HO<br>QBDIHO<br>OBDIHO; | 01-M                       | D-10               | Multidru<br>TLL1618  | Syne                                                    | Bact                          | NCBI<br>[1]              | SEQUI              | STRA         | MEDI                               | Nakaı    | Wataı                                                          | Kiyo                                                       | Shim                                                       | COM.                                           | Then                                  | DNA                       | EMBL                        | ĝ                                   | 8      | ŝ                 | Inte                               | Inte   | Pfam               | PRIN                          | TIGR                 | Comp               | SEQUENCE                | Query Match  | Best Local | Matches       |
| RESULT<br>QBDIHO<br>ID Q        | TO<br>TO                   | Į.                 | H Z                  | SO                                                      | ပ္ပ                           | X X                      | RР                 | RC<br>C      | XX                                 | Ş        | R.                                                             | RA                                                         | R.                                                         | RT                                             | RT                                    | IJ.                       | ద                           | DR.                                 | DR.    | DR<br>DR          | Z<br>Z                             | D<br>E | K<br>K             | DR.                           | DR<br>DR             | 3                  | Š                       | 8            | Be         | Ma            |

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NCBI_TaxID=4896
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 STRAIN=MAPF303099;
MEDIINE=21089309;
MEDIINE=21082930;
PubMed=11214968;
MEDIINE=21082930;
Nakamira Y., Sato S., Asamira E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kindida Y., Kiyokawa C., Kohara M., Mateumoto M., Mateuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Tabeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Gaps
 MEDLINE=22608415; PubMed=12721630;
MEDLINE=22608415; PubMed=12721630;
Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Ivanova N., Sorokin A., Anderson I.,
Kapatral V., Bhattacharyya A., Reznik G., Mikhailova M., Lapidus A.,
Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
Overbeek R., Kyrpides N.;
Genome sequence of Bacillus cereus and comparative analysis with
Bacillus anthracis.";
 ö
 Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Phyllobacteriaces, Mesorhizobium.
 Score 38; DB 16; Length 344;
Pred. No. 13;
2; Mismatches 2; Indels
 Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Firmicutes, Bacillales, Bacillaceae; Bacillus.
 344 AA; 38539 MW; C55268ACB7225995 CRC64;
 Mesorhizobium loti.";
DMA Res. 7:31-338 (2000).
EMBL; BAD0310.25 BAB50445.1; -.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0006237; F:metallopeptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR002933; Peptidase_M20.
 Created)
Last sequence update)
Last annotation update)
 OSISSA; PRE 344 AA. OSISSA; PRE 344 AA. OSISSA; SASSA; SASSA (TERBLE). 24, Created) OI-JUN-2003 (TERBLE). 24, Last sequence update) OI-OCT-2003 (TERBLE). 25, Last annotation update) BC5259.
 Nature 423:87-91(2003).
EMBL, AE017015; AAP12123.1; -. InterProc. IPP000437; Prok lipoprot S.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
 Rhizobium loti (Mesorhizobium loti).
 73.1%;
 01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-JUN-2003 (TrEMBLrel. 24,
 Local Similarity 60.0
 PRELIMINARY;
 |||:| |: ||
843 EEVLPNGIGYS 853
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152 EEIAPLGLSY 161
1 EEVVPXGMSYS 11
 1 EEVVPXGMSY 10
 Hippurate hydrolase
 NCBI_TaxID=226900;
 Complete proteome.
SEQUENCE 344 AA;
 Query Match
 Q98FX1;
 Q98FX1
 RESULT 3
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AC 098F.
AC 098F.
DT 01-0
DT 0
 RESULT 2
Q815A7
ID Q815
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 "Genomic analysis reveals chromosomal variation in natural populations of the uncultured psychrophilic archaeon Cenarchaeum symbiosum.";
J. Bacteriol. 180:5005-5009(1998).
EMBL: AF083072; AAC26699.1;
PIR; T31308; T31308.
GO; GO:00160215; Firansporter activity; IEA.
GO; GO:0006215; Piransporter activity; IEA.
GO; GO:0006215; Piransporter activity; IEA.
InterPro; IPR001580; WD40:
InterPro; IPR001680; WD40:
INTERPRO; IPR00168
 Gaps
 Gaps
 Archaea; Crenarchaeota; Thermoprotei; Cenarchaeales; Cenarchaeaceae;
 [1]
SEQUENCE FROM N.A.
STRAIN=972h-;
Hunt C., Aves S., McDougall R.C., Rajandream M.A., Barrell B.G.;
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 STRAIN=B;
MEDINE=98422450; PubMed=9748430;
Schleper C., DeLong E.F., Preston C.M., Feldman R.A., Wu K.Y.,
Swanson R.V.;
 Score 38; DB 1; Length 3472;
Pred. No. 1.7e+02;
4; Mismatches 1; Indels
 73.1%; Score 38; DB 16; Length 387; 60.0%; Pred. No. 15;
 3472 AA; 367058 MW; 37F80707030F9355 CRC64;
Pfam; PF01546; Peptidase M20; 1.
Hydrolase; Complete proteome.
SEQUENCE 387 AA; 41180 MW; 131BFF8E64306829 CRC64;
 Schizosaccharomyces pombe (Fission yeast).
Bukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
 01-MAY-2000 (TrEMBLrel. 13, Created)
.01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Probable sulfate permease.
 Last annotation update)
 Last sequence update)
 840 AA
 PRT; 3472 AA.
 PROSITE; PSOU40: "TRANSP_INN_MEMBR; 1.
Hypothetical protein.
SEQUENCE 3472 AA; 367058 MW. 37FBA77777
 2; Mismatches
 Created)
 PRT;
 73.1%;
 01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-OCT-2003 (TrEMBLrel. 25, Hypothetical protein.
 Query Match
Best Local Similarity 54.5'
Conservative
6;
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2294 EDVIPRGISFS 2304
 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
 PRELIMINARY;
 PRELIMINARY;
 1 EEVVPXGMSYS 11
 367 DEAIPHGMSY 376
 1 EEVVPXGMSY 10
 Cenarchaeum symbiosum
 SEQUENCE FROM N.A.
 NCBI_TaxID=46770;
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Local Similarity 60.0
 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
 PRELIMINARY;
 PRELIMINARY;
 226 EVIPAGASYN 235
 239 EVIPAGASYN 248
 SEQUENCE FROM N.A.
TISSUE=Salivary gland;
 2 EVVPXGMSYS 11
 2 EVVPXGMSYS 11
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A
 NCBI TaxID=10090;
 NCBI_TaxID=10090;
 SEQUENCE
 Query Match
 protein.
GLTSCR2.
 Q8VD18
Q8VD18;
 Q8BTX4
 RESULT 8
 RESULT 9
 Q8VD18
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 Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K., Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
"The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans.";
Nucleic Acids Res. 30:5293-5300(2002).
 Gape
 Gaps
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 Mycoplasma penetrans.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=28227;
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 Query Match
71.2%; Score 37; DB 16; Length 1123;
Best Local Similarity 70.0%; Pred. No. 81;
Matches 7; Conservative 1; Mismatches 2; Indels C
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
R FMBL; AL132779; CAB60015.1; -.
PIR; T39116; T39116.
GenebB SPombe, SPAC869.05c; -.
R GO; GO:0008271; F:sulfate porter activity; IEA.
GO; GO:0008271; F:sulfate transport; IEA.
R InterPro; IPR002645; STAS.
R InterPro; IPR01902; Sulph_transpt.
R Pfam; PF01740; STAS, 1.
R Pfam; PF01740; STAS, 1.
R Pfam; PF01740; STAS, 1.
R PROSTER; PSC80081; STAS, 1.
R PROSTER; PSC80081; STAS, 1.
R PROSTER; PSC80081; STAS, 1.
 Query Match 71.2%; Score 37; DB 3; Length 840; Best Local Similarity 77.8%; Pred. No. 59; Matches 7; Conservative 1; Mismatches 1; Indels
 1123 AA; 123636 MW; A4D707330E3DB4AC CRC64;
 QBR126;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
 Last sequence update)
Last annotation update)
 471 AA
 EMBL; AP004171; BAC44062.1; -.
InterPro; IPR008985; ConA like lec_gl.
InterPro; IPR007326; Lipoprotein_17.
Complete proteome: SEQUENCE 1123 AA; 123636 MW; A4D70
 Created)
 PRT;
 MEDLINE=22354719; PubMed=12466555;
 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, MYPE 2560 paralog, 57%.
 PRELIMINARY;
 PRELIMINARY;
 658 EYVPMGLSYS 667
 2 EVVPXGMSYS 11
 135 VVPQGMSYA 143
 3 VVPXGMSYS 11
 SEQUENCE FROM N.A. STRAIN=HF-2;
 QBR126
 Q8EWD4
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 STRAIN=NOD; TISSUE=Thymus; MEDLINE=22354683; PubMed=12466851; The FANTOM Consortium. The Party Consortium. The Party Consortium Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; Analysis of the mouse transcriptome based on functional annotation of
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 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TremBrel. 23, Last annotation update)
Similar to gliona tumor suppressor candidate region gene 2.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
 Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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 69.2%; Score 36; DB 11; Length 471; 60.0%; Pred. No. 51; tive 2; Mismatches 2; Indels
 69.2%; Score 36; DB 11; Length 484; 60.0%; Pred. No. 53; 2; Indels tive 2; Mismatches 2; Indels
Strausberg R.; Submitted (MAR-2002) to the BMBL/GenBank/DDBJ databases. EMBL; BC025810; AAH25810.1; -. MGD; MG1:2154441; Gltscr2. Hypothetical protein. 1
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 24, Last amnotation update)
01-UIN-2003 (TREMBLrel. 24, Last amnotation update)
Similar to glioma tumor suppressor CANDIDATE region gene
 Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; 8C017637; AAH17637.1; -.
MGD; MGI:2154441; G15tscr2.
SEQUENCE 484 AA, 55835 WW, BBB45F3B4BE02A36 CRC64;
 471 AA; 54506 MW; B0DA685C374A9760 CRC64;
 484 AA.
 484 AA.
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"Role of mobile DNA in the evolution of vancomycin-resistant
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 STRAIN-CSTBL/60; TISSUE-Pituitary;
MEDINE-225468; Pubmed=12466851;
The FANTON Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNs.";
Nature 420:563-573(2002)
RMEL: AROTA11; BAG36760.1;
SEQUENCE 484 AA; 55792 MW; EB67949BCBE92D44 CRC64;
 SEQUENCE FROM N.A.
STRAIN=VS83 / ATCC 700802;
MEDLINE=2250857; Pubmed=1265927;
MEDLINE=2250857; Pubmed=1265927;
Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Tettelin H., Dodson R.J., Unayam L., Brinkac L., Beanan M.,
Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
 Gaps
 0; Gaps
 Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
 Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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0
 Query Match
69.2%; Score 36; DB 11; Length 484;
Best Local Similarity 60.0%; Pred. No. 53;
Matches 6; Conservative 2; Mismatches 2; Indels
 69.2%; Score 36; DB 11; Length 484; 60.0%; Pred. No. 53; Live 2; Mismatches 2; Indels
 OBEK35;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to glioma tumor suppressor CANDIDATE region gene 2
 2; Indels
60,770 full-length cDNAs.";
Nature 420.563-573(2002).
BMBJ, AKO88461; BAC40367.1; -.
MAD). MGI: 2154441; Gltscr2.
SEQUENCE 484 AA; 55806 MW; B3056425B5EECAD8 CRC64;
 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pheromone binding protein, putative.
 PRT;
 Query Match
Best Local Similarity 60.0%
 PRELIMINARY;
 PRELIMINARY;
 239 EVIPAGASYN 248
 239 EVIPAGASYN 248
 2 EVVPXGMSYS 11
 2 EVVPXGMSYS 11
 SEQUENCE FROM N.A.
 08BK35
 Q839T9
 EF0063
 RESULT 10
08BK3
AC 08BK3
AC 08BK3
DT 01-MA
DT 01
 RESULT 11
10839T9
10839T9
AC 0839T9
DT 01-JU
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RC SUTAIN-DC3000;

RA BUELL R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D., RA Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D., RA Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M., RA Brinkac L., Beanan M., Haft D., Selengut J., Madupu R., Daugherty S., Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T., RA White O., Fraser C., Collmer A.;

R. Complete sequence of Pseudomonas syringae.";

R. Complete sequence of Pseudomonas syringae.";

R. EMBL, AR016588, AA054162.1;

DR ROG, GO0005634; C.nucleus; IRA.

GO, GO: 0005534; C.nucleus; IRA.

BR GO, GO: 0005534; C.nucleus; IRA.

DR GO, GO: 0005539; F: DNA-directed RNA polymerase activity; IEA.

BR GO, GO: 000539; F: DNA-directed RNA polymerase activity; IEA.

DR GO, GO: 000539; P: DNA-directed RNA polymerase activity; IEA.

DR InterPro; IPR007081; RNA pol Rpbl 3.

BR InterPro; IPR007081; RNA pol Rpbl 4.

DR InterPro; IPR007081; RNA pol Rpbl 3.

DR Pfam; PR04993; RNA pol Rpbl 3.

DR Pfam; PR04998; RNA pol Rpbl 3.

DR Pfam; PR04998; RNA pol Rpbl 3.

R. Pfam; PR04998; RNA pol Rpbl 3.

R. Pfam; PR04998; RNA pol Rpbl 3.

R. Pfam; PR04998; RNA pol Rpbl 4.

R. Pfam; PR04998; RNA pol Rpbl 4.

R. Pfam; PR04998; RNA pol Rpbl 5.

R. Pfam; PR04998; RNA pol Rpbl 5.

R. Pfam; PR04998; RNA pol Rpbl 4.

R. Pfam; PR04998; RNA pol Rpbl 5.

 Gaps
 Gaps
 .
0
 Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 ö
 69.2%; Score 36; DB 16; Length 1399; 66.7%; Pred. No. 1.7e+02; tive 2; Mismatches 1; Indels C
 Query Match 69.2%; Score 36; DB 16; Length 559; Best Local Similarity 66.7%; Pred. No. 62; Marches 6; Conservative 2; Mismatches 1; Indels
Enterococcus faecalis.";
L Science 299:2071-2074(2003).
ENEL, AEO16947.7 A-079943.1.
R TIGR; EF0063;
TIGR; EF006215; Firansport IRA.
R QO; GO:0005216; Firansport; IRA.
R QO; GO:0006910; P:transport; IRA.
R THREFFC; IPRO00943; Prok lipoprot_S.
R HTGEFFC; IPRO00943; SBP_bac_S; I.
R PROSITS; PSO0013; PROKAR_LIPOPROTEIN; 1.
R PROSITS; PSO0013; PROKAR_LIPOPROTEIN; 1.
R PROGIECE 559 AA; 61476 MW; CCI5418D33D53DE7 CRC64;
 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DNA-directed RNA polymerase, beta' subunit.
 PRT; 1399 AA.
 Pseudomonadaceae; Pseudomonas.
 PRELIMINARY;
 6; Conservative
 351 LIPEGMSYS 359
 581 QVVPAGLSÝ 589
 3 VVPXGMSYS 11
 2 EVVPXGMSY 10
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 RPOC OR PSPTO0620
 NCBI_TaxID=323;
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; 0

2; Indels

60.0%; Pred. No. 41; tive 2; Mismatches

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Best Local Similarity 60.0
Matches 6; Conservative
 2 EVVPXGMSYS 11
 Q9XVK4
 RESULT 15
 O9XVK
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 040129;
01-NOV-1996 (TTEMBLrel. 01, Created)
01-NOV-1996 (TTEMBLrel. 01, Last sequence update)
01-NOV-1996 (TTEMBLrel. 25, Last annotation update)
01-OCT-2003 (TTEMBLrel. 25, Last annotation update)
Hypothetical protein precursor.
Lycopersicon esculentum (Tomato).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
 Gaps
 MEDLINE-2282569B; PubMed=12917642;
Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
Angren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Angren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb E.A., Zinser E.R., Chisholm S.W.;
"Genome divergence in two Prochlorococcus ecotypes reflects oceanic
Nature 424:1042-1047(2003).
BMBL; BX57209B; CAR21267.1;
BMBL; BX57209B; CAR21267.1;
SEQUENCE 245 AA; 26907 MW; 106F7C4CBE2C6427 CRC64;
 STRANTS-VF56; TISSUE=Pistil;

X MEDLINE=5537523; PubMeda7647301;

A Milligan S.B., Gasser C.5.;

MILLIGAN S.B., Gasser C.5.;

Plant Mol. Biol. 28.691-711(1995).

R EMBL; U50592; AA840497.1; -..

R PIR; S57810; S57810.

R GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.

R InterPro.; IPR00137; Kunitz_lequme.

R Priore, PF00197; Kunitz_lequme.

R ProDom; PF00197; Kunitz_lequme.

R ProDom; PF00197; Kunitz_lequme.

R ProDom; PR00191; Kunitz_lequme.

R ProDom; PR00191; Kunitz_lequme.

R ProDom; PR00191; Kunitz_lequme.

R ProDom; PR001921; Kunitz_lequme.

R PROSTITE; PR00291; Kunitz_lequme.

R ProDom; PR001821; Kunitz_lequme.

R PROSTITE; PR002831; Kunitz_lequme.

R PROSTITE; PR002831; Kunitz_lequme.
 O7V604;
01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Phospholipid and glycerol acyltransferase (From 'motifs_6.msf').
 ö
 Prochlorococcus marinus (strain MIT 9313).
Bacteria, Cyanobacteria, Prochlorophytes, Prochlorococcaceae,
 67.3%; Score 35; DB 10; Length 225; 54.5%; Pred. No. 37;
 67.3%; Score 35; DB 16; Length 245;
 2; Indels
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SEQUENCE 225 AA; 25188 MW; 1074C261D20CFDAD CRC64;
 245 AA
 225 AA
 3; Mismatches
 POTENTIAL.
 PRT;
 PRT;
 6; Conservative
 PRELIMINARY;
 PRELIMINARY;
 DEVVPNGKTYA 42
 1 EEVVPXGMSYS 11
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Best Local Similarity
Matches 6; Conserv
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=74547;
 NCBI_TaxID=4081;
 32
 Query Match
 Q7V6Q4
 040129
 RESULT 14
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ö
 R10D12.10 -
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
 Gaps
 ö
 A "Genome sequence of the nematode C.elegans: A platform for investigating biology.";

L Science 281:2012-2013 (1998).

E EMBL, 281109; CAB03241.1; -.

R PRIS, 724111, 724111.

R PRIS, 724111, 724111.

R POSSESSE TATE BINDING IEA.

GO; GO:000524; F:ATP binding; IEA.

GO; GO:0006468; P:Drotein kinase activity; IEA.

GO; GO:0006468; P:Drotein amino acid phosphorylation; IEA.

R GO; GO:0006468; P:Drotein amino acid phosphorylation; IEA.

R PEAM: PPOONOS; Prot kinase.

R PEAM: PROONOS; Prot kinase.

R PRODOM; PDOMOSI; Rrot kinase.

R PROSITE; RSSOU1; RROTEIN KINASE DOM; 1.

R PROSITE; RSSOU1; RAMESERASE.
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67.3%; Score 35; DB 5; Length 425;
Best Local Similarity 50.0%; Pred. No. 75;
Matches 5; Conservative 3; Mismatches 2; Indels
 Percy C.M.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
R10D12.10 protein.
 425 AA
 Search completed: June 3, 2004, 11:57:32 Job time : 29.8667 secs
 PRT;
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MEDLINE=99069613; Pubmed=9851916;
 PRELIMINARY;
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179 QVVPVGLGYS 188
 335 EQIVPGGLQY 344
 1 EEVVPXGMSY 10
 SEQUENCE FROM N.A.
 WCBI_TaxID=6239;
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....

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Key
Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002.
 Synthetic
 ABB80523
 virucide
 protease
 ABB80523
 Hepatitis
Hepatitis
Hepatitis
 Hepatitis
Hepatitis
 Hepatitis
Hepatitis
Hepatitis
 Abb80523 Hepatitis
 Hepatitie
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 3, 2004, 11:31:01 ; Search time 45.9333 Seconds (without alignments) 67.664 Million cell updates/sec
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Abb 80550
Abb 80521
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Abb 80555
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Abb 80552
 1586107
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 otal number of hits satisfying chosen parameters:
 1586107 segs, 282547505 residues
 SUMMARIES
 Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 using sw model
 ABB80563
ABB80565
 ABB80528
 BLOSUM62
Gapop 10.0 , Gapext 0.5
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geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*
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geneseqp2001s:*
 A_Geneseq_29Jan04:*
 length: 0
length: 2000000000
 US-09-909-164-11
56
 1 BEVVPXGMHYS 11
 %
Query
Match Length I
 M protein - protein search,
 June
 ost-processing:
 linimum DB seq
Taximum DB seq
 Score
 scoring table:
 brfect score:
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| Hepatitis<br>Hepatitis<br>Hepatitis | 1                 |                      | iti. | 13 13 13                         | Hepatitis<br>Hepatitis<br>Hepatitis | Hepatitis<br>Hepatitis<br>Hepatitis |
|-------------------------------------|-------------------|----------------------|------|----------------------------------|-------------------------------------|-------------------------------------|
| Abb80526<br>Abb80564<br>Abb80568    | 944               | 3053<br>3053<br>3054 | 53   | 000                              | Abb80556<br>Abb80557<br>Abb80551    | Abb80553<br>Abb80552<br>Abb80545    |
| ABB80526<br>ABB80564                | 053<br>054<br>054 | 3053                 | 53   | ABB80549<br>ABB80547<br>ABB80544 | ABB80556<br>ABB80557<br>ABB80551    | ABB60553<br>ABB60552<br>ABB80545    |
|                                     |                   |                      |      |                                  |                                     |                                     |
| 111                                 | 1445              | ដេដដ                 | 11   | 클류큐                              | ###                                 | 111                                 |
| 4.08                                | 71.4              |                      |      |                                  |                                     | 69.6<br>69.6<br>69.6                |
| 4 4 4<br>70 70 71                   | 4444<br>9000      | 4 4 4                | 3.0  | თ თ თ<br>ო ო ო                   | 0 0 0<br>0 0 0                      | 0 0 0<br>0 0 0                      |
| 26                                  | 3005              | 1 64 66 44           | 36.5 | 37<br>38<br>39                   | 4 4 4<br>0 4 4                      | 44<br>44<br>5                       |

## ALIGNMENTS

```
/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 virus
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #3.
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 /note= "D-form residue"
 Location/Qualifiers
ABB80523 standard; peptide; 11 AA
 Claim 17; Page 64; 69pp; English.
 Brunck
 19-JUL-2001, 2001WO-US023169
 21-JUL-2000; 2000US-0220101P.
 (first entry)
 (CORV-) CORVAS INT INC
 Lim-Wilby M, Levy OE,
 WPI; 2002-361643/39.
 Misc-difference
 WO200208251-A2
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Gaps

ö

Length 11; 0; Indels

96.4%; Score 54; DB 5; Le 100.0%; Pred. No. 0.00071; ive 0; Mismatches 0;

Query Match Best Local Similarity 100. Matches 11; Conservative

7

EEVVPXGMHYS 11

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Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;

Synthetic

virucide.

Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #40.

(first entry)

08-OCT-2002

ABB80560;

ABB80560 standard; peptide; 11 AA.

RESULT

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Gaps

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0; Indels

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invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingradient is useful for treating disorders associated with hepatitis C virus
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7^{\rm n}
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #38.
 DB 5; Length 11; 0.00071;
 96.4%; Score 54; DB 100.0%; Pred. No. 0.0 iive 0; Mismatches
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 'note= "Oxymethionine"
 location/Qualifiers
 TK;
 ABB80558 standard, peptide, 11 AA.
 Claim 17; Page 65; 69pp; English.
 Brunck
 19-JUL-2001; 2001WO-US023169.
 21-JUL-2000; 2000US-0220101P.
 (first entry)
 11; Conservative
 1 BEVVPXGMHYS 11
 1 EEVVPXGMHYS 11
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39
 Query Match
Best Local Similarity
Matches 11; Conserv
 Sequence 11 AA
 WO200208251-A2
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002.
 Synthetic
 protease
 ABB80558
 ABB80558
 RESULT
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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 ingredient
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 The sequence represents a peptide compound of the invention having Lepatitis C virus (HCV) protease inhibitory activity. The peptides of invention are alpha-ketcamide peptide analogues. The peptides have viruside activity, and are useful for treating and in the manufacture a medicament to trat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredicts useful for treating disorders associated with hepatitis C virus
 Gaps
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
 ö
 DB 5; Length 11;
0.00071;
hes 0; Indels
 Query Match
96.4%; Score 54; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 11; Conservative 0; Mismatches
 note= "N-terminal acetyl"
 /note= "C-terminal amide"
 'note= "D-form residue"
 note= "D-form residue"
 note= "Oxymethionine"
 Location/Qualifiers
 Brunck TK;
 Claim 17; Page 65; 69pp; English.
 19-JUL-2001, 2001WO-US023169.
 21-JUL-2000; 2000US-0220101P
 Levy OE,
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39.
 Misc-difference
 Misc-difference
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 31-JAN-2002.
 protease.
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus

Sequence 11 AA,

RESULT 4 ABB80527

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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #17.
 note= "N-terminal acetyl"
 /note= "C-terminal amide"
 note= "D-form residue"
 Location/Qualifiers
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169.
 (first entry)
 Levy OE,
 (CORV-) CORVAS INT INC
 EEVVPXGQHYS
 WPI; 2002-361643/39
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 08-OCT-2002
 31-JAN-2002
 Synthetic
 ABB80541;
 ABB80537;
 protease
 RESULT 6
 ABB8054
 日
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 ö
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 note= "Norvaly1 carbony1 forming keto-amide linkage with
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #7.
 ö
 DB 5; Length 11;
0.00071;
thes 0; Indels
 96.4%; Score 54; DB 100.0%; Pred. No. 0.C ive 0; Mismatches
 note= "N-terminal acetyl"
 /note= "C-terminal amide"
 note= "D-form residue"
 Location/Qualifiers
 Ŧ,
 ABB80537 standard; peptide; 11 AA.
 11 AA
 Claim 17; Page 64; 69pp; English.
 Brunck
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169
 ABB80527 standard; peptide;
 residue 7"
 11; Conservative
 EEVVPXGMHYS 11
 1 EEVVPXGMHYS 11
ij
 EEVVPXGMHYS 11
 o
E
 (CORV-) CORVAS INT INC
EEVVPXGMHYS
 WPI; 2002-361643/39.
 Levy
 Query Match
Best Local Similarity
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 Synthetic
 ABB80527;
 virucide.
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Brunck TK;

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ö
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #21
 .
0
 87.5%; Score 49; DB 5; Length 11; 90.9%; Pred. No. 0.0069; ive 0; Mismatches 1; Indels
 Ä
Claim 17; Page 64; 69pp; English.
 7
 ABB80541 standard; peptide;
 (first entry)
 Query Match
Best Local Similarity 90.5
Matches 10; Conservative
 1 EEVVPXGMHYS 11
 디
```

Matches

à d RESULT 5 ABB80537 ID ABB80

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WPI; 2002-361643/39
 Query Match
Best Local Similarity
 Misc-difference
 Sequence 11 AA;
 Key
Modified-site
 WO200208251-A2
 Modified-site
 Key
Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 Synthetic
 Synthetic.
 ABB80546;
 virucide
 protease
 Matches
 RESULT 7
 ABB80546
```

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ö
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\sf C}
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #34.
 ö
 Match 11; Score 48; DB 5; Length 11; Local Similarity 90.9%; Pred. No. 0.011; Local 10; Conservative 0; Mismatches 1; Indels
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 /note= "C-terminal amide"
 note= "D-form residue"
 Location/Qualifiers
 Brunck TK;
 ABB80554 standard; peptide; 11 AA.
 Claim 17; Page 65; 69pp; English.
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 08-OCT-2002 (first entry)
 1 EEVVPXGMHYS 11
 1 EEVVPXGTHYS 11
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 Modified-site
 31-JAN-2002
 31-JAN-2002
 Synthetic
 ABB80554;
 virucide.
 Query Match
 protease
 Best Loc
Matches
 RESULT 8
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 셤
 ö
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmacceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #26.
 ö
 Score 49; DB 5; Length 11;
Pred. No. 0.0069;
0; Mismatches 1; Indels
 /note= "N-terminal acetyl"
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 'note= "D-form residue"
 Location/Qualifiers
 Location/Qualifiers
 Brunck TK;
 ABB80546 standard; peptide; 11 AA
 Claim 17; Page 65; 69pp; English
 87.5%;
90.9%;
 19-JUL-2001; 2001WO-US023169.
 21-JUL-2000; 2000US-0220101P.
 (first entry)
 10; Conservative
 1 EEVVPXGMHYS 11
 7
 Levy OE,
 (CORV-) CORVAS INT INC
 EEVVPXGQHYS
 virucide.
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Brunck TK,

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The sequence represents a peptide compound of the invention having hepatitis C virus (RCV) procease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #30.
 ABB80550 standard; peptide; 11 AA.
 Claim 17; Page 65; 69pp; English.
 19-JUL-2001; 2001WO-US023169.
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
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Best Local Similarity 90.9
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 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 Synthetic
 protease.
 ABB80550;
 RESULT 9
ò
 g
```

(first entry)

/note= "N-terminal acetyl"

Location/Qualifiers

/note= "C-terminal amide" note= "D-form residue"

Brunck TK;

Levy OE,

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ò
 The sequence represents a peptide compound of the invention having bepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV prorease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 virus
 Gaps
 Hepatitis C virus, HCV, serine protease, inhibitor, alpha-ketoamide, virucide.
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\tt C}
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #35.
 ;
0
 11 13 14; Score 48; DB 5; Length 11; 12 90.9%; Pred. No. 0.011; Conservative 0; Mismatches 1; Indels
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 /note= "D-form residue"
 note= "D-form residue"
 Location/Qualifiers
 Brunck TK;
 ABB80555 standard; peptide; 11 AA.
 Claim 17; Page 65; 69pp; English.
 19-JUL-2001; 2001WO-US023169.
 21-JUL-2000; 2000US-0220101P.
 (first entry)
 1 EEVVPXGMHYS 11
 EEVVPXGSHYS 11
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39
 WPI; 2002-361643/39
 Best Local Similarity
Matches 10; Conser
 Misc-difference
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002
 Synthetic.
 ABB80555;
 protease.
 protease
 Query Match
 RESULT 10
 HILKEKKEKEKEKEKELLLLLLLLKEKKKEKELKY
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 ö
 /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
```

Gaps

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Score 48; DB 5; Length 11; Pred. No. 0.011; 0; Mismatches 1; Indels

85.7%;

7

EEVVPXGSHYS

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Gaps

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Length 11; 1; Indels

DB 5; 0.011;

Score 48; DB Pred. No. 0.0110; Mismatches

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```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 'note= "Norvalyl carbonyl forming keto-amide linkage with
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C ^\circ
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #12.
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 note= "D-form residue"
 Location/Qualifiers
 Claim 17; Page 64; 69pp; English.
 Claim 17; Page 65; 69pp; English.
 ABB80532 standard; peptide; 11
 85.7%;
90.9%;
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 (first entry)
 residue 7"
 Conservative
 1 EEVVPXGMHYS 11
 검
 Levy OE,
 (CORV-) CORVAS INT INC
 1 EEVVPXGSHYS
 Query Match
Best Local Similarity
Thes 10; Conserve
 WPI; 2002-361643/39
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Novel peptide
 Key
Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 activity protease.
 Synthetic
 ABB80532;
 virucide
 RESULT 11
 ABB8053
 g
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```

Brunck TK;

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 "Norvaly1 carbonyl forming keto-amide linkage with
pharmaceutical composition comprising the peptide as an active ingredient
is useful for treating disorders associated with hepatitis C virus
 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
 Gaps
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #11.
 ö
 ö
 Length 11;
 1; Indels
 Length 11;
 1; Indels
 Score 46; DB 5;
Pred. No. 0.027;
 Score 46; DB 5;
Pred. No. 0.027;
0; Mismatches
 Mismatches
 'note= "N-terminal acetyl"
 11
/note= "C-terminal amide"
 Location/Qualifiers
 Brunck TK;
 Ā
 Claim 17; Page 64; 69pp; English.
 ö
 ABB80531 standard; peptide; 11
 21-JUL-2000; 2000US-0220101P.
 82.1%;
90.9%;
 82.1%;
 19-JUL-2001; 2001WO-US023169
 /note= "No
residue 7"
 10; Conservative
 Conservative
 1 EEVVPXGMHYS 11
 1 EEVVPXGMHYS 11
 EEVVPXGGHYS 11
 Levy OE,
 WPI; 2002-361643/39.
 Query Match
Best Local Similarity
Matches 10; Conserv
 (CORV-) CORVAS INT
 Local Similarity
nes 10; Conserv
 Sequence 11 AA;
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 peptide
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 Synthetic.
 Novel pep
activity
 ABB80531;
 protease
 virucide.
 Query Match
 Best Loc
Matches
 RESULT 12
 ABB80531
 δ
 SSSS
 ઠ
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```

/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"

/note= "C-terminal amide" 'note= "D-form residue" 'note= "Oxymethionine"

WO200208251-A2

31-JAN-2002

Misc-difference

Modified-site

Modified-site

'note= "N-terminal acetyl"

Location/Qualifiers

Key Modified-site Modified-site

Synthetic

virucide

Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;

Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41

08-CCT-2002

ABB80561;

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```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5.
 Score 45; DB 5; Length 11;
Pred. No. 0.042;
0; Mismatches 1; Indels
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 note= "D-form residue"
 Location/Qualifiers
 Brunck TK;
 Ź
 Claim 17; Page 64; 69pp; English.
 .
 ABB80525 standard; peptide; 11
 80.4%;
illarity 90.9%;
Conservative (
 21-JUL-2000; 2000US-0220101P
 (first entry)
 1 EEVVPXGMHYS 11
 Levy OE,
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39.
 Query Match
Best Local Similarity
Matches 10; Conserv
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 Synthetic
 virucide.
 ABB80525;
 protease
RESULT 13
```

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hopatitis C virus
 Gaps
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1.
 ö
 DB 5; Length 11; 0.042;
 1; Indels
 Score 45; DB 9
Pred. No. 0.042
0; Mismatches
 ABB80521 standard; peptide; 11 AA.
 Claim 17; Page 65; 69pp; English.
 80.4%;
90.9%;
 (first entry)
 Local Similarity 90.3
 1 EEVVPXGMHYS 11
 EEVVPXGMDYS 11
 Sequence 11 AA;
 08-OCT-2002
 ABB80521;
 Query Match
 Best Loc
Matches
 RESULT 15
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Gaps

.; 0

RESULT 14 ABB80561 ID ABB80561 standard; peptide; 11 AA. XX

EEVVPXGMSYS

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virus

Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C

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Brunck

Lim-Wilby M, Levy OE, (CORV-) CORVAS INT INC

WPI; 2002-361643/39

protease.

virus

19-JUL-2001; 2001WO-US023169. 21-JUL-2000; 2000US-0220101P us-09-909-164-11.rag

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 'note= "Norvaly1 carbony1 forming keto-amide linkage with
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
Hepatitis C virus, HCV, serine protease, inhibitor, alpha-ketoamide, virucide.
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 Location/Qualifiers
 Lim-Wilby M, Levy OE, Brunck TK;
 Claim 17; Page 64; 69pp; English.
 19-JUL-2001; 2001WO-US023169.
 21-JUL-2000; 2000US-0220101P
 residue 7"
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39.
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 31-JAN-2002.
 Synthetic
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Search completed: June 3, 2004, 11:48:23 Job time: 45.9333 secs 1 EEVVPXGMHYS 11 1 EEVVPXGMSYS 11 ઠે g

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Gaps

. 0

Score 45, DB 5, Length 11; Pred. No. 0.042; 0, Mismatches 1; Indels

Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative (

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Sequence 4794, Ap Sequence 21444, A Sequence 19, Ap Sequence 19, Appli Sequence 26515, A Sequence 28613, A Sequence 213, Appli Sequence 31, Appli Sequence 31, Appli Sequence 41, Appli Sequence 41, Appli Sequence 41, Appli Sequence 21, Appli Sequence 22, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 22, Appli Sequence 6, Appli Appli Sequence 6, Appli Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 June 3, 2004, 11:36:47; Search time 11.7333 Seconds (without alignments) 48.399 Million cell updates/sec
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2: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/pcrits_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 US-09-134-001C-4794

US-09-252-991A-21444

US-08-821-119-19

US-08-821-118-2

US-08-252-991A-26415

US-09-252-991A-27834

US-09-252-991A-27834

US-09-252-991A-27834

US-09-134-01C-4

US-09-134-01C-4

US-09-134-01C-4

US-09-134-01C-4

US-09-134-01C-4

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US-08-1995A-3

US-08-1995A-3

US-08-460-674-4

US-08-460-711B-4

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US-08-216-01
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US-08-464-517-22
US-08-246-361A-22
US-08-463-772-22
PCT-US93-05000-22
US-08-464-517-6
 Total number of hits satisfying chosen parameters:
 389414 segs, 51625971 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Minimum DB seg length: 0 Maximum DB seg length: 2000000000
 US-09-909-164-11
56
1 EEVVPXGMHYS 11
 DB
 *
Query
Match Length D
 Fitle:
Perfect score:
Sequence:
 Scoring table:
 Score
 Database :
 Searched:
 Result
No.
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| Sequence 6, Appli<br>32 57.1 289 3 US-08-246-361A-6<br>Sequence 4, Appli<br>Sequence 4, Appli<br>Sequence 4, Appli<br>Sequence 4, Appli<br>Sequence 5, Appli<br>Sequence 23, Appli<br>Sequence 24, Appli<br>Sequence 24, Appli<br>Sequence 26, Appli<br>Sequence 27, Appli | RESULT 1  US-09-134-001C-4794  Sequence 4794, Application US/09134001C  Sequence 4794, Application US/09134001C  GENERAL INFORMATION:  APPLICANT: Lynn Doucette-Stamm et al  APPLICANT: Lynn Doucette-Stamm et al  TITLE OF INVENTION: WUCHEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  TITLE OF INVENTION NUMBER: US/09/134,001C  CURRENT APPLICATION NUMBER: US 60/064,964  PRIOR PILING DATE: 1997-11-08  PRIOR PILING DATE: 1997-08-14  PRIOR PILING DATE: 1997-08-14  NUMBER OF SEQ ID NOS: 5674  LENGTH: 1037  TYPE: PRT  TYPE: PRT  VERSION Staphylococcus epidermidis  US-09-134-001C-4794                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | <pre>Query Match</pre>                | RESULT 2 US-09-252-991A-21444 Sequence 21444, Application US/09252991A Sequence 21444, Application US/09252991A Sequence 21444, Application US/09252991A Sequence 21444, Application US/09252991A Factor No. 6551795 GENERAL INFORMATION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ASPLICATION NUMBER: US/09/252,991A CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 21444 LENGTH: 856 TYPE: PRI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
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| 00010000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | RESULT 1 US-09-134- Sequence Sequence Sequence Sequence PELICY TITLE C TITLE C TITLE C TITLE C FILE RE FILE RE CURRENT PRIOR F | Query Ma<br>Best Loc<br>Matches<br>Qy | RESULT 2 US-09-252-1 Sequence: Sequence: GENERAL APPLICE: TITLE CTILE R TITLE CURREN CURREN CURREN PRIOR 1 PRI |

us-09-909-164-11.rai

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 Pacence 2, Application US/08821118
Sequence 2, Application US/08821118
Pacent No. 5989889
GENERAL INFORMATION:
APPLICANT: Rey, Michael
APPLICANT: Golightly, Elizabeth
TITLE OF INVENTION: HAVING TRIPEPTIDE AMINOPEPTIDES
TITLE OF INVENTION: ACTIVITY
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59898990 No. 5989899disk of No. 5989889th America, Inc.
STREET: 405 Lexington Avenue
 Gaps
 .
0
 ö
 Length 600;
 Score 34; DB 2; Length 600
Pred. No. 1.2e+02;
0; Mismatches 2; Indels
 COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCTHARE: FESTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,118
FILING DATE: 19-MAR-1997
CIASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Lambiris, Elias J
RECISTRATION NUMBER: 33,728
RECISTRATION NUMBER: 33,728
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
 Score 34; DB 2;
Pred. No. 1.2e+02
 0; Mismatches
 60.7%;
 TELEX:
INFORMATION FOR SEQ ID NO: 19:
 Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
 INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 600 amino acids
TYPE: amino acid
STRANDEDNESS: single
TELEPHONE: 212-867-0123
TELEPAX: 212-878-9655
 SEQUENCE CHARACTERISTICS:
LENGTH: 600 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Matches 6; Conservative
 TELEPHONE: 212-867-013
TELEFAX: 212-878-9655
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 MOLECULE TYPE: protein
FRAGMENT TYPE: internal
) MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-821-119-19
 4 VPXGMHYS 11
 31 VPKGWHYS 38
 linear
 linear
 USA
 10174
 US-08-821-118-2
 COUNTRY:
 g
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 APPLICANT: GARY BRETON
TITLE OF INVENTION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER: OF SEQ ID NOS: 8344
SEQ ID NO 7304
LENGTH: 323
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 Sequence 19, Application US/08821119
Sequence 19, Application US/08821119
Sequence 19, Application US/08821119
Sequence 19, Application US/08821119
Sequence 19, Application US/08821119
Sequence 19, Application US/08821104
APPLICANT: Holm, Kaj Andre
APPLICANT: Halkier, Torben
APPLICANT: Lehnbeck, Jan
TITLE OF INVENTION: Tripeptidyl Aminopeptidase
NUMBER OF SEQUENCES: 23
CORRESSENDENCE ADDRESS:
ADDRESSEE: NO. 5821104th America, Inc.
 Gaps
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 ö
 60.7%; Score 34; DB 4; Length 323; 55.6%; Pred. No. 63;
 DB 4; Length 856;
48;
 Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM COMPATIBLE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,119
FILING DATE: 19-MAR-1997
CLASSIPRCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Blias J
REGISTRATION NUMBER: 33,728
RECISTRATION NUMBER: 33,728
RECISTRATION NUMBER: 33,728
RECISTRATION NUMBER: 33,728
RECISTRATION NUMBER: 34,728
RECISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 Mismatches
 Score 37;
Pred. No.
 Sequence 7304, Application US/09543681A
Patent No. 6605709
 No. 58211040 No. 58

CITY: A05 Lexington Avenue

CITY: New York

STATE: NY

COUNTRY: TGT
 , ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21444
 Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
 TYPE: PRT ORGANISM: Proteus mirabilis
 1 EEVVPXGMHY 10
 64 EAVVPGGEHY 73
 2 EVVPXGMHY 10
 : | | |:||
75 DVCPAGVHY 83
 Local Similarity
 USA
10174
RF
 US-09-543-681A-7304
 US-09-543-681A-7304
 Query Match
 Matches
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US-09-134-001C-3950

US-09-134-001C-3950

Sequence 3950, Application US/09134001C

Sequence 3950, Application US/09134001C

Sequence 3950, Application US/09134001C

SERETAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDEMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: B998-08-13

FILE REFERRANCE: GTC-007

CURRENT FILING DATE: 1998-08-13

PRIOR PILING DATE: 1997-11-08

PRIOR PLILOG DATE: 1997-11-08

PRIOR PLILOG DATE: 1997-08-14

NUMBER: US 60/055,779

NUMBER OF SEQ ID NOS: 5674

NUMBER OF SEQ ID NOS: 5674

LENGTH: 70
, LILLE OF INVENTION: by the polynucleotides and methods for their use.; FILE REPERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT PILLING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. NO. 6380362 60/171,678
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 747
; TYPE: PRI
; ORGANISM: Rat
 ö
 ö
 Sequence 4, Application US/09408020

Fatent No. 6632937

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Swanson, Robert A.
APPLICANT: Scheper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/09/408,020
CURRENT FILING DATE: 1999-09-29
PRIOR PILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
 Gaps
 Gaps
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0
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0
 Length 3472;
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 2; Indels
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Best Local Similarity 45.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 4; Mismatches 2.
 NUMBER OF SEQ ID NOS: 123
SCPTWARE: FastSEQ for Windows Version 3.0
SEQ ID VIEW 3472
 TYPE: PRT
ORGANISM: Cenarchaeum symbiosum
 2294 EDVIPRGISFS 2304
 1 EEVVPXGMHYS 11
 627 PGGLHYS 633
 5 PXGMHYS 11
 US-09-408-020-4
 US-09-408-020-4
 à
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 Parente 27834, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT:

MARC J. Rubenfield et al.

TITLE OF INVENTION:

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.

TITLE OF INVENTION:

TITLE OF INVENTION:

PREPRIENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27834

LENGTH: 285
 GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PAPLICATION NUMBER: US/00/252, 991A
CURRENT FILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-7
NUMBER OF SEQ ID NOS: 33142
LENGTH: 277
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 Gaps
 Gaps
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 APPLICANT: Watson, James D
APPLICANT: Murison, James G.
IITLE OF INVENTION: Polynucleotides, polypeptides expressed
 Score 33; DB 4; Length 277;
Pred. No. 83;
0; Mismatches 4; Indels
 58.9%; Score 33; DB 4; Length 385;
44.4%; Pred. No. 1.2e+02;
tive 3; Mismatches 2; Indels
 US-09-252-991A-26615
; Sequence 26615, Application US/09252991A
; Patent No. 6551795
 Sequence 36, Application US/09724864
Patent No. 6380362
GENERAL INFORMATION:
) OKGANISM: Pseudomonas aeruginosa
JS-09-252-991A-26615
 ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27834
 Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
 Query Match
Best Local Similarity 44.4
Matches 4; Conservative
 1 EEVVPXGMHYS 11
 48 EETVPGGGHTS 58
 201 EILPAALHY 209
 2 EVVPXGMHY 10
 US-09-252-991A-27834
 RESULT 8
US-09-724-864-36
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ANTI-SENSE:
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 TITLE OF INVENTION: Tumor Necrosis Factor
TITLE OF INVENTION: Tumor Necrosis Factor
TITLE OF INVENTION: For Its Use
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Benjamin A COTTON OF SECTION O
) IOCATION: 96
) OTHER INFORMATION: Xaa = * ,Ala,Glu,Gly,Ile,Lys,Leu,Arg,Ser,Thr,Val
US-09-621-976-6096
 .
0
 57.1%; Score 32; DB 4; Length 101; 83.3%; Pred. No. 43;
 Score 32; DB 4; Length 70;
Pred. No. 29;
1; Mismatches 2; Indels
 Indels
 APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dobert S.
APPLICANT: Jobert G.
APPLICANT: Jobert G.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 1054 PR2.
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
; SEQ ID NO 6096
LENGTH: 101
 COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,988A
PITING DATE: January 3, 1996
 Sequence 6096, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3950
 S-08-580-988A-23
Sequence 23, Application US/08580988A
Patent No. 5856161
GENERAL INFORMATION:
APPLICANT: Aggarwal et al.
 Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
 Best Local Similarity 83.3
Matches 5, Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
 4 VPXGMHYS 11
 5 PXGMHY 10
 40 PRGMHY 45
 CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071
 NAME/KEY: UNSURE
 JS-09-621-976-6096
 Query Match
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57.1%; Score 32; DB 2; Length 102; 60.0%; Pred. No. 44;
 APPLICANT: Hilman, Jennifer L.
APPLICANT: Lal Preeti
APPLICANT: Lal Preeti
APPLICANT: Lal Preeti
APPLICANT: Raser, Matthew R.
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Comparible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEC for Windows Version 2.0

CURENT APPLICATION DATA:

APPLICATION NUMBER: US/08/879,995A

FILING DATE: Herewith

CLASSIPFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:
 NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5721CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEPHONE: 713-777-6908
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS:
 1; Mismatches
 RESULT 13
US-08-879-995A-3
; Sequence 3, Application US/08879995A
Patent No. 5985606
 FILING DATE:
- ATTORNEY/AGENT INFORMATION:
NAME: B111ings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERRICE/DOCKET NUMBER: PP-0
TELECOMMUNICATION INFORMATION:
 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 126 amino acide TYPE: amino acid STRANDEDNESS: single
FILING DATE:
ATTORNEY/AGENT INFORMATION
 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
 TELEPHONE: 415-855-05:
TELEFAX: 415-845-4166
 FRAGMENT TYPE: internal
CORIGINAL SOURCE:
US-08-580-988A-23
 DESCRIPTION: protein HYPOTHETICAL: no
 1 EEVVPXGMHY 10
 24 EEVFPLAMNY 33
 linear
 8
 TOPOLOGY: lin
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0
 DB 2; Length 126;
 57.1%; Score 32; DB 3; Length 126;
66.7%; Pred. No. 55;
tive 1; Mismatches 2; Indels
 Indels
 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,096
 57.1%; Score 32; DB 66.7%; Pred. No. 55; tive 1; Mismatches
 NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0326 US
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,995
 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
 FILING DATE:
ATTORNEY/AGENT INFORMATION:
 126 amino acids
 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
 28 EQVVPGGGH 36
; TOPOLOGY: linear; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 163590
US-08-879-995A-3
 1 EEVVPXGMH 9
 TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
 ; LIBRARY: GenBank
; CLONE: 163590
US-09-215-096-3
 FILING DATE:
CLASSIFICATION:
 LENGTH:
 RESULT 14
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Gaps
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 Score 32; DB 2; Length 152;
Pred. No. 68;
1; Mismatches 3; Indels
Date of the control o
 Search completed: June 3, 2004, 12:03:07 Job time: 11.8 secs
 ss: not relevant
linear
 57.1%;
 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
 TOPOLOGY: linear
MOLECULE TYPE: peptide
 1 EEVVPXGMHY 10
 20 EEVFPLAMNY 29
 US-08-460-694-4
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RESULT 15

EQVVPGGGH 36

1 EEVVPXGMH 9

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Sequence 7, Appli
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 June 3, 2004, 11:57:42; Search time 33.7333 Seconds (without alignments) 91.741 Million cell updates/sec
 Sequence 11, Sequence 21, Sequence 25, Sequence 30, Sequence 34, Sequence 39, Sequence 42, Sequence 15, Sequence 15, Sequence 6, M. Sequence 8, M. Sequence
 Description
 | Cgn2 6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/US06 NEM PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/US06 NEM PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/US08 NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/US09 NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/US00 NEW PUB.pep:*
 1155919
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 US-09-909-164-7

US-09-909-164-11

US-09-909-164-25

US-09-909-164-36

US-09-909-164-34

US-09-909-164-38

US-09-909-164-38

US-09-909-164-44

US-09-909-164-15

US-09-909-164-16
 Total number of hits satisfying chosen parameters:
 1155919 seqs, 281338677 residues
 SUMMARIES
 Published Applications AA:*
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Minimum DB seg length: 0
Maximum DB seg length: 200000000
 US-09-909-164-11
56
1 EEVVPXGMHYS 11
 Query
Match Length
 Score
 Title:
Perfect score:
 Scoring table:
 Database :
 Sequence:
 Searched:
 Run on:
 Result
No.
 7
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| Sequence 9, Appli<br>Sequence 10, Appl<br>Sequence 12, Appl<br>Sequence 13, Appl | equence 49, equence 49, equence 50, equenc | 4444444                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ednence<br>ednence<br>ednence<br>ednence<br>ednence<br>ednence                               | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                         |
|----------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------|---------------------------------------------------------------|
| US-09-909-164-9<br>US-09-909-164-1<br>US-09-909-164-1                            | 2 US-09-909-16<br>2 US-09-909-16<br>2 US-09-909-16<br>3 US-09-909-16                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | US-09-909-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064-15-1064 | 09-909-164-2<br>09-909-164-2<br>09-909-164-2<br>09-909-164-3<br>09-909-164-3<br>09-909-164-3 | 606-60-SN<br>606-60-SN<br>606-60-SN<br>606-60-SN<br>606-60-SN |
| ннан                                                                             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 144444                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 1 <b>111111</b>                                                                              | =======                                                       |
|                                                                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 711.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 4 0 0 0 1 1 4 4 0 0 0 1 1 4 4 0 0 0 0 0                                                      | 0000000<br>000000                                             |
| 1111<br>124<br>188                                                               | 200000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 4 W & C & C & C & C & C & C & C & C & C &                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~                                                        | W 4 4 4 4 4 4<br>W 0 4 6 4 6 4 6                              |

## ALIGNMENTS

|                                                                                                                                                                                                                                           | S OF HEFATITIS C                                                                                                                                                                                                                                                                                                   |                                                                       |                                                                                                                                                   |                                                                                                                                                                                        |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ·                                                                                                                                                                                                                                         | TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS FILE REPERENCE: IN01192-US CURRENT APPLICATION NUMBER: US(09/909,164 CURRENT FILING DATE: 2003-03-25 PRIOR APPLICATION NUMBER: 60/220,101 PRIOR FILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 62 SOFTWARE: PACENTIN VERSION 3.1 |                                                                       | example 1                                                                                                                                         |                                                                                                                                                                                        |
|                                                                                                                                                                                                                                           | S NS-3-SERINE PR                                                                                                                                                                                                                                                                                                   |                                                                       | ed according to                                                                                                                                   |                                                                                                                                                                                        |
| ULT 1 09-909-164-7 equence 7, Application US/09909164 ublication No. US20020068702A1 APPLICAT: Corvas International, Inc. APPLICANT: Lim-Wilby, Marguerita APPLICANT: Levy, Odile E APPLICANT: Tery, Caile E APPLICANT: Frunck, Terence K | TITLE OF INVENTION: NOVEL PEPTIDES AS NS-<br>FILE REFERENCE: IN01192-US CURRENT APPLICATION NUMBER: US/09/909,164 CURRENT FILING DATE: 2003-03-25 PRIOR APPLICATION NUMBER: 60/220,101 PRIOR FILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 62 SOFTWARE: Patentin version 3.1                                       | l sequence                                                            | OTHER INFORMATION: 11-mer synthesized according to example SABJURE: NAME/KEY: MOD RES LOCATION: (1). (1) PURBER INFORMATION: ACETYLATION PRATURE: | URE norvaline-(CO) URE D-amino acid                                                                                                                                                    |
| SULT 1 Sequence 7, Application US/09909164 Sequence 7, Application US/09909164 Publication No. US20020068702A1 APPLICANT: Corvas International, ID APPLICANT: Lim-Wilby, Marguerita APPLICANT: Leneck, Terence K                          | TITLE OF INVENTION: NOVEL PEPTID FILE REFERENCE: IN01192-US CURRENT APPLICATION NUMBER: US/O CURRENT FILING DATE: 2003-03-25 PRIOR APPLICATION NUMBER: 60/220 PRIOR PILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 62 SOFTWARE: PARENTI NOVERSON 3.1                                                                | Q ID NO 7<br>LENGTH: 11<br>TYPE: PRT<br>ORGANISM: artificial sequence | OTHER INFORMATION: 11-mer synt<br>FRATURE:<br>LOCATION: (1) (1)<br>OTHER INFORMATION: ACETYLATION<br>PERATURE:                                    | NAME/KEY: MISC_FEATURE LOCATION: (6)(6) OTHER INFORMATION: norvaline-(CO) TEARURE: NAME/KEY: MISC_FEATURE LOCATION: (9)(9) OTHER INFORMATION: D-amino acid PEATURE: LOCATION: (11)(11) |
| RESULT 1 US-09-909-164-7 ; Sequence 7, A ; Publication N ; GENNERAL INFOR APPLICANT: ; APPLICANT:                                                                                                                                         | TITLE R FILE R CURREN CURREN PRIOR PRIOR PRIOR NUMBER SOFTWAR                                                                                                                                                                                                                                                      | SEQ ID NO 7 LENGTH: 1 TYPE: PRT ORGANISM: FEATURE:                    | CTHER IN FEATURE: NAMB/KEY LOCATION OTHER IN FEATURE:                                                                                             | NAMB/KEY  LOCATION  OTHER IN  FEATURE:  NAMB/KEY  LOCATION  LOCATION  LOCATION  LOCATION                                                                                               |

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ASPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Levy, Odile E
APPLICANT: Lavy, Odile E
APPLICANT: BANGA, Tereance K
TILE REFERENCE: INOIL92-US
FILE REFERENCE: INOIL92-US
CURRENT PELLOATE: 2003-03-25
FILE REFERENCE: 2003-03-25
FILE REFINED DATE: 2003-03-25
FILE REFERENCE: SOURCE TO NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEQ TRANE: PATENT VILING PATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEQ ID NO 25
LEMETER: LEMET
 FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
 OTHER INFORMATION: 11-mer synthesized according to example 1 PEATURE:
NAME/KEY: MOD_RES
 Query Match 87.5%; Score 49; DB 12; Length 11; Best Local Similarity 90.9%; Pred. No. 0.0067; Matches 10; Conservative 0; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 21
LENGTH: 11
 PRATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
 NAME/KEY: MISC_FEATURE
COCATION: (9)...(9)
OTHER INFORMATION: D-amino acid
US-09-909-164-21
 NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
 LOCATION: (1).(1)
OTHER INFORMATION: ACETYLATION
 TYPE: PRT
ORGANISM: artificial sequence
 TYPE: PRT ORGANISM: artificial sequence
 FRATURE:
NAME/KRY: MOD RES
LOCATION: (11)
OTHER INFORMATION: AMIDATION
 LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 1 EEVVPXGMHYS 11
 1 EEVVPXGQHYS 11
 FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6). (6)
 NAME/KEY: MOD RES
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 RESULT 2
US-09-164-11

SQUENCE 11, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Corver International, Inc.

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Brunck, Terence K

TITLE OF INVENTION: NOVEL PEFTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: IN01182-US

CURRENT PAPLICATION NUMBER: US/09/909,164

CURRENT PAPLICATION NUMBER: 60/220,101

PRIOR FILING DATE: 2003-03-25

PRIOR FILING DATE: 2003-07-21

NUMBER OF SEQ ID NOS: 62

SOOFWARE: Patentin version 3.1

LENGTH: 11

TYPE: PRI
 RESULT 3
US-09-164-21
US-09-909-164-21
Sequence 21, Application US/09909164
; Publication No. US20020068702A1
; Publication No. US20020068702A1
; FAREZAL INFORMATION:
 APPLICANT: Corvas International, Inc.
; APPLICANT: Lim-Wilby, Marguerita
; APPLICANT: Lim-Wilby, Marguerita
; APPLICANT: Brunck, Telence
; APPLICANT: Brunck, Telence
; TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS (
; FILE REFERENCE: IN01192-US
 ö
 Gaps
 0; Gaps
 INFORMATION: 11-mer synthesized according to example 1
 Query Match 96.4%; Score 54; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.0007; Matches 11; Conservative 0; Mismatches 0; Indels
 Query Match 96.4%; Score 54; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.0007; Matches 11; Conservative 0; Mismatches 0; Indels
 FEATURE:
NAME/KEY: MISC_FEATURE
COCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
 ; LOCATION: (8). (8)
; OTHER INFORMATION: D-amino acid
US-09-909-164-11
 NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 ORGANISM: artificial sequence
 FEATURE:
NAME/KEY: MOD RES
LOCATION: (11). (11)
OTHER INFORMATION: AMIDATION
; OTHER INFORMATION: AMIDATION US-09-909-164-7
 1 EEVVPXGMHYS 11
 1 EEVVPXGMHYS 11
 1 BEVVPXGMHYS 11
 1 BEVVPXGMHYS 11
 NAME/KEY: MISC_FEATURE
 FEATURE:
 FEATURE:
 OTHER
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Sequence 38, Application US/09909164

publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Levy, Odile E

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN101192-UB

CURRENT APPLICANTON NUMBER: US/09/909,164

CURRENT FILING DATE: 2003-03-25

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR PILLAG DATE: 2000-7-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: 2000-7-21

SOFTWARE: 2000-7-21

LENGTH: 11

LENGTH: 11
 ö
 Gaps
 ö
 FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
 OTHER INFORMATION: 11-mer synthesized according to example 1
 1; Indels
 Score 48; DB 1; Pred. No. 0.01; 0; Mismatches
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 34
 LOCATION: (6). (6) OTHER INFORMATION: norvaline-(CO)
 FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (9)...(9)
OTHER INFORMATION: D-amino acid
US-09-909-164-34
 LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
 TYPE: PRT ORGANISM: artificial sequence
 85.7%;
 ORGANISM: artificial sequence
 FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 Local Similarity 90.9
Les 10; Conservative
 1 EEVVPXGMHYS 11
 1 EEVVPXGSHYS 11
 PEATURE:
NAME/KEY: MISC_FEATURE
 NAME/KEY: MISC FEATURE LOCATION: (8)..(8)
 OTHER
FEATURE:
NAME/KEY: MOD RES
 FEATURE:
NAME/KEY: MOD_RES
 TYPE: PRT
 Best Loca
Matches
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 APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile B
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERBNCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
WINDER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
 Sequence 34, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Nove PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
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 FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
 DB 12; Length 11;
 DB 12; Length 11;
 1; Indels
 1; Indels
 Score 49; DB 12;
Pred. No. 0.0067;
0; Mismatches
 85.7%; Score 48; DB
90.9%; Pred. No. 0.01
tive 0; Mismatches
 Sequence 30, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
 OTHER INFORMATION: norvaline-(CO) FEATURE:
 i LOCATION: (6)...(6); OTHER INFORMATION: norvaline-(CO) US-09-909-164-30
 NAME/KEY: MOD_RES

LOCATION: (1)...(1)

COATION: (1)...(1)

PEATURE:

NAME/KEY: MOD RES

LOCATION: (11)...(11)

OTHER INFORMATION: AMIDATION
 ; LCCATION: (8)...(8); OTHER INFORMATION: D-amino acid
 87.5%;
 TYPE: PRT
ORGANISM: artificial sequence
 Query Match
Best Local Similarity 90.9.
 Query Match
Best Local Similarity 90.5
Matches 10; Conservative
 1 EEVVPXGTHYS 11
 1 EEVVPXGMHYS 11
 1 EEVVPXGQHYS 11
 1 EEVVPXGMHYS 11
 NAME/KEY: MISC FEATURE
 NAME/KEY: MISC_FEATURE
 RESULT 6
US-09-909-164-34
 SEQ ID NO 30
LENGTH: 11
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Page 4

APPLICANT: Levy, Odile E

APPLICANT: Brunck, Terence K

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: IN01192-US

CURRENT PILLON NUMBER: 00/220,101

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR PLILUE DATE: 2000-0-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQ ID NO 42

LENGTH: 11

TYPE:
 RESULT 10
US-09-909-164-44

JUSTON 10200200068702A1

SUDJICATION NO. US200200068702A1

SUDJICATION TO COVAS INTERNATION:

APPLICANT: COVAS INTERNATION:

APPLICANT: Levy, Odile B

APPLICANT: Levy, Odile B

APPLICANT: Brunck, Terence K

TITLE OF INVENTION NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: IN01192-US

FURRARY PILING DATE: 2003-03-25

PRIOR PAPLICATION NUMBER: 60/220,101

PRIOR PLING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PATENTIN OF 44

SORTWARE: PATENTIN OF 44

SORTWARE: PATENTIN OF 44
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 TYPE: PRT ORGANISM: artificial sequence FRATURE: OFFICE ORGANISM: CONTINE OTHER INFORMATION: 11-mer synthesized according to example 1
 INFORMATION: 11-mer synthesized according to example 1
 DB 12; Length 11;
 Query Match
Best Local Similarity 90.9%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches
 LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
 FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
FEATURE:
 LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 TYPE: PRT
ORGANISM: artificial sequence
 NAME/KEY: MISC FEATURE
LOCATION: (8). (8)
OTHER INFORMATION: Met(0)
 1 EEVVPXGMHYS 11
 1 EEVVPXGXHYS 11
 NAME/KEY: MISC_FEATURE
 NAME/KEY: MOD RES
 US-09-909-164-42
 g
 APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPREMENCE: INO1192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR PRILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENT NOS: 63
LENGTH: 11
 0
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 Gaps
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0
 OTHER INPORMATION: 11-mer synthesized according to example 1 PERTURE:
NAME/KEY: WOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 Score 48; DB 12; Length 11;
Pred. No. 0.01;
0; Mismatches 1; Indels
 DB 12; Length 11;
 1; Indels
 Query Match 85.7%; Score 48; DB 12
Best Local Similarity 90.9%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches
 APPLICANT: Corvas International, Inc. APPLICANT: Lim-Wilby, Marguerita
 Sequence 39, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
 US-09-909-164-42; Sequence 42, Application US/09909164; Publication No. US20020068702A1; GENERAL INFORMATION:
 PEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
COTHER INFORMATION: norvaline-(CO)
US-09-909-164-38
 LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
 NAME/KEY: MISC FEATURE
LOCATION: (8)...(9)
COTHER INFORMATION: D-amino acids
US-09-909-164-39
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
 TYPE: PRT
ORGANISM: artificial sequence
 FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
FEATURE:
 1 EEVVPXGMHYS 11
 1 EEVVPXGSHYS 11
 1 EEVVPXGSHYS 11
 1 EEVVPXGMHYS 11
 NAME/KEY: MISC_FEATURE
 FEATURE:
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Sequence 5 Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lewy, Odile B

APPLICANT: Lewy, Odile B

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: IN104192-US

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT PILING DATE: 2003-03-25

PRIOR PILING DATE: 2003-03-25

PRIOR APPLICATION NUMBER: 60/220,101

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PATENTING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SED ID NO 5

LENGTH: 11
Publication No. US202020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE CF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERBNCE: 1001192-08
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PEACENTIN VERSION 3.1
SEQ ID NO 16
LENGTH: 11
 ö
 Gaps
 OTHER INFORMATION: 11-mer synthesized according to example 1
 OTHER INFORMATION: 11-mer synthesized according to example 1
 Score 46; DB 12;
Pred. No. 0.026;
0; Mismatches
 LOCATION: (6). (6) OTHER INFORMATION: norvaline-(CO)
 LOCATION: (9). (9)
CTHER INFORMATION: D-amino acid
US-09-909-164-16
 LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative (
 ORGANISM: artificial sequence
 ORGANISM: artificial sequence
 NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 1 EEVVPXGMHYS 11
 1 EEVVPXGGHYS 11
 NAME/KEY: MISC FEATURE LOCATION: (9)..(9)
 NAME/KEY: MISC FEATURE
 NAME/KEY: MOD RES
 셤
 APPLICANT: Corvas International, Inc.
APPLICANT: Lim Wilby, Marguerita
APPLICANT: Lim Wilby, Marguerita
APPLICANT: Lim Wilby, Marguerita
APPLICANT: Lim Wilby, Marguerita
APPLICANT: Lim Wilby, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
URRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTION VINBER: 2000-07-21
SOFTWARE: PATENTION VINBER: 2000-07-21
SOFTWARE: PATENTION OF SEQ ID NOS: 62
IENGTH: 11
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0
 TYPE: PRT ORGANISM: artificial sequence FEATURE: OFFICE ORGANISM: OTHER INFORMATION: 11-mer synthesized according to example 1
 Score 48; DB 12; Length 11; Pred. No. 0.01;
 Query Match

82.1%; Score 46; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.026;
Matches 10; Conservative 0; Mismatches 1; Indels
 1; Indels
 0; Mismatches
 RESULT 12
US-09-909-164-16
; Sequence 16, Application US/09909164
 Sequence 15, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
 NAME/KEY: MISC_FEATURE
; LOCATION: (6)...(6)
; OTHER INFORMATION: norvaline-(CO)
US-09-909-164-15
 NAME/KEY: MISC_FEATURE
LCGATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
 FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (8)._(9)
OTHER INFORMATION: D-amino acids
FEATURE:
 LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
 85.7%;
90.9%;
 NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 OTHER INFORMATION: AMIDATION
 Query Match
Best Local Similarity 90.9
Matches 10; Conservative
 LOCATION: (8)...(8)
CTHER INFORMATION: Met(0)
US-09-909-164-44
 1 EEVVEXGGHYS 11
 1 EEVVPXGMHYS 11
 1 EEVVPXGXHYS 11
 NAME/KEY: MISC FEATURE
 FEATURE:
NAME/KEY: MOD_RES
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GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lin-Wilby, Marguerita
APPLICANT: Lin-Wilby, Marguerita
APPLICANT: Lin-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Le
 ö
 TYPE: PRT
ORGANISM: artificial sequence
FRATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
 Query Match 80.4%; Score 45; DB 12; Length 11; Best Local Similarity 90.9%; Pred. No. 0.041; Matches 10; Conservative 0; Mismatches 1; Indels
 Search completed: June 3, 2004, 12:57:15
Job time : 33.7333 secs
 NAME/KEY: MOD RES

LOCATION: (1) ... (1)

OTHER INFORMATION: ACETYLATION

FEATURE:

NAME/KEY: MISC_FEATURE

LOCATION: (6) ... (6)

OTHER INFORMATION: norvaline-(CO)

FEATURE:
 NAME/KEY: MISC FEATURE
LOCATION: (9). (9)
OTHER INFORMATION: D-amino acid
Publication No. US20020068702A1
 NAME/KEY: MOD_RES

LOCATION: (11)...(11)

OTHER INFORMATION: AMIDATION

US-09-909-164-8
 1 EEVVPXGMHYS 11
 1 EEVVPXGMDYS 11
 셤
 APPLICANT: Corvas International, Inc.
APPLICANT: Lim-wilby, Marguerita
APPLICANT: Lim-y, Odile E
APPLICANT: Levy, Odile E
TILLE REFERENCE: INO1192-US
CURRENT APPLICATION NUMBER: US/99/909,164
CURRENT PILING DATE: 2003-013-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
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 Gaps
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 TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
 Score 45; DB 12; Length 11; Pred. No. 0.041; 0; Mismatches 1; Indels
 80.4%; Score 45; DB 12; Length 11; 90.9%; Pred. No. 0.041;
 1; Indels
 0; Mismatches
 Sequence 6, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
 RESULT 15
US-09-909-164-8
; Sequence 8, Application US/09909164
 NAME/KEY: MISC FEATURE
LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
 FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
 FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (9) ...(9)
OTHER INFORMATION: D-amino acid
 NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
OTHER INFORMATION: ACETYLATION
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
 NAME/KEY: MOD RES

LOCATION: (11)...(11)

CTHER INFORMATION: AMIDATION
US-09-909-164-6
 FEATURE:
NAMEN KEX:
NOTHER INFORMATION: AMIDATION
US-09-909-164-5
 10; Conservative
 1 EEVVPXGMHYS 11
 1 EEVVPXGMSYS 11
 1 EEVVPXGMHYS 11
 1 EEVVPXGMSYS 11
 Query Match
Best Local Similarity
Matches 10, Conserva
 FEATURE:
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hypothetical prote 3-dahydroquinate s probable DNA ligas cell division prote hypothetical prote Slal protein precure ATP-dependent DNA hypothetical prote polyamine transpor conserved hypothet
 carbamoyl-phosphat
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hypothetical prote
hypothetical prote
hypothetical prote
conserved hypothet
DNA binding protei
GMP syntherase, su
Hypothetical protei
TSIB.1 protein - A
diphthine synthase
 cytochrome-c3 hydr
coenzyme F420-quin
hypothetical prote
 ftsH proteinase ac
 probable amino aci
amino acid antipor
finger protein (cl
 (without alignments)
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 June 3, 2004, 11:35:47 ; Search time 9 Seconds
 283366
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 283366 seqs, 96191526 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 A72207
A89892
A89892
A82892
A82001
A82001
B82618
B82618
B724111
G86430
G75538
B7562
B7581
B75
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 H81697
 length: 0
length: 2000000000
 US-09-909-164-11
56
 Query
Match Length DB
 1 EEVVPXGMHYS
 PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
 sed
sed
 Scoring table:
 Title:
Perfect score:
 Score
 Minimum DB s
Maximum DB s
 Sequence:
 Searched:
 Database
 Run on:
 Result
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| DNA mismatch repaimacrophage-stimula | C14B9.8 protein - | L-shaped tail fibe | hypothetical 367K | tachykinin B precu | heme exporter prot | hypothetical prote | ribosomal protein | ribosomal protein | probable ThuA prot | hypothetical prote | cyclin D2 - rat | cyclin D2 - rat | cyclin D2 - mouse | cyclin D2 - human |
|--------------------------------------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|-----------------|-----------------|-------------------|-------------------|
| A69663<br>JC5061                     | 844754            | 836851             | T31308            | A25905             | D71640             | 857810             | E97120            | T07215            | C95881             | T25737             | JC4011          | 158372          | A41984            | A42822            |
| 24                                   | (7)               | 0                  | 0                 | ~                  | 0                  | 0                  | ~                 | ~                 | 7                  | ~                  | 0               | ~               | 7                 | 03                |
| 627                                  | 1257              | 1396               | 3472              | 126                | 197                | 225                | 233               | 267               | 270                | 283                | 288             | 288             | 289               | 289               |
| 58.9                                 | 58.9              | 58.9               | 58.9              | 57.1               | 57.1               | 57.1               | 57.1              | 57.1              | 57.1               | 57.1               | 57.1            | 57.1            | 57.1              | 57.1              |
| e e                                  | 33.6              | 33                 | 33                | 32                 | 32                 | 32.                | 32                | 32                | 32                 | 35                 | 32.             | 32              | 32                | 32                |
| (1)                                  |                   |                    |                   |                    |                    |                    |                   |                   |                    |                    |                 |                 |                   |                   |

## ALIGNMENTS

|           | RESULT 1                                                                                                                                             |
|-----------|------------------------------------------------------------------------------------------------------------------------------------------------------|
| · · · · · | ftsH proteinase activity modulator HflK - Thermotoga maritima (strain MSB8)                                                                          |
|           | C;Species: Thermotoga maritima<br>C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000                                        |
|           | C; Accession: A/2207<br>R; Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey                                    |
|           | Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.,<br>C.M.                                                     |
|           | Nature 399, 323-329, 1999                                                                                                                            |
|           | A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome set<br>a.Beference number: a72200; MITD:99287316; DMID:10360571 |
|           | A.Accession: A72207                                                                                                                                  |
|           | A;Status: preliminary                                                                                                                                |
|           | A; Molecule Cype: DNA A; Molecule Cype: DNA                                                                                                          |
|           | A, NCD 2014 - JOS - AND 11 - JOS - AND 119 GB: AEO00512; NID: G4982396; PIDN: AAD36885.1; PID: G498240                                               |
|           | A;Experimental source: strain MSB8                                                                                                                   |
|           | CjGenetics:<br>b.Gene. mwisos                                                                                                                        |
|           | C;Superfamily: erythrocyte band 7 integral membrane protein                                                                                          |
|           | Query Match 66.1%; Score 37; DB 2; Length 308;                                                                                                       |
|           | Best Local Similarity 75.0%; Pred. No. 10;<br>Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;                                             |
|           | Qy 3 VVPXGMHY 10                                                                                                                                     |
|           | Db 41 VVPSGIHY 48                                                                                                                                    |
|           | RESULT 2<br>F89892                                                                                                                                   |

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Score 37, DB 2; Length 1057; Pred, No. 39; 2; Mismatches 2; Indels

Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative 7.

|:| |:| || 190 EIVSNGLHYS 199 2 EVVPXGMHYS 11

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Conserved hypothetical protein XF1950 [imported] - Xylella fastidiosa (strain 9a5c)
C/Species: Xy/ella fastidiosa
C/Species: Xy/ella fastidiosa
C/Species: Xy/ella fastidiosa
C/Species: Xy/ella fastidiosa
C/Species: Sylella fastidiosa
C/Species: Sylella fastidiosa
C/Species: The Xylella fastidiosa Consortium of the Organization for Nucleotide Seque
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A82515; MUID:20365717; PXID:10910347
A/Rocession: D82618
A/Reference number: A82515; MUID:20365717; PXID:10910347
A/Rocession: D82618
A/Reference number: A82515; MUID:20365717; PXID:10910347
A/Rocession: D82618
A/Residues: 1-156 <81N
A/Rosines: GB:ABC04014; GB:AEC03849; NID:g9107044; PIDN:AAF84752.1; GSPDB:GNO
A/Rosinental source: strain 95c
R/SImpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Brionés, M.R.S.; Bunno, M.R.P.; Camargo, L.B.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer,
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A/Rombors: Rerreira W.C., Frange, M.L.; Kemper, B.L.; Kitajima, J.B.; Kraider, J.B.; Kraider, J.B.; Kraider, M.L.; Kamper, B.L.; Kitajima, J.D.; Junqueira, M.L.; Kemper, B.L.; Kitajima, J.D.; Junqueira, M.L.; Kemper, B.L.; Kitajima, J.D.; Margues, M.V.; Martins,
 Ajaccession: S69046
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosiduca: 1-460 «HAL»
A;Cross-references: EMBL:U43703; NID:g1244769; PIDN:AAB68221.1; PID:g1244776; MIPS:YPL1
C;Genetics:
A;Genetics:
A;Genes: SGD:UMS1
A;Cross-teferences: SGD:S0006060; MIPS:YPL139c
A;Agrap position: 16L
C;Superfamily: Saccharomyces cerevisiae transcription modulator WTM1
 A; Molecule type: DNA
A; Residues: 1-43 < VAB.
A; Cross-references: EMBL: 228292; NID: 9486536; PIDN: CAA82146.1; PID: 9486537; MIPS: YKR067
A; Experimental source: strain S288C
 ö
 hypothetical protein YBL011w homolog YKR067w - yeast (Saccharomyces cerevisiae)
 ö
 C; Species: Saccharomyces cerevisiae
C; Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-Apr-2002
C; Accession: 538143
R; Van Vliet-Reedijk, J.C.; Planta, R.J.
submitted to the Protein Sequence Database, March 1994
A; Reference number: 538130
 Gaps
 Gabs
 ö
 64.3%; Score 36; DB 2; Length 460; 62.5%; Pred. No. 25; tive 2; Mismatches 1; Indels
 Query Match
64.3%; Score 36; DB 2; Length 743;
Batc Local Similarity 75.0%; Pred; No. 43;
Matches 6; Conservative 1; Mismatches 1; Indels
 A; Map position: 11R
C; Keywords: transmembrane protein
 Local Similarity 62.5%;
tes 5; Conservative
 A;Gene: SGD:GPT2
A;Cross-references: SGD:S0001775
A; Reference number: $69040
 294 VVPCGLHY 301
 3 VVPXGMHY 10
 85 IVPLGLHY 92
 3 VVPXGMHY 10
 A; Accession: S38143
 Query Match
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 VI protein - tobacco yellow dwarf virus (strain Australia)
C;Species: tobacco yellow dwarf virus
C;Species: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Accession: A42452
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
Virology 187, 633-642, 1992
A;Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yelld A;Reference number: A42452; MUID:92188538; PMID:1546458
 hypothetical protein alr1563 [imported] - Nostoc sp. (strain PCC 7120)
C)Specias: Nostoc sp. PCC 7120
C)Specias: Nostoc sp. PCC 7120
C)Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C)Accession: ARZ001
Nakazaki, N.; Nakamuxa, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, 8
N;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
 hypothetical protein YPL139c - yeast (Saccharomyces cerevisiae)
()Species: Saccharomyces cerevisiae
()Species: Saccharomyces cerevisiae
()Chace: 2-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 17-Mar-2000
()Accession: S69046
(SPRIAL) J.; Debaulo, T.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K. submitted to the EMBL Data Library, December 1995
A;Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
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 A;Accession: AE2001
A;Status: preliminary
A;Molecule trianinary
A;Molecule 220 vMA
A;Reaidues: 1-252 vMA
A;Residues: 1-252 vMA
A;Cross-references: GB:BA000019; PIDN:BAB77929.1; PID:g17135383; GSPDB:GN00179
A;Experimental source: strain PCC 7120
A;Genetics:
A;Gene: alr1563
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A;Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
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64.3%; Score 36; DB 2; Length 102; 60.0%; Pred. No. 5; tive 3; Mismatches 1; Indels

6; Conservative

Matches

Query Match Best Local Similarity

2 EVVPXGMHYS 11

.; 0

64.3%; Score 36; DB 2; Length 252; 50.0%; Pred. No. 13; Live 3; Mismatches 2; Indels

Best Local Similarity 50.0 Matches 5, Conservative

Query Match

235 EMIVPAGLHF 244

1 EEVVPXGMHY 10

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TSIB.1 procein - Arabidopsis thaliana (Forest) (Species: Arabidopsis thaliana (mouse-ear cress) (Forest (C) Arabidopsis thaliana (mouse-ear cress) (Forest (C) Arabidopsis thaliana (mouse-ear cress) (Forest (C) Arabidopsis (C) Arabidopsis (Forest (C) Arabidopsis (C) Arabidopsis (Forest (C) Arabidopsis (C) Arabidopsis (C) Arabidopsis (C) Arabidopsis (Forest (C) Arabidopsis (C) Arabidopsis (Forest (C) Arabidopsis (C) Arabidopsis (Forest (Forest (C) Arabidopsis (Forest (Forest (C) Arabidopsis (Forest (Forest (C) Arabidopsis (Forest
 A; Reference number: 219842
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A; Reference number: 229842
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C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 15-Oct-1999
C;Accession: T24111
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C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 25-Aug-2003
C;Accession: G69117
 G69117
diphthine synthase - Methanobacterium thermoautotrophicum (strain Delta H)
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 Ouery Match 62.5%; Score 35; DB 2; Length 510; Best Local Similarity 60.0%; Pred. No. 45; Masmatches 2; Indels Matches 6; Conservative 2; Mismatches 2; Indels
 2; Indels
 A;Map position: 1
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Pred. No. 37;
3; Mismatches
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 62.5%;
 5; Conservative
 219 EEVVESGLHES 229
 335 EQIVPGGLQY 344
 1 EEVVPXGMHY 10
 1 EEVVPXGMHY 10
 ||| | |:|:
EEVKPPGIHF 21
 Query Match
Best Local Similarity
Matches 5; Conserv
 A; Accession: G86430
 RESULT 12
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4, Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunse, L.R.; Oliveira, M.A.; de Oliveira, R.C.; Palniteri, D.B. Acdrigues, V.; Rose, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A.Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, H.; Taulako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; d., Contents: annotation
 C.) Accession: H69194
S.) Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
S. Smith, D.R.; Doucette-Stamm, L.A.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
Oliu, D., Spadafora, R.; Vicalie, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A; Reference number: A69000; MUID: 98037514; PMID: 9371463
 A,Accession: H69194
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Rolecule type: DNA
A,Residues: 1-311 «MIT»
A,Cross-references: GB.AE000850; GB:AE000666; NID:g2621794; PIDN:AAB85215.1; PID:g262179
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 DAA binding protein EREBP-2 - common tobacco
Dispecies: Nicotiana tabacum (common tobacco)
Dispecies: Nicotiana tabacum (common tobacco)
Dibace: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 21-Jul-2000
Dibacession: T02590
Cionme-Takagi, M.; Shinshi, H.
Plant Cell 7, 173-182, 1995
A;Title: Ethylene-inducible DNA binding proteins that interact with an ethylene responsible A;Reference number: Z14671; MUID:95276459; PMID:7756828
 GMP synthetase, subunit B - Methanobacterium thermoautotrophicum (strain Delta H) C;Species: Methanobacterium thermoautotrophicum C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
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A;Cross.references: EMBL:D38126; NID:q790362; PIDN:BAA07324.1; PID:g1208498
A;Experimental source: Btrain BY4; tissue-type leaf
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Pred. No. 13;
3; Mismatches 1; Indels
 Score 35; DB 2; Length 311;
Pred. No. 27;
1; Mismatches 3; Indels
 Score 35; DB 2; Length 233;
Pred. No. 19;
1; Mismatches 3; Indels
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 63.5%;
 62.5%;
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Best Local Similarity 60.0
Matches 6; Conservative
 Conservative
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 1 EEVVPXGMHYS 11
 ||::| |:|
EEILPQGVH 127
 1 EEVVPXGMHY 10
 OAVVPKGRHY 99
 Query Match
Best Local Similarity
 1 EEVVPXGMH 9
 Query Match
Best Local Similarity
Matches 5; Conserv
 A;Gene: MTH710
A;Start codon: GTG
 C;Genetics:
A;Gene: XF1950
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Gaps

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Gaps

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A;Experimental source: strain R1
C;Genetics:
A;Genetics:
A;Genetics:
A;Map position: 1
C;Superfamily: 3-dehydroquinate synthase; 3-dehydroquinate synthase homology
 R;Seeger, S.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, June 1999
A;Reference number: Z21565
 A,Residues: 1-355 <SEE>
A,Residues: 1-355 <SEE>
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A,Experimental source: strain A3(2)
C,Genetics:
A,Gene: SCOEDB:SC4C6.17c
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 C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
 Gaps
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60.7%; Score 34; DB 2; Length 355;
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 Search completed: June 3, 2004, 12:00:00
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 2 EVVPXGMHYS 11
 4 VPXGMHY 10
 20 IPPGMHY 26
 A; Accession: T35025
 C,Accession: T35025
 Job time : 9 secs
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 g
 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-279 <#HT.
A;Tossa references: GB:AE001889; GB:AE000513; NID:g6457944; PIDN:AAF09867.1; PID:g645795
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;Experimental source: strain Delta H

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 hypothetical protein - Deinococcus radiodurans (strain R1)
C; Species: Deinococcus radiodurans
C; Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C; Date: 03-Dec-1990 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-199
 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A;Tille: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463
 A.Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A;Reference number: A75250; MUID:20036896; PMID:10567266
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 Status: preliminary; nucleic acid sequence not shown; translation not shown; Molecule type: DNA
 Gaps
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Length 264;

A,Gene: WTH1874 C,Superfamily: diphthamide biosynthesis methyltransferase

1; Indels

Score 34; DB 2; Pred. No. 35; 2; Mismatches

Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative 2

à 셤 Cjaccession: B75478
RiWhite, O.; Bisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.;
RiWhite, O.; Bisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Scienne 286, 1571-1577, 1999
Scienne 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266

A; Status: preliminary A; Molecule type: DNA A; Residues: 1-350 <WHI> A, Accession: B75478

3-dehydroquinate synthase - Deinococcus radiodurans (strain R1) C;Species: Deinococcus radiodurans C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000

- Deinococcus radiodurans (strain R1)

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Gaps

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Length 279; 2; Indels

Score 34; DB 2; Pred. No. 38; 0; Mismatches

Match 60.7%; Local Similarity 75.0%; les 6; Conservative

Query Match

100 VPLGRHYS 107

RESULT 14

4 VPXGMHYS 11

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C; Superfamily: Deinococcus radiodurans hypothetical protein DR0271

A;Gene: DR0271 A;Map position: 1

A; Accession: C75538

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Run on:

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 SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RP SEQUENCE 1228;

RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,

RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,

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RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,

RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,

RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,

RA Zhang Y.-Q., Maco G.-P., Qu D., Danchin A., Wen Y.-M.;

RA Zhang Y.-Q., Maco G.-P., Qu D., Danchin A., Wen Y.-M.;

RA Zhang Y.-Q., Maco G.-P., Qu D., Danchin A., Wen Y.-M.;

ROBENTAL ACTIVITY 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + L-GORACTOR: Binds 3 mangarese ions per subunit (By similarity).

RATHWAY: Pyrimidine biosynthesis; first step.

RATHWAY: Pyrimidine biosynthesis; first step.

ROBENTI: Composed of two chains; the small (or glutamine) chain

Promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By Similarity).
 buchnera ap
saccharomyc
schizosacch
 bacillus an
drosophila
 homo sapien
homo sapien
 rattus norv
 chimpanzee
 15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annoration update)
15-MAR-2004 (Rel. 43, Last annoration update)
6arbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
 099vwp4 089a96 K P32784 8 0074377 8 009kv29 V P15823 K P17280 0 P97885 x
P39948
P40595
P19887
 Staphylococcus epidermidis.
Bacteria, Firmicutes, Bacillales, Staphylococcus.
NCBI_TaxID=1282;
 -! - SIMILARITY: Belongs to the carB family.
 ALIGNMENTS
 CGD1_RAT
T2RB_ACON
T2RB_BACAN
SUOX_DROWE
WDLB_BUCBP
SCT1_YERAF
SULH_SCHPO
RPOC_VIBCH
ZEB1_HUMAN
ZEB1_HUMAN
ZEB1_HUMAN
ZEB1_HUMAN
ZEB1_HUMAN
ZEB1_HUMAN
 HAMAP, ME 01210; -; 1.
InterPro; IRRO06275; CarA_L glu.
InterPro; IRRO06245; CarA_L glu.
InterPro; IRRO06493; CPase_L_D.
InterPro; IRRO05499; CPase_L_D.
InterPro; IRRO05499; CPase_L_D.
InterPro; IRRO04962; MGS Ike.
InterPro; IRRO0199; SBDFOL acsite.
Fam; PRO2796; CPSase_L_D2; 2.
Ffam; PRO2796; CPSase_L_D2; 2.
Ffam; PRO2192; MGS; 1.
Ffam; PRO2142; MGS; 1.
Fran; PRO2142; MGS; 1.
 EMBL; AE016746; AA004476.1; -.
 295
341
353
353
573
759
1401
2717
847
124
 STAEP
 QBCPJ4;
 RESULT 1
CARE STAEP
ID CARE S'
 P31619 tobacco yel

003010 saccharomyc

035586 mesthanobact

026806 methanobact

026806 methanobact

02702 methanobact

029158 yarrowna al

P4621 vibrio para

P4621 vibrio para

P4336 deaulfovibr

P49850 bacillus su

P34335 caenorhabdi

P1330 baccariopha

P08858 bos tearus

076217 anopheles g

087586 clostridium

P56351 chlorella v

074827 rattus norv

P30280 mus musculu
 xenopus lae
gallus gall
 homo sapien
homo sapien
mus musculu
 brachydanio
xenopus lae
 Q8cpj4 staphylococ
Q8rg86 fusobacteri
 gallus gall
 vibrio para
 3, 2004, 11:32:06 ; Search time 4.86667 Seconds (without alignments) 117.693 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 mus
 087qx9
 Q90459
P50755
P49706
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 141681 seqs, 52070155 residues
 SUMMARIES
 CARB STRAM
CARB STRAM
YILK
YILK
YEAT TYDVA
WHEL YEAST
IDII MESAU
IDII MESAU
DPHB METTH
SLSI YARLI
SLSI YARLI
SLSI YARLI
SLSI YIBPA
PHSL_DESBA
MUTL BACSU
WUTL BACSU
VLTF BPTS
TKNK BOVIN
RRA CARBL
YUNGA
RRZ CGLOAB
RRZ CGLUVU
CGD2_RANN
 CARB_STAEP
CARB_FUSNN
AROA_VIBPA
CARB_STAAM
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 MOUSE
BRARE
XENLA
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 4inimum DB seq length: 0
4aximum DB seq length: 2000000000
 US-09-909-164-11
56
1 BEVVPXGMHYS 11
 DB
 SwissProt 42:*
 Length
 Query
 Title:
Perfect score:
 Scoring table:
 Database :
 Sequence:
 searched:
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Result No.

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SOLUTION TO THE TENERAL TO THE TENER
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 CTRAIN=ATCC 25586;

XX MEDLINE=21886394; PubMed=11889109;

XA MEDLINE=21886394; PubMed=11889109;

XA MEDLINE=21886394; PubMed=11889109;

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XA Battacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,

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A Fonstein M., Kyrpides N., Overbeek R.;

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A Fonstein N., Kyrpides N., Overbeek R.;

A Fonstein ATCC 25586 ";

C Bacteriol. 184:2005-2018(2002).

C CAPLYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +

Dhosphate + L-glutamate + carbamoyl phosphate.

C CORACYOR: Binde 3 manganese ions per subunit (By similarity).

C -- PATHWAY: Pyrimidine biosynthesis; first step.

C -- PATHWAY: Pyrimidine biosynthesis; the small (or glutamine) chain

C -- SUBNNT: Composed of two chains; the small (or glutamine) chain

C -- SUBNNT: Composed of two chains; the small (or glutamine) chain

C -- SUBNNT: Composed of two chains; the small (or glutamine) chain

C -- SUBNNT: Composed of two chains; the small (or glutamine) chain

C -- SUBNNT: Composed of two chains; the small (or glutamine) chain

C -- SUBNNT: Composed of two chains; the small (or glutamine) chain

C -- SUBNNT: Composed of two chains; the small (or glutamine) chain

C -- SUBNNT: Composed of two chains; the small (or glutamine) chain

C -- SUBNNT: Composed of two chains; the small (or glutamine) chain

C -- SUBNNT: Composed of two chains; the small (or glutamine) chain

C -- SUBNNT: Composed of two chains; the small (or glutamine) chain

C -- SUBNNT: Composed of two chains; the small (or glutamine) chain

C -- SUBNNT: Composed of two chains; the small (or glutamine) chain

C -- SUBNNT: Composed of two chains; the small (or glutamine) chain

C -- SUBNNT: Composed of two chains; the small (or glutamine) chain
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 ö
R TIGRPAMS; TIGRO1369; CPSasell_lrg; 1.

R PROSITE; PSCO866; CPSASE 1; 2.

R PROSITE; PSCO866; CPSASE 1; 2.

R Arginine biosynthesis; biosynthesis; Ligase; Repeat;

M ATP-binding; Manganese; Complete proteome.

T DOMAIN 401 GARBOXYPHOSPHATE SYNTHETIC DOMAIN.

T DOMAIN 547 929 CARBANOYL PHOSPHATE SYNTHETIC DOMAIN.

T DOMAIN 547 929 CARBANOYL PHOSPHATE SYNTHETIC DOMAIN.

T REPEAT 1057 ALLOSTERIC DOMAIN.

T REPEAT 547 1057 ALLOSTERIC DOMAIN.

T NP_BIND 302 352 ATP (POTENTIAL).

T NP_BIND 302 352 ATP (POTENTIAL).

T METAL 284 284 MANGANESE 1 (BY SIMILARITY).

T METAL 300 MANGANESE 2 (BY SIMILARITY).

T METAL 300 RANGANESE 3 (BY SIMILARITY).
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
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55-FEB-2003 (Rel. 41, Last annotation update)
56-FEB-2003 (Rel. 41, Last annotation update)
57-FEB-2003 (Rel. 41, Last annotation update)
58-FEB-2003 (Rel. 41, Last annotation u
 10 ATP (POTENTIAL).
52 ATP (POTENTIAL).
84 MANGANEEE 1 (BY SIMILARITY).
98 MANGANEEE 2 (BY SIMILARITY).
00 MANGANEEE 2 (BY SIMILARITY).
00 MANGANEEE 3 (BY SIMILARITY).
01 MANGANEEE 3 (BY SIMILARITY).
02 MANGANEEE 3 (BY SIMILARITY).
03 MANGANEEE 3 (BY SIMILARITY).
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 Score 39; DB 1; Length 1057;
Pred. No. 7.3;
2; Mismatches 2; Indels
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Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
Fusobacterium.
 -!- SIMILARITY: Belongs to the carB family.
 PRT; 1058 AA
 69.68;
 Conservative
 189 KEVVSNGLHYS 199
 STANDARD;
 1 EEVVPXGMHYS 11
 832 83;
1057 AA;
 Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=76856;
 CARB FUSNN
ID CARB FUSNN
AC QBRGB6;
 METAL
SEQUENCE
 Query Match
 Best Loca
Matches
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Gaps
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STRAIN-RIMD 2210633 / Serotype O3:K6;

MEDLINE-2208454; PubMed=12620739;

MEDLINE-2208454; FubMed=12620739;

MAKINO K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

Tijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
 Q87QXS;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last samotation update)
10-OCT-2003 (Rel. 42, Last samo
 --- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate.
--- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
 ATP (POTENTIAL).

ATP (POTENTIAL).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).
 ..
0
 Score 38; DB 1; Length 1058; Pred. No. 12; 1; Indels 3; Mismatches 1; Indels
 sixth step.
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable)
 ALLOSTERIC DOMAIN
 426 AA.
 67.9%;
 117451
 Local Similarity 60.0
les 6; Conservative
 STANDARD;
 190 EIVPNGLNYS 199
 2 EVVPXGMHYS 11
 1058 AA;
 AROA VIBPA
 SEQUENCE
 Query Match
 NP BIND
 DOMAIN
DOMAIN
DOMAIN
 REPEAT
 METAL
 Best Loc
Matches
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Lancet 359:1819-1827(2002).

-i- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP
phosphate + L-glutamate + carbamoyl phosphate.

-i- CORCIOR: Binds 3 manganese ions per subunit (By similarity).

-i- PATHWAY: Arghnine blosynthesis.
 MEDIINE-22040117; Pubmed-12044378; Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Baba T., Tawam N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramateu K.; Rimanteu K.; Rimance M., Gui M., Gu
 Complete protecme.
CarboxyPHOSPHATE SYNTHETIC DOMAIN.
CARBOXYPRIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB OR PYRAB OR MW1086.
 ATP (POTENTIAL).

ATP (POTENTIAL).

ATP (POTENTIAL).

ATP (POTENTIAL).

ANANGANESE 1 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

ANANGANESE 3 (BY SIMILARITY).

117171 MW; E3E179EF0591F0F8 CRC64;
 PROSITE; PS00666; CFSASE 1; 2. PROSITE; PS00867; CPSASE 2; 2. Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat; ATP-binding; Manganese; Complete proteome.
 DB 1; Length 1057;
 2; Indels
 Staphylococcus aureus (strain MW2).
Bacteria, Firmicutes, Bacillales, Staphylococcus.
 ALLOSTERIC DOMAIN.
 Score 37; DB 1; Pred. No. 19; 2; Mismatches
 PRT; 1057 AA.
 EMBJ, AP003361, BAB57365.1; -
PIR, P89892, F89892.
HSSP, P00968, 1CSO.
HANAP, MF 01210; -; 1.
InterPro; IPR005483; CPase_L.
InterPro; IPR005483; CPase_L.
InterPro; IPR005480; CPase_L.
InterPro; IPR005481; CPase_L.
InterPro; IPR005481; CPase_L.D2.
InterPro; IPR005481; CPase_L.D3.
InterPro; IPR005481; CPase_L.D3.
InterPro; IPR005481; CPase_L.D3.
Pfam; PF00289; CPasee_L.D3.
Pfam; PF00289; CPasee_L.D3, 2.
Pfam; PF00289; CPasee_L.D3, 2.
Pfam; PF01878; MGS, 11.
PRINTS; PR00189; CPSASE.
IIRRPAMS; ILGAR01369; CPSASE.
send an email to license@isb-sib.ch)
 66.18;
 Query Match
Best Local Similarity 60.0.
 STANDARD;
 190 KIVSNGLHYS 199
 2 EVVPXGMHYS 11
 832 85.
1057 AA;
 NCBI_TaxID=196620;
 SEQUENCE FROM N.A.
 SEQUENCE
 DOMAIN
 DOMAIN
 REPEAT
 ଧ
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 ö
 CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + phosphate + L-glutamate + carbamoyl phosphate.

-!- CORACTOR: Binds 3 manganes ions per subunit (By similarity).
-!- PATHWAY: Arginine biosynthesis.
-!- PATHWAY: Pyrimidine biosynthesis; first step.
-!- PATHWAY: Composed of two chains; the small (or glutamine) chain promotes the hydrolygis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
 Gaps
 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=21311952; PubMed=11418146;

MEDLINE=21311952; PubMed=11418146;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Kuroda M., Ohta T., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,

Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

Sekimizu K., Hizakawa H., Kuhara S., Goto S., Yabuzaki J.,

Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba S.

Hattori M., Ogasawara N., Hayashi H., Hiramateu K.,

"Whole genome sequencing of meticillin-resistant Staphylococcus
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Carbamoyl-phosphate synthese large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthese large chain).
CARB OR PYRAB OR SAV1203 OR SA1046.
Staphylococcus aureus (strain N35) / ATCC 700699), and Staphylococcus aureus (strain N35).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
 HAMAP: NF_00210; -; 1.
InterPro; IRROD1986; BPSP_synth.
Pfam; PF00275; BPSP_synthase; 1.
PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
PROSITE; PS00885; BPSP_SYNTHASE_2; 1.
Aromatic amino acid biosynthesis; Transferase; Complete proteome.
SEQUENCE 426 AA; 46094 MW; 373D39CCSBA1F70F CRC64;
 ö
 66.1%; Score 37; DB 1; Length 426; 60.0%; Pred. No. 7.3;
 3; Indels
 SIMILARITY: Belongs to the EPSP synthase family.
 -!- SIMILARITY: Belongs to the carB family.
 1; Mismatches
 EMBL; AP005076; BACS9283.1; -.
 Lancet 357:1225-1240(2001).
 Query Match
Best Local Similarity 60.00,
 STANDARD;
 223 EFVIPAGOHY 232
 1 EEVVPXGMHY 10
 CARB STAAM
ID CARB STAAM
 099UR5;
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 ö
 Pfam; Froz.

REMINES, PRO1042; MGS; 1.

REMINES, PRO1059; CPSASE.

REMINES, PRO1059; CPSASE.

REMOSITE; PRO1086; CPSASE 1; 2.

DR PROSITE; PRO1086; CPSASE 2; 2.

XW Arginine blosynthesis; Dyrimidine blosynthesis; Ligase; Repeat;

XW Arginine blosynthesis; Pyrimidine blosynthesis; Ligase; Repeat;

XW Arginine blosynthesis; Dyrimidine blosynthesis; Ligase; Repeat;

XW Arginine blosynthesis; Dyrimidine blosynthesis; Ligase; Repeat;

XW Arginine blosynthesis; Dyrimidine blosynthesis; Ligase; Repeat;

XW Arginine blosynthesis; Domain.
PATHWAY: Pyrimidine biosynthesis; first step.
SUBUNIT: Composed of two Chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
 Gape
 SEQUENCE FROM N.A.
MEDLINE-92188538; PubMed=1546458;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
 10 ATP (POTENTIAL).

52 ATP (POTENTIAL).

84 MANGANESE 1 (BY SIMILARITY).

98 MANGANESE 1 AND 2 (BY SIMILARITY).

00 MANGANESE 2 (BY SIMILARITY).

10 MANGANESE 3 (BY SIMILARITY).

117185 MW, D8E3B09F9BCGF152 CRC64;
 ô
 Score 37; DB 1; Length 1057; pred. No. 19; 2; Mismatches 2; Indels
 Tobacco yellow dwarf virus (strain Australia) (TVDV)
Viruses, ssDNA viruses, Geminiviridae, Mastrevirus.
NCBI_TaxID=31599;
 Last sequence update)
Last annotation update)
 similarity).
SiMiLARITY: Belongs to the carB family.
 HAWAP; MF 01210; -; 1.
InterPro; IPR006275; CarA L glu.
InterPro; IPR005493; CPase L.
InterPro; IPR005493; CPase L. D2.
InterPro; IPR005480; CPase L. D3.
InterPro; IPR005480; CPase L. D3.
InterPro; IPR005481; CPase L. D3.
InterPro; IPR005481; CPase L. D3.
InterPro; IPR005482; MSS 11ke
Pfam; PP02786; CPSase L. Chain; 2.
Pfam; PP02786; CPSase L. D3; 1.
Pfam; PP02142; MGS; 1.
 EMBL; AP004825; BAB94951.1; -. HAMAP; MF_01210; -; 1.
 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last seq
01-OCT-1993 (Rel. 27, Last ann
Hypothetical 11.2 kDa protein.
 66.1%;
60.0%;
 Local Similarity 60.0 es 6; Conservative
 STANDARD,
 190 EIVSNGLHYS 199
 2 EVVPXGMHYS 11
 547 1057
153 21(
202 35;
294 29
298 29
300 82
820 82
832 83
 YIIK_TYDVA
ID YIIK_TYDVA
AC P31619;
 METAL
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RESIDENCE FROW N. N. Barrell B.G. Albermann K., Allen B., Ansorge W., Ansure B., Storma R.K., Almed A., Carpenter T., Cherry J.M., Araujo R., Bowman S., Brucher M., Carpenter T., Cherry J.M., Annorn M., Floeth M., Fortin W., Friesen J.D., Fritz C., Goffeau A., Annorn M., Floeth M., Fortin W., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebling U., Heumann K., Hilbert H., Hiller L.W., Annorn M., Floeth M., Fortin W., Mirtipati S., Mosetl D., Kamp C., Kurdi O., Lashkari D., Lew H., Mirtipati S., Mosetl D., RA, Amarthe R., Messenguy F., Mewes H.-W., Mirtipati S., Mosetl D., RA, Menler-Auer S., Namath A., Nentwich U., Oefner P., Pearson D., RA, Petel F.X., Pohl T.W., Purnelle D., Schafer M., Scharfe M., Scharfe M., Scharfe M., Scharfe M., Scharfe M., Scharen B., Schramm S., Schroeder M., Sdicu A.M., Tettelin H., Schorg W.W., Zollner A., Vo D.H., Hani J.;

RA Urrestarazu L.A., Ushinsky S., Vierendeels F., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H., Hani J.;

RIC Thwallow And SILENCING. NEGATION WITH ROLES IN WEIGHIG C. - FRUNCION TERMINALING NEGATION REGULATION OF MEIOSIS.

- SEMILARITY: STRONG, TO YEAST WITH AND WITH.
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 Gaps
"The nucleotide sequence of the infectious cloned DNA component of tobacco yellow dwarf virus reveals features of geminiviruses infecting monocotyledonous plants."; Virology 187:633-642(1992).
 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Melosis negative regulator UME1.
UME1 OR WIM3 OR YPL139C OR LPF7C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Pungi; Ascomycota; Saccharomycetes;
 ó
 64.3%; Score 36; DB 1; Length 102; 60.0%; Pred. No. 2.7;
 1; Indels
 STRAIN=A364A;
Mallory M.J., Strich R.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
 al protein. 1102 AA; 11178 MW; A40ECF1EOAF55B67 CRC64;
 Saccharomycetales; Saccharomycetaceae; Saccharomyces
 460 AA
 3; Mismatches
 EMBL; M81103; AAA47947.1; -.
PIR; A42452; A42452.
InterPro; IPRO2651; Gemini_mov.
Pfam; PF01708; Gemini_mov; I.
Hypothecical procein.
SEQUENCE 102 AA; 11178 MW; A4
 60.08;
 6; Conservative
 STANDARD;
 16
 2 EVVPXGMHYS 11
 |||::|||::|
| QVVPSGINYS
 Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=4932;
 UMEL YEAST
ID UMEL YEAST
AC Q03010; P87330;
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 ö
 Gaps
 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 SEQUENCE FROM N.A.
STRAIN=S288c;
van Vliet-Reedijk J.C., Planta R.J.;
submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELIVILAR LOCATION: Integral membrane protein (Probable).
-!- SUBCELIVILAR STRONG, TO YEAST YBL011W.
 ö
 Refine the state of the state o
 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
14-Ypothetical 83.6 kDa protein in CCPI-MET1 intergenic region.
YKRO67W.
 64.3%; Score 36; DB 1; Length 460; 62.5%; Pred. No. 13; cive 2; Mismatches 1; Indels
 411 451 WD 4;
460 AA; 51022 MW; AA6F60448B7BCBA9 CRC64;
 743 AA.
 EMBL; U10280; AAB40937.1; -.
EMBL; U43703; AAB68221.1; -.
 PRT;
 EMBL; Z28292; CAA82146.1; -. PIR; S38143; S38143.
 Query Match
Best Local Similarity 62.5
Matches 5; Conservative
 STANDARD;
 3 VVPXGMHY 10
 :|| |:||
85 IVPLGLHY 92
 GermOnline; 140046;
SGD; S0001775; GPT2.
 NCBI_TaxID=4932;
 YK47 YEAST
P36148;
 SEQUENCE
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 MEDINE=97373600; PubMed=9228075;
Paton V.G., Shackelford V.E., Krieans S.K.;
Paton V.G., Shackelford V.E., Krieans S.K.;
Cloning and subcellord Localization of hanster and rat isopentenyl diphosphate dimethylallyl diphosphate isomerase. A PTS1 motif targets the enzyme to peroxisomes.";
J. Biol. Chem. 272:18946-18950(1997).
-I- FUNCTION: CATALYZES THE 1,3-ALIXLIC REARRANGEMENT OF THE HOMOALINIC SUBSTRATE ISOSCHERY. IPP) TO ITS HIGHLY ELECTROPHILIC ALIXLIC ISOMER, DIMETHYLALIZE DIPHOSPHATE (DMAPP).
 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
130opentenyl-diphosphate delta-isomerase 1 (EC 5.3.3.2) (IPP isomerase
 InterPro; IPR000267; IPP isomerase.
InterPro; IPR000086; NUDIX_hydrolase.
Pfam; PF00293; NUDIX, 1.
Probom; PD004109; IPP isomerase; 1.
Carotenoid biosynthesis; Cholesterol biosynthesis;
Isoprene biosynthesis; Sterol biosynthesis; Isomerase; Peroxisome; Magnesium.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Soiurognathi; Muridae; Cricetinae;
Mesocricetus.
 GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0004366; F:glycerol.3-phosphate O-acyltransferase acti.
GO; GO:000864; P:phospholipid biosynthesis; IDA.
InterPro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
SMART; SM00563; P18C; 1.
Hypothetical protein; Transmembrane.
TRANSMEM 31
 .
 Score 36; DB 1; Length 743;
Pred. No. 21;
1; Mismatches 1; Indels
 84B9946E56B82F15 CRC64;
 POTENTIAL.
POTENTIAL.
POTENTIAL.
 Mesocricetus auratus (Golden hamster)
 31 55 PO
69 85 PO
50 524 PO
539 555 PO
743 AA; 83644 MW;
 EMBL; AF003836; AAC53283.1; -.
 64.3%;
75.0%;
 6; Conservative
 STANDARD;
 294 WPCGLHY 301
 3 VVPXGMHY 10
 Local Similarity
 [1]
SEQUENCE FROM N.A.
 NCBI_TaxID=10036;
 IDI1 MESAU
035586;
 TRANSMEM
TRANSMEM
 SEQUENCE
 TRANSMEM
 Query Match
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us-09-909-164-11.rsp

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1 EEVVPXGMHYS 11
 DPHB OR MTH1874.
 DPHB METTH
 Query Match
 RESULT 11
DPHB_METTH
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 ö
 STRAINE-BORGASTA4, PubMed-9371463;

A Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Addredge T., Bashirzadeh R., Blackelly D., Cook R., Gilbert K., Addredge T., Bashirzadeh R., Blackelly D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Addredge T., Bash D., Safer H., Patwell D., Prabhakar S., Jamin N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Patwell D., Prabhakar S., McComplete genome sequence of Methanobacterium thermoautotrophicum deltaff: functional analysis and comparative genomics.", J. Bacteriol. 179:7135-7155(1997).

I. CATALYTIC ACTIVITY: ATP + xanthosine 5'-phosphate + L-glutamine + H(2)O = AMP + diphosphate + GMP + L-glutamate.

I. PATHWAY: GMP biosynthesis.

I. SUBUNIT: Heterodiam a GMP synthase subunit (B) (Potential).
 Gaps
 16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
GMP synthase [glutamine-hydrolyzing] subunit B (EC 6.3.5.2) (GMP
 ö
 Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanothermobacter.
 HAMAP; MF_00345; -; 1.
InterPro; IPR001674; GMP synth_C.
Pfan; PF00958; GMP_synt_C; 1.
TIGRPAMs; TIGRO0884; guaA_cterm; 1.
Ligase; GMP blosynthesis; Purine biosynthesis; ATP-binding;
 Similarity 63.6%; Score 35; DB 1; Length 308; Similarity 63.6%; Pred. No. 13; 7; Conservative 1; Mismatches 3; Indels
 Score 35; DB 1; Length 227; Pred. No. 9.8;
 33 184 GMP-BINDING (BY SIMILARITY).
29 35 ATP (BY SIMILARITY).
308 AA; 34403 MW; F2DCF6EDZ02CAECI CRC64;
 86 BY SIMILARITY.
148 148 BY SIMILARITY.
225 227 MICROBODY TARGETING SIGNAL.
227 AA; 26317 NW; FSOOA6586385E803 CRC64;
 3; Indels
 308 AA.
 0; Mismatches
 GÜAAB OR MTH710.
Methanobacterium thermoautotrophicum.
 EMBL; AE000850; AAB85215.1; ALT_INIT.
HSSP; P04079; 1GPM.
 62.5%;
 7; Conservative
 STANDARD;
 121 EEVDPNEMHY 130
 1 EEVVPXGMHY 10
 Query Match
Best Local Similarity
Matches 7; Conserv
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 STRAIN=Delta H;
 synthetase)
 GAAB METTH
 ACT_SITE
ACT_SITE
SITE
 SEQUENCE
 SEQUENCE
 BIND
 026806;
 RESULT 10
GAAB_METTH
 Matches
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Gaps

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 ö
 Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
Aldredge T., Bashirzadeh R., Blakely D., Cock R., Gilbert K.,
Aldredge T., Bashirzadeh R., Blakely D., Cock R., Gilbert K.,
A spadafora R., Vicare R., Wange P., Lumm W., Pothier B., Qiu D.,
Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
A jwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
A mcDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
Daniels G.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
T. Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
J. FUNCTION: Required for the methylation step in diphthamide
Diosynthesis (By similarity).
J. CARALYIIC ACTIVITY: S-adenosyl-L-methionine + 2-(3-carboxy-3-aminopropyl)-L-histidine = S-adenosyl-L-homocysteine + 2-[3-carboxy-3-(methylatmonio)propyl]-L-histidine.
J. STMILARITY: Belongs to the diphthine synthase family.
 Gaps
 10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
Probable diphthine synthase (EC 2.1.1.98) (Diphthamide biosynthesis
 ô
 Methanobacterium thermoautotrophicum.
Archaea, Buryarchaeota, Methanobacteria, Methanobacteriales,
Methanobacteriaceae, Methanothermobacter.
 60.7%; Score 34; DB 1; Length 264; 62.5%; Pred. No. 18; tive 2; Mismatches 1; Indels
 Transferase; Methyltransferase; Complete proteome.
SEQUENCE 264 AA; 28858 MW; 366BAB4B4D992C21 CRC64;
 426 AA.
 264 AA
 EMBL; AE000940; AAB86340.1; -.
PIR; G69117; G69117; G69117;
InterPro; IPR00189; -; 1.
InterPro; IPR00459; Cor/por_Metransf:
InterPro; IPR00459; Dphthn Bynthase.
Pfam; PP00590; TP methylase; 1.
IGRPAMS; IIGR00522; dph5; 1.
 PRT;
 STRAIN=Delta H;
MEDLINE=98037514; PubMed=9371463;
 RESULT 12
SIS1_YARL1
ID SIS1_YARL1 STANDARD; 1
AC Q99158;
DT 01-NOV-1997 (Rel. 35, Created)
 5; Conservative
216 EEVVESGLHES 226
 STANDARD;
 235 VVPAGLHF 242
 3 VVPXGMHY 10
 methyltransferase).
 Local Similarity
 NCBI_TaxID=187420;
 [1]
SECUENCE FROM N.A.
```

```
Lancet 361:743-749(2003).
 363
419
441 AA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=899;
 McCarter L.L.;
 DESBA
 baculatus:
 TRANSMEM
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PHSL_DESBA
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 ö
 Gaps
 STRAIN-ATCC 20460 / W29;

MEDLINE=96216076; PubMed=8662639;

MEDLINE=96216076; PubMed=8662639;

Boistane A., Beckerich J.-M., Gaillardin C.;

Boistane A., Beckerich J.-M., Gaillardin C.;

Boistane A. Involved in the yeast Yarrowia lipolytica.";

J. Biol., Chem. 271-11668-11675(1996).

-i- FUNCTION: Involved in the protein translocation process May interact directly with translocating polypeptides to facilitate their transfer and/or help their folding in the ER. It is not required for viability but is essential for optimal growth at elevated temperatures.

-i- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 SEQUENCE FROM N.A.
STRAINERIND 210633 / Serotype O3:K6;
MEDLINE=22508454; PubMed=12620739;
MEDLINE=22508454; PubMed=12620739;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasuunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. Cholerae.";
 SLSI PROTEIN.
PREVENT SECRETION FROM ER (POTENTIAL).
, OACD7EF17540B8E2 CRC64;
 Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
 ö
 Vibrio parahaemolyticus.
Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales,
 60.7%; Score 34; DB 1; Length 426; 44.4%; Pred. No. 30; ive 4; Mismatches 1; Indels
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
SLS1 protein precursor.
 01-NOV-1995 (Rel. 32, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
 441 AA
 POTENTIAL
 Hypothetical protein VP2115 (ORF3) VP2115.
 InterPro; IPR00838; ARM.
InterPro; IPR00886; ER target_S.
PROSITE; PS00014; ER TARGET; 1.
Endoplasmic reticulum; Signal.
SIGNAL
 47201 MW;
 EMBL; Z50154; CAA90516.1; -. PIR; S58132; S58132.
 Local Similarity 44.4
 STANDARD;
 426
 ::|:| |:|
52 DQVIPAGLH 60
 Vibrionaceae; Vibrio.
NCBL_TaxID=670;
 1 EEVVPXGMH 9
 423 4
426 AA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=4952;
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 ó
 01-305;
01-30N-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-1990 (Rel. 42, Last annotation update)
Periplasmic (NiFeSe) hydrogenase large subunit (BC 1.12.99.6) (NiFeSe hydrogenlyse chain).
Desulfovibrio baculatus (Desulfomicrobium baculatus).
Bacteria, Proteobacteria, Deltaproteobacteria, Desulfowicrobium.
 Gaps
 MEDINE=88058744; PubMed=3316183;
Manon N.K., Peck H.D. Jr., le Gall J., Przybyla A.E.;
"Cloning and sequencing of the genes encoding the large and small
subunits of the periplasmic (NIPeSe) hydrogenase of Desulfovibrio
 "Moty, a component of the sodium-type flagellar motor.";
d. Bacteriol. 176:4219-4225(1994).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: STRONG, TO H.INFLUENZAE H10325.
 ó
 Score 33; DB 1; Length 441;
Pred. No. 50;
2; Mismatches 3; Indels
 Complete proteome.
 451969FE307E4D46 CRC64;
 Menon N.K., Pect H.D. Jr., le Gall J., Przybyla A.E.;
 513 AA.
 POTENTIAL.
POTENTIAL.
POTENTIAL.
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POTENTIAL.
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 POTENTIAL
 EMBL; AP005080; BAC60378.1; -.
EMBL; U06949; AAA21571.1; -.
InterPro; IPR004770; Antiport nhaC.
InterPro; IPR01991; Na/diCo_gymport.
Pfan; Pf03553; Na H antiporter; 1.
PRINTS; PR00173; EDTRNSPORT.
 PRINTS, PROOL/3; EDTRNSPORT.
Hypothetical protein; Transmembrane;
TRANSMEM 21 41 POTENTIA
 MEDLINE=94292449; PubMed=8021208;
 Bacteriol. 169:5401-5407(1987)
 45961 MW;
 58.9%;
 54.58;
SEQUENCE OF 1-140 FROM N.A.
 Query Match 58.9
Best Local Similarity 54.5
Matches 6; Conservative
 STANDARD;
 417 ETVVPTFIHYN 427
 1 EEVVPXGMHYS 11
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Score 33; DB 1; Length 513;
Pred. No. 58;
1; Mismatches 1; Indels
 MUTL BACSU

1D MUTL BACSU

AC P49850,

DT 01-0CT-1996 (Rel. 34, Created)

DT 01-0CT-2093 (Rel. 42, Last sequence update)

DT 10-0CT-2003 (Rel. 42, Last sequence)

DE DNA mismatch repair protein mutl.

GN MUTL OR BSU17050.

GN BSU11us subtilis.

OS Bacillus subtilis.

OC Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
 56683 MW; AC8285A6F80576FC CRC64;
 Query Match 58.9%;
Best Local Similarity 71.4%;
Matches 5; Conservative 1
 297 PGGLHYS 303
 493 4
513 AA;
 PXGMHYS 11
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 MEDLINE=99306038; PubMed=10378275;

MEDLINE=99306038; PubMed=10378275;

MEDLINE=99306038; PubMed=10378275;

MEDLINE=99306038; PubMed=10378275;

Removal of the bridging ligand atom at the Ni-Fe active site of finitel hydrogenae upon reduction with H2, as revealed by X-ray structure analysis at 1.4 A resolution.";

Structure 7:557-566(1999);

In CATALYTIC ACTIVITY: H(2) + acceptor = 2 H(+) + reduced acceptor. In CATALYTIC ACTIVITY: H(2) + acceptor = 2 H(+) + reduced acceptor. In CATALYTIC ACTIVITY: H(2) + acceptor = 2 H(+) + reduced acceptor. In CATALYTIC ACTIVITY: H(2) + acceptor = 2 H(+) + reduced acceptor. In CATALYTIC ACTIVITY: H(2) + acceptor = 2 H(+) + reduced acceptor. In CATALYTIC ACTIVITY: H(2) + acceptor = 2 H(+) + reduced acceptor. In CATALYTIC ACTIVITY: H(2) + acceptor = 2 H(+) + reduced acceptor. In CATALYTIC ACTIVITY: H(2) + acceptor = 2 H(+) + reduced acceptor. In CATALYTIC ACTIVITY: H(2) + acceptor = 2 H(+) + reduced acceptor. In CATALYTIC ACTIVITY: H(2) + acceptor = 2 H(+) + reduced acceptor. In CATALYTIC ACTIVITY: H(2) + acceptor = 2 H(+) + reduced acceptor. In CATALYTIC ACTIVITY: H(2) + acceptor = 2 H(+) + reduced acceptor. In CATALYTIC ACTIVITY: H(2) + acceptor = 2 H(+) + reduced acceptor. In CATALYTIC ACTIVITY: H(2) + acceptor = 2 H(+) + reduced acceptor. In CATALYTIC ACTIVITY: H(2) + acceptor = 2 H(+) + reduced acceptor. In CATALYTIC ACTIVITY: H(2) + acceptor = 2 H(+) + reduced acceptor. In CATALYTIC ACTIVITY: H(2) + acceptor = 2 H(+) + reduced acceptor. In CATALYTIC ACTIVITY: H(2) + acceptor = 2 H(4) + reduced acceptor. In CATALYTIC ACTIVITY: H(2) + acceptor = 2 H(4) + reduced acceptor. In CATALYTIC ACTIVITY: H(4) + acceptor = 2 H(4) + reduced acceptor. In CATALYTIC ACTIVITY: H(4) + acceptor = 2 H(4) + reduced acceptor. In CATALYTIC ACTIVITY: H(4) + acceptor = 2 H(4) + reduced acceptor. In CATALYTIC ACTALYTIC ACTALYTIC ACTALYTIC ACTALYTIC ACTALYTIC ACCEPTOR ACTALYTIC ACTALYTIC ACTALYTIC ACTALYTIC ACTALYTIC ACTALYTIC ACCEPTOR ACTALYTIC ACTALYTIC ACTALYTIC ACTALYTIC ACTALYTIC ACCEPTOR ACTALYT
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 Bacteriol. 170:4429-4429(1988)
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 FUNCTION: This protein is involved in the repair of mismatches in DNA. It is required for dam-dependent methyl-directed DNA mismatch repair. May act as a "molecular matchmaker", a protein that promotes the formation of a stable complex between two or more promotes the formation of a stable complex between two or more DNA-binding proteins in an ATP-dependent manner without itself being part of a final effector complex (By similarity). SIMILARITY: Belongs to the DNA mismatch repair mutt/hexB family.
 IIGRFAMS; TIGR00585; mutl; 1.
PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
 EMBL; U27343; AAB19236.1; -.
EMBL; 299112; CAB13578.1; -.
EMBL; A69663; A69663.
HSSP; P23367; 1BKN;
Subclidat; BG11402; mutL.
HAMAP; MF 00149; -: 1.
InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR002099; NA_mis_repair.
Pfam; PP02119; DNA_mis_repair.
Pfam; PP02189; HATPase_c; 1.
 SM00387, HATPase c
s; TIGR00585; mutl
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RA KUNDINES 9044031; Pubmace3384377;
RA KUNSTINES 9044031; Pubmace3384377;
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Blochert S.,
RA Borriss R., Boursler L., Brans A., Braun M., Briganell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Brington J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Bronizot F., Devine K.M., Dusterhoft A., Erhlich S.D., Emmerson P.T.,
RA Britz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Eritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Eritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Eritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Eritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Hibbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kuria K., Lapidus A., Lardinois S., Lauber J., Laya M., Jones L.,
RA Kuria K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Medina N., Mallado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Presecan E., Pujic P., Purnelle B., Ropoport G., Rey M., Sadaie Y.,
RA Schulun E., Schleich S., Schroeter R., Scoffene F.,
Schleich J., Seror E., Schleich S., Schroeter R., Scoffene F.,
RA Toseconi E., Roche B., Roch B., Nose M., Sadaie Y.,
RA Toseuchi M., Tamakoshi A., Tanaka T., Tarkahashi H., Takemaru K.,
A Viari A., Wambutt R., Wadler E., Wedler E., Wedler E., Wedler E.,
Waltiers P., Wipat A., Yamamoco H., Yamane C., Yamanoto H., Yamane C., Yamanoto R., Yam
 MEDLINE=96349107; PubMed=8760914;
Ginetti F., Perego M., Albertini A.M., Galizzi A.;
"Bacillus subtilis mutS mutL operon: identification, nucleotide
 MEDLINE=98044033; PubMed=9384377;
 sequence and mutagenesis:";
Microbiology 142:2021-2029(1996).
 SEQUENCE FROM N.A.
STRAIN=168;
SEQUENCE FROM N.A.
```

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Nature 390:249-256(1997).
```

ö Score 33; DB 1; Length 627; Pred. No. 71; 1; Mismatches 4; Indels DNA repair; Complete proteome. SEQUENCE 627 AA; 70431 MW; 068A0509CC265343 CRC64; 58.9%; 54.5%; Query Match
Best Local Similarity 54.5
6; Conservative 488 EMIVPLIFHYS 498 1 EEVVPXGMHYS 11 셤 ઠ

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Gaps

Search completed: June 3, 2004, 11:49:53 Job time: 4.86667 secs

Q7t1g5 gallus gall Q2trn9 deinococcus Q9trn9 deinococcus Q9trw92 deinococcus Q2xam3 streptomyce Q2f79 methanobact Q9kbal bacillus ha Q8call mus musculu Q87629 aspergillus Q970y6 drosophila Q9y0y6 cercopithec

09xvk4 caenorhabdi 09sa71 arabidopsis 08tz07 methanopyru

09yron ranid herpe 08bnlo mus musculu 08ylil brucella me 08c6x2 mus musculu 09vq17 drosophila 01479 saccharomyc 08p6p8 xanthomonas 08pcq4 candidatus 09rdc1 streptomyce

07v6q4 prochloroco QBpib0 xanthomonas O99011 prototheca Q96n44 homo sapien

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Gaps

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Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; BC021953, AAH32195.1;
GO; GO:0030374; F:11gand-dependent nuclear receptor transcrip. . .; IDA.
GO; GO:0005515; F:protein binding; IPI.
SEQUENCE 413 AA; 46621 MW; A9B8A1DC70CDA0D5 CRC64;
 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to expressed sequence A1987856.
TADA31 OR 1110004B19RIK.
Mus musculus (Mouse).
Bukaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musl. TaxID=10090;
 Match
Local Similarity 63.6%; Pred. No. 7.1;
Local Similarity 63.6%; Pred. No. 7.1;
Leg 7; Conservative 1; Mismatches 3; Indels
 Last sequence update)
Last annotation update)
 PRT; 1057 AA
 ALIGNMENTS
 Created)
 Q7T1G5
Q9RXN9
Q98HU6
Q9RW92
Q9XAM3
 Q9KBA1
Q8CAL1
Q16912
Q87629
Q9Y0Y6
Q9Y1X6
 Q8C6X2
Q9VQL7
Q12479
Q8P6P8
Q8KTQ4
Q9KTQ1
 PRT;
 Q8BNL0
 (TrEMBLrel. 23, C
(TrEMBLrel. 23, I
(TrEMBLrel. 25, I
168 EEIPPLGKHYS 178
 PRELIMINARY;
 PRELIMINARY;
 1 EEVVPXGMHYS 11
 [1]
SEQUENCE FROM N.A.
Q8CPJ4;
01-MAR-2003
01-MAR-2003
01-OCT-2003
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 QBCPJ4
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 RESULT 2
Q8CPJ4
ID Q8CP,
AC Q8CP,
DT 01-M
DT 01-M
 RESULT 1
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 Q8k289 mus musculu
Q8cpj4 staphylococ
Q9x22 thermotoga
Q911ha thermotoga
Q911ha thermotoga
Q911ha synechococc
Q87wpl anabaens
Q87wpl anabaens
Q87wpl anabaens
Q97wpl anabaens
Q97wpl puccides
Q97ds xylella fas
Q97ds xylella fas
Q97ds nicotiana t
Q97w50 nicotiana t
 (without alignments)
116.206 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 June 3, 2004, 11:35:06 ; Search time 29.8667 Seconds
 1017041
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1017041 segs, 315518202 residues
 Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - protein search, using sw model
 SPTREWBL 25:*
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4: Sp_human:*
5: Sp_human:*
5: Sp_mammal:*
5: Sp_mhc:*
6: Sp_phage:*
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 08K289
08C2E4
09C2E4
09C2E4
09HLH8
046486
048WP1
09AW4
057WP1
09PC35
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
 length: 0
length: 2000000000
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56
1 EEVVPXGMHYS 11
 Query
Match Length DB
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 Title:
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 Scoring table:
 Score
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 Minimum DB
Maximum DB
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Gaps

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Indels

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Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
 66.1%; Score 37; DB 16; Length 308; 75.0%; Pred. No. 34;
 66.1%; Score 37; DB 17; Length 322; 75.0%; Pred. No. 36;
 Thermoplasma acidophilum.
Archaea; Buryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
 TLL1618.
Synechococcus elongatus (Thermosynechococcus elongatus)
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 Protease, Complete proteome.
SEQUENCE 308 AA; 34778 MW; ADE03603E5101A9D CRC64;
 322 AA; 36918 MW; B8C239E71009D167 CRC64;
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Multidrug efflux transporter.
 O9HIHB;
01-MRR-2001 (TrEMBLrel. 16, Created)
01-MRR-2001 (TrEMBLrel. 16, Last sequence update)
01-UJUN-2003 (TrEMBLrel. 24, Last annotation update)
Glucose-fructose oxidoreductase related protein.
TA0250.
 Nature 407::09 513 (2000).

EMBL, AL445063; CAC11395.1; -.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0006118; P:electron transport; IEA.

InterPro; IPR000683; GFO_IDH_MocA.

Pfam, PFOTO, GFO_IDH_MocA; 1.

Complete proteome.

SEQUENCE 322 AA; 36918 MW; B8C239E71009D167
 PRT; 1044 AA.
 322 AA.
 1; Mismatches
 1; Mismatches
 GO; GO:0016020; C:membrane; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
InterPro; IPR001107; Band 7.
InterPro; IPR001972; Stomatin.
PERM: PR007011, STOMATIN.
SWART; SM00244; PHB; I.
 PRT;
 STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001;
 EMBL, AE001819; AAD36885.1; -. PIR; A72207; A72207.
 Local Similarity 75.0
ses 6; Conservative
 PRELIMINARY;
 6; Conservative
 PRELIMINARY;
Nature 399:323-329(1999)
 3 WPXGMHY 10
 ||| |:||
66 VVPDGLHY 73
 3 VVPXGMHY 10
 41 VVPSGIHY 48
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=2303;
 Query Match
 QBDIHO
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 RESULT 5
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 A Zhangard 12228;
A Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z., Chang Y., Ren Z., Wen Y.,
Chen Z., Wen Y.,
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
R EMBL, AEG16746; AA004476.1;
R GO; GO:0005737; C:cyttoplasm; IEA.
GO; GO:0005737; C:cyttoplasm; IEA.
GO; GO:0004189; F:cyttoplasm; IEA.
R GO; GO:0004189; F:cyttoplasm; IEA.
R GO; GO:0004189; F:cyttoplasm; IEA.
R GO; GO:000680; P:cyttoplasm; IEA.
R GO; GO:000680; P:cyttoplasm; IEA.
R GO; GO:000680; P:proteolysis and peptidolysis; IEA.
R GO; GO:0006808; P:proteolysis and peptidolysis; IEA.
R GO; GO:0006808; P:proteolysis and peptidolysis; IEA.
R GO; GO:0008809; P:pyrimidine base biosynthesis; IEA.
 STRAIN-MSB6 / DSM 3109,
STRAIN-MSB6 / DSM 3109,
MEDLINE-99287316; PubMed=10360571;
MEDLINE-99287316; PubMed=10360571;
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A., McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M., Malek J.A., Linher K.D., Garrett M.M., Heidelberg J., Sutton M.D., Frat W.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M., Mite O., Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.",
 Gaps
 Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
NCBL_TaxID=2336;
 ö
 Score 39; DB 16; Length 1057;
Pred. No. 49;
2; Mismatches 2; Indels C
 Complete proteome.
SEQUENCE 1057 AA; 117391 MW; 8944D7D8DB1CAE59 CRC64;
 Q9X2E2 PRELIMINARY; PRT; 308 AA. 09X2E2. 01-100-1-1999 (TrEMBLrel. 12, Created) 01-100-1999 (TrEMBLrel. 12, Last sequence update) 01-10M-2003 (TrEMBLrel. 24, Last annocation update) PTSH protease activity modulator HFLK.
 Staphylococcus epidermidis.
Bacteria, Firmicutes, Bacillales, Staphylococcus.
NGBI_TaxID=1282;
 Carbamoyl-phosphate synthase large chain.
 PRINTS; PRODOSS; CPSASE.
TIGREAMS; TIGRO1369; CPSASE.1.
PROSITE; PSO0866; CPSASE.1; 2.
PROSITE; PSO0867; CPSASE.2; 2.
PROSITE; PSO0639; THIOL_PROTEASE_HIS; 1.
 InterPro; IPR006275; Cara Lglu.
InterPro; IPR00543; CPase L.
InterPro; IPR005443; CPase L. D2.
InterPro; IPR005440; CPase L. D2.
InterPro; IPR005440; CPase L. D3.
InterPro; IPR005411; CPase L. N3.
InterPro; IPR004162; MGS IIRe.
InterPro; IPR00109; SMprot acsite.
Pfam; PP00289; CPSase L. Chain; 2.
Pfam; PP002197; CPSase L. D3; 1.
Pfam; PP02142; MGS; 1.
 63.6%;
 Query Match
Best Local Similarity 65...
7; Conservative
 189 KEVVSNGLHYS 199
 1 EEVVPXGMHYS 11
 Thermotoga maritima.
 [1]
SEQUENCE FROM N.A.
 RESULT 3
Q9X2E2
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MEDLINE=22225144; PubMed=12240834;

A Makamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
A Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
A Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N.,
A Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the thermophilic cyanobacterium
Thermosynechococcus elongatus BP-1.";
DNA Res. 9:123-130(2002).
I. DNA Res. 9:123-130(2002).
I. RMBL; APPOG514; BAC09170.1; -
RR GO; GO:0016021; F:transporter activity; IRA.
GO; GO:0016021; F:transporter activity; IRA.
RO; GO:001634; Acrfluin_res.
RICEPEPO; IPRO0136; Acrfluin_res.
RICEPEPO; IPRO0136; Acrfluin_res.
RICEPEPO; IPRO0136; Acrfluin_res.
 SPECIES=C.striatum; STRAIN=M82B;
MEDLINE=20194806; PubMed=10732668;
Tauch A., Krieft S., Kalinowski J., Puhler A.;
"The 51,409-bp R-plasmid pTP10 from the multiresistant clinical
"Solate Corynebacterium striatum M82B is composed of DNA segments
initially identified in soil bacteria and in plant, animal, and human
 SEQUENCE FROM N.A.
SPECIES—C.xerosis; STRAIN=M82B;
MEDLINE=96117603; PubMed=8559800;
MEDLINE=96117603; PubMed=8559800;
Tauch A., Kassing F., Kalinowski J., Puhler A.;
"The Corynebacterium xerosis composite transposon Tn5432 consists of two identical insertion sequences, designated IS1249, flanking the erythromycin resistance gene ermCX.";
Plasmid 34:119-131(1995).
 Query Match 66.1%; Score 37; DB 16; Length 1044; Best Local Similarity 63.6%; Pred. No. 1.2e+02; Matches 7; Conservative 2; Mismatches 2; Indels (
 Corynebacterium striatum.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 1044 AA; 113205 MW; 00E9C13F0F636D2F CRC64;
 1 protein; Plasmid.
208 AA; 23012 MW; P1504BE1ECDE85A6 CRC64;
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (GCrA).
 Mol. Gen. Genet. 263:1-11(2000).
EMBL; U21300; AA:055478.1; -.
EMBL; AF:024666; AA:0390.1; -.
GO; GO:0046821; C:extrachromosomal DNA; IEA.
 208 AA
 PRT;
 InterPro; IPR004764; HAEL.
Pfam; PF00873; ACR tran; 1.
PRINTS; PR0702; ACRIFLAVIRP.
TIGRFAMS; TIGR00915; 2A0602; 1.
 Corynebacterium xerosis, and
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843 EEVLPNGIGYS 853
 PRELIMINARY;
 1 EEVVPXGMHYS 11
 NCBI_TaxID=1725, 43770;
 SEQUENCE FROM N.A.
 SEOUENCE FROM N.A.
 Complete proteome
SEQUENCE 1044 A
NCBI_TaxID=32046;
 Q46486;
01-NOV-1996 (
01-NOV-1996 (
 Hypothetical
SEQUENCE 20
 046486
 RESULT 6
 046486
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Length 208;

64.3%; Score 36; DB 2;

Query Match

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 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
NCBI_TaxID=3888;
 X MEDIZINE-21595285; PubMed=11759840; Xuritz T., Sasamoto S., A Matenaboto T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., A Matenaboto T., Nakamura Y., Wolar, W., Ishikawa A., Kawashima K., Kimura T., A Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., A Makazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Tabata S., Sugimoto of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.", DNA Res. 8:205-213(2001).

R PIRJ, ABZ001; ABZ7729:1; -. R REMIJ, ABC701; ABZ7001; Complete protecome.
 SEQUENCE FROM N.A.
STRAIN=CV. Alaska;
MEDLINE=21231727;
PubMed=11333309;
Sassa N., Matsushita Y., Nakamura T., Nyunoya H.;
Cassa Nakamura Y., Nakamura T., Nyunoya H.;
Cassa Nakamura Y., Nakamura T., Nyunoya H.;
Cassa Nakamura Y., Nakamu
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 64.3%; Score 36; DB 16; Length 252; 50.0%; Pred. No. 44; 25; ive 3; Mismatches 2; Indels
 Cyanobacteria; Nostocales; Nostocaceae; Nostoc
 Indels
 1 protein; Complete proteome.
252 AA; 28831 MW; 925572DA5D1CA519 CRC64;
 TRANSFAC; T05513; ---
GO; GO:0009288; C:flagellum (sensu Bacteria); IEA.
GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0005199; P:structural molecule activity; IEA.
 01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Alr1563.
 Created)
Last sequence update)
Last annotation update)
 ,
,
 252 AA
 Pred. No. 36;
 PRT;
 PRT;
 Anabaena sp. (strain PCC 7120).
.0%;
 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-OCT-2003 (TrEMBLrel. 25, SCARECROW.
 Query Match
Best Local Similarity 50.00,
 Pisum sativum (Garden pea)
 Best Local Similarity 50.0
Matches 5; Conservative
 PRELIMINARY;
 PRELIMINARY;
 :|:| | ||:
130 DVIPEGKHYA 139
 | :|| |:|:
235 EMIVPAGLHF 244
 11
 1 EEVVPXGMHY 10
 2 EVVPXGMHYS
 Bacteria; Cyanobace
NCBI_TaxID=103690;
 SEQUENCE
 Q9AVK4;
 Q8YWP1
 Q9AVK4
 PSSCR
 RESULT 7
08YWP1
 RESULT 8
 Q9AVK4
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RESULT 9 Q57489 ID Q5748

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Rubulnuscussoli; rubuncallylusus,
Rimpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
Alvarenga R., Alves L.M.C., Arruda P., Abreu F.A., Acencio M.,
Alvarenga R.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
Barros M.H., Canargo L.D., Carraro D.M., Carrer H.,
Calouto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Colutton L.L., Cristofani M., Dias Neto B., Docena C., Bl-Dorry H.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Lomes M.V.F., Lopes E.L., Kitajima J.P.,
R. Hop.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
R. Hop.L., Madeira B.A.L., Martins B.M.F., Matsukuma A.Y.,
Machado M.A., Madeira B.A.D., Martins E.M.F., Matsukuma A.Y.,
Mardues M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Mardues M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Mardues M.V., Martins E.A.L., Martins E.S.,
Mani A. Jr., Nobrega F.G., Miyaki C.Y., Montairo-Vitorello C.B.,
RA Mannik J.Y., Nobrega F.G., Miyaki C.Y., Montairo-Vitorello C.B.,
RA Peixoto D.B., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
A de Sliva A.C., de Oliveira R.C., Palmieri D.A., Paris A.
A de Silva A.C., de Salva M.M.Z., Squeira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Teai S.M., Tsuhako M.H.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.,
RA Matha Gelles M. Van Sulya M.A., Verjovski-Almeida S., Vettore A.L.,
RA Matha Genome sequence of the plant pathogen Xylella fastidiosa.";
REMRI. ARGALIS.
 SEQUENCE FROM N.A.
MEDLINE=22421331; Pubmed=12533478;
Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
Van Kluys K., Furlan L.R., Camargo L.B.A., da Silva A.C.R., Moon D.H.,
 PD0850.

Xylella fastidiosa (strain Temeculal / ATCC 700964).

Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceas; Xylella.

NCBI_TaxID=183190;
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
NCBI_TaxID=2371;
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SEQUENCE 156 AA; 17144 MW; D8358619C6671ASD CRC64;
 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 GO; GO:0005622; C:intracellular; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0006935; P:clemotaxis; IEA.
GO:0007165; P:signal transduction; IEA.
InterPro; IPR002545; CheW.
 156 AA.
 Conserved hypothetical protein.
 EMBL; AE004014; AAF84752.1; -. PIR; D82618; D82618.
 55.6%;
 5; Conservative
 PRELIMINARY;
 InterPro; IPR002545; Che
PROSITE; PS50851; CHEW;
 119 EEILPQGVH 127
 1 REVVPXGMH 9
 Query Match
Best Local Similarity
 MEDLINE=20365717;
 Q87D36
Q87D36;
 Matches
 RESULT 11
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 SEQUENCE FROM N.A.

MEDLINES-5257263; Pubmed-8654969;

MEDLINES-5257263; Pubmed-8654969;

A Billington S.J.; Sinistaj M., Cheetham B.F., Ayres A., Moses E.K.,

A Katz M.E., Rood J.I.;

"Identification of a native bichelobacter nodesus plasmid and

"Identifications for the evolution of the vap regions.";

Gene 172:111-116(1996).

EMBL; U02462; AAB12366.1; -.

EMBL; U02462; C:Intracellular; IEA.

GO; GO:00016874; F:Itgase activity; IEA.

InterPro; IPR001357; BRCT.

SMART; SM00292; BRCT; 1.
 "A multiple site-specific DNA-inversion model for the control of Ompl phase and antigenic variation in Dichelobacter nodosus."; Mol. Microbiol. 17:183-196(1995).
 Gaps
 SEQUENCE FROM N.A.
MEDLINE=56020672; PubMed=7476204;
MSDSINE=56020672; PubMed=7476204;
MSSSS E.K., Good R.T., Sinistaj M., Billington S.J., Langford C.J.,
Rood J.I.;
 Bacteria, Proteobacteria, Gammaproteobacteria, Cardiobacteriales, Cardiobacteriaceae, Dichelobacter.
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 ;
 64.3%; Score 36; DB 10; Length 819; 45.5%; Pred. No. 1.5e+02; Live 4; Mismatches 2; Indels
 62.5%; Score 35; DB 2; Length 139; 55.6%; Pred. No. 37; ive 3; Mismatches 1; Indels
 InterPro; IPR001444; Flag_bb_rod.
InterPro; IPR005202; GRAS.
Pfam; PF03514; GRAS.1
PF03TTE; PS00568; FLAGELLA BB ROD; 1.
SEQUENCE 819 AA; 90372 WW; 41B67BD6DC72ADFA CRC64;
 Ligase.
NOW TER
SEQUENCE 139 AA; 15052 MW; E0E110AA4B7D4708 CRC64;
 01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TN-2003 (TrEMBLrel. 24, Last annotation update)
Hypotherical protein Xf1950.
XR1950.
Xylella fastidiosa.
 (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
 DNA ligase (Fragment).
Bacteroides nodosus (Dichelobacter nodosus).
 139 AA
 PRT;
 Query Match
Best Local Similarity 45.5
Matches 5, Conservative
 Local Similarity 55.6 tes 5; Conservative
 PRELIMINARY;
 343 DDVVPTSLHFS 353
 PRELIMINARY;
 1 EEVVPXGMHYS 11
 3 VVPXGMHYS 11
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21 IVPAGVHWS 29
 057489
057489;
01-NOV-1996 (
01-NOV-1996 (
 Query Match
 Q9PC35;
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RESULT 10

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099C35 1D 099 AC 099 DT 011 DT 014 GN XF

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1 EEVVPXGMHY 10
 NCBI_TaxID=4096;
 Q7WNB7
 09LW50
 Q7WNB7
 RESULT 13
Q9LW50
 RESULT 14
 O7WNB7
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Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R., Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Teasi S.M., Carrer H., Carraro D.M., de Oliveira R.C., Nunes D.R., Siqueira W.J., Marchio L.L., Kimura B.T., Ferro E.S., Harakava R., Kurames B.E., Marino C.L., Giglioti B., Abreu I.L., Alves L.M.C., do Amaral A.M., Bala G.S., Blanco S.R., Britto M.S., Cannavan F.S., Celestino A.V., da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T., Leoni S.G., Oliveira A.R., Rosa V.E. Ur., Sassaki F.T., Sena J.A.D., de Souza A.A., Turffi D., Tankumo F., Yanai G.M., Zaros L.G., Civerlo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Nicotiana.
NCBI_TaxID=4097;
 Gaps
 Kitajima J.P.; "Comparative analyses of the complete genome sequences of Pierce's disease and citrus variegated chlorosis strains of Kylella
 .
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 62.5%; Score 35; DB 10; Length 233; 60.0%; Pred. No. 65; 3; Indels iive 1; Mismatches 3; Indels
 62.5%; Score 35; DB 16; Length 156; 55.6%; Pred. No. 42; tive 3; Mismatches 1; Indels
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 233 AA; 25563 MW; 6CD16783582C0CB5 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UTM-2003 (TrEMBLrel. 24, Last annotation update)
EREBP-2.
 fastidiosa.";
J. Bacteriol. 185:1018-1026 (2003).
BMBL; ARDISE5, AAO28718.1;
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0006935; P:chemotaxis; IEA.
GO; GO:0007165; P:chemotaxis; IEA.
Interpro; IPR002545; Chéw.
PROSITE; PS50851; CHÉW.
 233 AA
 PRT;
 Nicotiana tabacum (Common tobacco)
 llarity 55.6%;
Conservative
 Best Local Similarity 60.0
Matches 6, Conservative
 PRELIMINARY;
 119 EEILPOGVH 127
 SMART; SM00380; AP2;
SEQUENCE 233 AA; 2
 1 EEVVPXGMH 9
 Best Local Similarity
Matches 5; Conserv
 Query Match
 Query Match
 040479;
 040479
 RESULT 12
 040479
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Gaps

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 MEDLINE=22827954; PubMed=12910271;
MEDLINE=22827954; PubMed=12910271;
Parkill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
Parkill J., Sebaihia M., Temple L., James K., Harris B., Quail M.A.,
Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
Chillingworth T., Collins W., Cronin A., Davis P., Doggett J.,
Peltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
Leather S., Morberzak H., O'Neil S., Ormon D., Perice C.,
Rabbinowitsch E., Rutter S., Sanders M., Seaunders D., Seeger K.,
Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Nicotiana.
 Gaps
 GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; PR00471; TF_ERP.
PRINTS; PR00367; ETHKSPELEMNT.
PRINTS; PR00367; ETHKSPELEMNT.
SMART; SM0380; AP2; 1.
SMART; SM0380; AP2; 1.
SEQUENCE 237 AA; 26243 MM; 01BC3EEB51E46298 CRC64;
 .
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 BB1123.

Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales;
Alcaligenaceae; Bordetella.
NCBI_TaxID=518;
 62.5%; Score 35; DB 10; Length 237; 60.0%; Pred. No. 66; ive 1; Mismatches 3; Indels
 01-OCT-2000 (TrEMBLrel. 15, Created)
U-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Ethylene-responsive element binding factor.
 Last sequence update)
Last annotation update)
 262 AA.
 237 AA
 01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequ
01-0CT-2003 (TrEMBLrel. 25, Last anno
 Nicotiana sylvestris (Wood tobacco)
 PRT;
 PRT;
 Putative encyl-CoA hydratase.
 SEQUENCE FROM N.A.
 Query Match
Best Local Similarity 60..
60..
 PRELIMINARY;
 PRELIMINARY;
 94 QAVVPKGRHY 103
 1 EEVVPXGMHY 10
90 OAVVPKGRHY 99
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 527954; PubMed=12910271;

MEDLINE=2287954; PubMed=12910271;

A Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,

Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

A Cardeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,

A Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach T.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Relivell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Unwin L., Whitchead S., Barrell B.G., Maskell D.J.,

"Comparative analysis of the genome sequences of Bordetella pertussis,

R Dordetella parapertussis and Bordetella bronchiseptica.",

EMBL, BK640425; CAR403321.1; -.

SCHEMBL, BK640425; CAR403321.1; -.
 ô
Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
"Comparative analysis of the genome sequences of Bordetella pertussis,
Bordetella parapertussis and Bordetella bronchiseptica.";
Nat. Genet. 35:32-40(2003).
EMBL: BX640440; CAE31621.1; -.
CCMPLete proteome.
SEQUENCE 262 AA; 28907 NW; B3CA29331CB776B2 CRC64;
 Gaps
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 Bordetella parapertussis.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
NCBL_TaxID=519;
 62.5%; Score 35; DB 16; Length 262; 66.7%; Pred. No. 73; 2; Indels iive 1; Mismatches 2; Indels
 62.5%; Score 35; DB 16; Length 262; 66.7%; Pred. No. 73; tive 1; Mismatches 2; Indel8
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 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Putative encyl-CoA hydratase.
 262 AA
 01-OCT-2003 (TrEMBLrel. 25, Created)
 PRT;
 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
 6; Conservative
 PRELIMINARY;
 :||| | |
182 QEVVPYGQH 190
 :|||| | |
182 QEVVPYGQH 190
 1 EEVVPXGMH 9
 1 EEVVPXGMH 9
 Query Match
Best Local Similarity
 SEQUENCE
 Q7W0Z3
 Matches
 RESULT 15
 Q7W0Z3
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Search completed: June 3, 2004, 11:57:33 Job time: 30.8667 secs

Hepatitis Hepatitis Hepatitis Hepatitis

Hepatitis Hepatitis

Abb80558 |
Abb80657 |
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Abb80653 |
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Abb80536 |
Abb80540 |
Abb80540 |
Abb80541 |
Abb80551 |
Abb80551 |
Abb80552 |
Abb80552 |
Abb80555 |

Hepatitis Hepatitis Hepatitis Hepatitis Hepatitis

Hepatitis Hepatitis

Hepatitis Hepatitis

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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
 'note= "N-terminal acetyl"
 ALI GNMENTS
 /note= "C-terminal amide"
 note= "D-form residue"
 'note= "Oxymethionine"
 ABB80527
ABB80634
ABB80633
ABB80634
ABB80634
ABB80634
ABB80634
ABB80644
ABB80634
ABB80634
ABB80634
ABB80654
ABB80654
ABB80655
 Location/Qualifiers
 Brunck TK;
 ABB80561 standard; peptide; 11 AA
 Claim 17; Page 65; 69pp; English
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 (first entry)
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39
Misc-difference
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002
 Synthetic
 ABB80561;
 protease
 RESULT 1
 ABB8056
 QQQQEEEEEEEEEEEE
 Abb80561 Hepatitis
Abb80529 Hepatitis
Abb80529 Hepatitis
Abb80542 Hepatitis
Abb80542 Hepatitis
Abb80543 Hepatitis
Abb80543 Hepatitis
Abb80548 Hepatitis
Abb80525 Hepatitis
Abb80521 Hepatitis
Abb80521 Hepatitis
Abb80521 Hepatitis
Abb80551 Hepatitis
Abb8056 Hepatitis
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 (without alignments)
67.664 Million cell updates/sec
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 June 3, 2004; 11:31:01; Search time 45.9333 Seconds
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 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 otal number of hits satisfying chosen parameters:
 1586107 segs, 282547505 residues
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 Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 M protein - protein search, using sw model
 ABB60524
ABB60529
ABB60529
ABB60524
ABB60542
ABB60542
ABB60543
ABB60543
ABB60543
ABB6054
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Gapop 10.0 , Gapext 0.5
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11: geneseqp1980s:*

2: geneseqp2000s:*

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5: geneseqp2001s:*

6: geneseqp2003as:*

7: geneseqp2003as:*

8: geneseqp2003bs:*
 DB seq length: 0
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 US-09-909-164-12
54
1 EEVVPXGMDYS 11
 B
 Length
 Query
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Perfect score:
Requence:
 scoring table:
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Sequence 11

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha **Aetoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 note= "Norvalyl carbonyl forming keto-amide linkage with
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
 ô
 DB 5; her.
 Match 96.3%; Score 52; DB Local Similarity 100.0%; Pred. No. 0.0 (es 11; Conservative 0; Mismatches
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 'note= "D-form residue"
 Location/Qualifiers
 Brunck TK;
 ABB80524 standard; peptide; 11 AA.
 Claim 17; Page 64; 69pp; English.
 21-JUL-2000; 2000US-0220101P
 19-JUL-2001; 2001WO-US023169
 residue 7"
 (first entry)
 1 EEVVPXGMDYS 11
 1 REVVPXGMDYS 11
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39.
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002
 Synthetic
 ABB80524;
 protease
 Query Match
 virucide
 Matches
 ABB80524
 RESULT
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 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 virus
 Gaps
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C ^\circ
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9.
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 96.3%; Score 52; DB 5; Length 11;
ilarity 100.0%; Pred. No. 0.0024;
Conservative 0; Mismatches 0; Indels
 Length 11;
 0; Indels
 Score 52; DB 5;
Pred. No. 0.0024;
 Mismatches
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 /note= "D-form residue"
 'note= "D-form residue"
 Location/Qualifiers
 Brunck TK;
 ABB80529 standard; peptide; 11 AA.
96.3%; Scc.
100.0%; Pre
 Claim 17; Page 64; 69pp; English.
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001, 2001WO-US023169.
 (first entry)
 Conservative
 1
 7
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 1 EEVVPXGMDYS
 1 EEVVPXGMDYS
 WPI; 2002-361643/39.
 Query Match
Best Local Similarity
Matches 11; Conserv
 Query Match
Best Local Similarity
Matches 11; Conserv
 Misc-difference
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002.
 Synthetic.
 ABB80529;
 protease
 virucide
 RESULT 3
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us-09-909-164-12.rag

note= "Norvalyl carbonyl forming keto-amide linkage with

/note= "C-terminal amide"

WO200208251-A2

31-JAN-2002.

Modified-site

'note= "D-form residue" note= "D-form residue"

Misc-difference Misc-difference

Modified-site

note= "Oxymethionine"

residue 7"

'note= "N-terminal acetyl"

Location/Qualifiers

Key Modified-site

Synthetic

virucide

Modified-site

Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #42.

08-OCT-2002

ABB80562;

EEVVPXGMDYS 11 1 EEVVPXGMDYS 11

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 'note= "Norvaly1 carbony1 forming keto-amide linkage with
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
 Hepatitis C virus, HCV, serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8.
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 note= "D-form residue"
 Location/Qualifiers
 Brunck TK;
 ABB80528 standard; peptide; 11 AA.
 Claim 17; Page 64; 69pp; English.
 21-JUL-2000; 2000US-0220101P
 19-JUL-2001; 2001WO-US023169
 residue 7"
 (first entry)
 (CORV-) CORVAS INT INC.
 Levy OE,
 WPI; 2002-361643/39.
 Misc-difference
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 Synthetic
 ABB80528;
RESULT 4
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ö
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Gabs
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 Length 11;
 0, Indels
 96.3%; Score 52; DB 5; 1
100.0%; Pred. No. 0.0024;
cive 0, Mismatches 0;
 ABB80542 standard; peptide; 11 AA.
 Claim 17; Page 65; 69pp; English.
 Local Similarity 100.
es 11; Conservative
 1 EEVVPXGMDYS 11
 11
 1 EEVVPXGMDYS
 Sequence 11 AA;
 08-OCT-2002
 ABB80542;
 Query Match
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Matches
 ABB80542
ID ABB8
XX ABB8
AC ABB8
XX 08-C
 RESULT 6
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Gaps

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96.3%; Score 52; DB 5; Length 11; 100.0%; Pred. No. 0.0024; ive 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.
Matches 11, Conservative

Sequence 11 AA;

1 EEVVPXGMDYS 11 EEVVPXGMDYS 11

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ABB80562 standard; peptide; 11 AA.

RESULT 5 ABB80562 ID ABB81

Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus

Brunck TK;

(CORV-) CORVAS INT INC Lim-Wilby M, Levy OE,

WPI; 2002-361643/39.

protease.

19-JUL-2001; 2001WO-US023169. 21-JUL-2000; 2000US-0220101P.

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Hepatitis C virus, HCV, serine protease, inhibitor, alpha-ketoamide, virucide.
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #23.
Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #22
 87.0%; Score 47; DB 5;
90.9%; Pred. No. 0.023;
iive 0; Mismatches
 note= "N-terminal acetyl"
 /note= "C-terminal amide"
 'note= "D-form residue"
 Location/Qualifiers
 ŢĶ;
 ABB80543 standard; peptide; 11 AA.
 Claim 17; Page 65; 69pp; English.
 Brunck
 21-JUL-2000; 2000US-0220101P
 19-JUL-2001; 2001WO-US023169
 (first entry)
 Conservative
 1
 1 EEVVPXGMDYS 11
 œ,
 (CORV-) CORVAS INT INC.
 EEVVPXGODYS
 WPI; 2002-361643/39.
 Local Similarity
ses 10; Conserv
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 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Lim-Wilby M,
 Modified-site
 08-OCT-2002
 31-JAN-2002
 Synthetic
 Synthetic
 ABB80543;
 virucide
 protease
 Query Match
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Matches
 ABB80543
 RESULT
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 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 "Norvalyl carbonyl forming keto-amide linkage with
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #18.
 .;
0
 Length 11;
 1; Indels
 Score 47; DB 5;
Pred. No. 0.023;
0; Mismatches 1
 /note= "N-terminal acetyl"
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 'note= "D-form residue"
 'note= "D-form residue"
 Location/Qualifiers
Location/Qualifiers
 ż
 Brunck TK;
 Claim 17; Page 65; 69pp; English.
 ABB80538 standard; peptide; 11
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169.
 87.0%;
 residue 7"
 Local Similarity 90.9
Les 10; Conservative
 1 BEVVPXGMDYS 11
 H
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 EEVVPXGQDYS
 WPI; 2002-361643/39
 Misc-difference
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-Bite
 Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002
 Synthetic
 ABB80538;
 virucide
 protease.
 Query Match
 Matches
 RESULT 8
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Gaps

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Length 11; 1; Indels Ŋ

19-JUL-2001; 2001WO-US023169

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The sequence represents a peptide compound of the invention having the peptides of the peptides of the peptides of the invention are alpha *ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with NGV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 'note= "Norvaly1 carbony1 forming keto-amide linkage with
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5
 87.0%; Score 47; DB 5; Length 11; 90.9%; Pred. No. 0.023; ive 0; Mismatches 1; Indels
 'note= "N-terminal acetyl"
 11
/note≂ "C-terminal amide"
 _note= "C-terminal amide'
 /note= "D-form residue"
 note= "D-form residue"
 Location/Qualifiers
 Brunck TK;
 ABB80525 standard; peptide; 11 AA.
 Claim 17; Page 64; 69pp; English
 19-JUL-2001; 2001WO-US023169.
 21-JUL-2000; 2000US-0220101P.
 (first entry)
 residue 7"
 Query Match
Best Local Similarity 90.5
Matches 10; Conservative
 1 EEVVPXGMDYS 11
 1 EEVVPXGQDYS 11
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39.
Misc-difference 9
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 WO200208251-A2
 Modified-site
 Key
Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002
 31-JAN-2002
 Synthetic.
 protease.
 ABB80525;
 virucide.
 ESULT 9
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 The sequence represents a peptide compound of the invention having the peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with NGV procease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 virus
 Gaps
 Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide;
 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #28
 ö
 Score 46; DB 5; Length 11;
Pred. No. 0.036;
 1; Indels
 0, Mismatches
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 note= "D-form residue"
 Location/Qualifiers
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 Brunck TK;
 ABB80548 standard; peptide; 11 AA.
 Claim 17; Page 64; 69pp; English
 85.28;
 21-JUL-2000; 2000US-0220101P
 19-JUL-2001; 2001WO-US023169.
 21-JUL-2000; 2000US-0220101P
 (first entry)
 10; Conservative
 1 EEVVPXGMDYS 11
 11
 Lim-Wilby M, Levy OE,
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 (CORV-) CORVAS INT INC
 1 REVVPXGMSYS
 WPI; 2002-361643/39.
 Similarity
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Novel peptide
 Key
Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 11-JAN-2002
 Synthetic.
 ABB80548;
 virucide.
 activity
 protease
 Query Match
 Local
 Matches
 RESULT 10
 ABB80548
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Gaps

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WPI; 2002-361643/39

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The sequence represents a peptide compound of the invention having the peptides of the invepatities C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketchanide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Gaps
Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
 .
0
 Length 11;
 1; Indels
 Score 46; DB 5;
Pred. No. 0.036;
 English.
 Claim 17; Page 65; 69pp;
 Seguence 11 AA;
 protease
 Query Match
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Mismatches ö 85.2%; Conservative EEVVPXGTDYS 11 1 EEVVPXGMDYS 11 Local Similarity es 10; Conserv Best Loc Matches ઠે d

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RESULT 11

ABB80521 standard; peptide; 11 AA. ABB8052

Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide. Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1. 08-OCT-2002 Synthetic. ABB80521; 

/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7" 'note= "N-terminal acetyl" Location/Qualifiers Key Modified-site Modified-site

/note= "C-terminal amide" Modified-site

WO200208251-A2

31-JAN-2002

19-JUL-2001; 2001WO-US023169. 21-JUL-2000; 2000US-0220101P.

(CORV-) CORVAS INT INC

ŢĶ; Brunck Levy OE, Lim-Wilby M,

WPI; 2002-361643/39

Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.

Claim 17; Page 64; 69pp; English.

sequence represents a peptide compound of the invention having Che

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 the sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 carbonyl forming keto-amide linkage with
 inhibitory activity. The peptides of the
 ingredient
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hepatitis C virus (HCV) protease inhibitory activity. The peptides of invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredits useful for treating disorders associated with hepatitis C virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C ^{\circ}
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2.
 ö
 Score 46; DB 5; Length 11;
Pred. No. 0.036;
); Mismatches 1; Indels
 "N-terminal acetyl"
 "C-terminal amide"
 note= "D-form residue"
 Location/Qualifiers
 Ä
 Brunck TK;
 Claim 17; Page 64; 69pp; English.
 'note= "Norvalyl
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 ABB80522 standard; peptide; 11
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 85.2%;
90.9%;
 residue 7"
 10; Conservative
 1 EEVVPXGMDYS 11
 11
 'note=
 /note=
 (CORV-) CORVAS INT INC
 œ,
 EEVVPXGMSYS
 WPI; 2002-361643/39.
 Levy
 Similarity
 Misc-difference
 Sequence 11 AA;
 Sequence 11 AA;
 WO200208251-A2
 Novel peptide
 Modified-site
 Key
Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 Synthetic
 ABB80522;
 protease
 Query Match
Best Local &
 virucide
 Best Loc
Matches
 RESULT 12
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carbonyl residue forming a keto
 hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 The sequence represents a peptide compound of the invention having
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46.
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #36.
 Length 11;
 1; Indels
 /note= "2-aminoisobutyryl carb
-amide linkage with residue 7"
 Score 46; DB 5;
Pred. No. 0.036;
0; Mismatches
 'note= "N-terminal acetyl"
 11
/note= "C-terminal amide"
 Location/Qualifiers
 ŦĶ;
 ABB80566 standard; peptide; 11 AA
 ABB80556 standard; peptide; 11 AA.
 Claim 17; Page 65; 69pp; English
 Brunck
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169
 85.2%;
90.9%;
 (first entry)
 (first entry)
 Query Match
Best Local Similarity 90.5
Matches 10; Conservative
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 (CORV-) CORVAS INT INC
 Levy OE,
 EEVVPXGMDYS
 BEVVPXGMSYS
 WPI; 2002-361643/39.
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Novel peptide
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 08-OCT-2002
 31-JAN-2002
 Synthetic
 protease.
 ABB80556;
 ABB80566;
 virucide
 Н
 RESULT 15
 ABB80556
ID ABB8
XX ABB6
XX ABB6
XX DT 08-C
XX XX Heps
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 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"
 virus
 Gaps
 Hepatitis C virus, HCV; serine protease, inhibitor, alpha-ketoamide, virucide.
 Gaps
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C '
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #27.
 .
0
 ö
 85.2%; Score 46; DB 5; Length 11; 90.9%; Pred. No. 0.036; ive 0; Mismatches 1; Indels
 DB 5; Length 11; 0.036;
 1; Indels
 Score 46; DB 5
Pred. No. 0.036
0; Mismatches
 /note= "C-terminal amide'
 Location/Qualifiers
 'note= "N-terminal
 Ą.
 Brunck TK;
 Claim 17; Page 65; 69pp; English.
 0;
 ABB80547 standard, peptide, 11
 21-JUL-2000; 2000US-0220101P.
90.9%;
 19-JUL-2001; 2001WO-US023169
 (first entry)
 Similarity 90.9 10; Conservative
 Local Similarity 90.
 1 EEVVPXGMDYS 11
 디
 1 EEVVPXGMDYS 11
 EEVVPXGTDYS 11
 Levy OE,
 (CORV-) CORVAS INT INC
 EEVVPXGMSYS
 WPI; 2002-361643/39
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002.
 Synthetic.
Query Match
Best Local S:
Matches 10
 ABB80547;
 protease.
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Gaps

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Query Match

Best Loc Matches

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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"

/note= "C-terminal amide" /note= "D-form residue"

note= "N-terminal acetyl"

Location/Qualifiers

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
Hepatitis C virus, HCV, serine protease, inhibitor, alpha-ketoamide, virucide.
 Claim 17; Page 65; 69pp; English.
 19-JUL-2001; 2001WO-US023169.
 21-JUL-2000; 2000US-0220101P.
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC.
 WPI; 2002-361643/39.
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2.
 Key
Modified-site
 Modified-site
 Modified-site
 31-JAN-2002.
 Synthetic.
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Brunck TK;

Search completed: June 3, 2004, 11:48:23 Job time: 45.9333 secs

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Gaps

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Score 46; DB 5; Length 11; Pred. No. 0.036; 0; Mismatches 1; Indels

us-09-909-164-12.rai

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Sequence 4, Application US/08853948B

Patent No. 6210943

GENERAL INFORMATION:

APPLICANT: MATHAMA, TOYOTA

TITLE OF INVENTION: THE SAME

CURRENT APPLICATION NUMBER: US/08/853,948B

CURRENT PILING DATE: 1997-05-09

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 4

SEQ ID NO 4

LENGTH: 341
 FEATURE:
OTHER INFORMATION: Xaa at position 109 is one of Ala, Arg,
OTHER INFORMATION: Cys, Gln, Glu, Gly, His, Ile, Leu, Lys,
 5177197-51

US-08-580-988A-23

US-08-460-694-4

US-08-460-744-4

US-08-19-977-7

US-08-19-977-7

US-08-464-517-21

US-08-464-517-21

US-08-464-517-21

US-08-464-517-21

US-08-464-517-22

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US-08-464-517-22

US-08-464-517-22

US-08-464-517-22

US-08-463-772-22

US-08-463-772-22

US-08-926-8428-21

US-08-926-8428-21

US-08-926-8428-21
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 TYPE: PRT ORGANISM: Enterococcus faecalis
 Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
 145 EEVVPTSEDY 154
 TYPE: PRT
ORGANISM: Citrus unshiu
 1 EEVVPXGMDY 10
US-09-134-000C-4848
 US-09-134-000C-4848
 RESULT 2
US-08-853-948B-4
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 Sequence 24, Appl
Sequence 10, Appl
Sequence 7, Appli
Sequence 7, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 11, Appl
Sequence 76, Appli
Sequence 76, Appli
Sequence 31637, A
 Sequence 4848, Ap
Sequence 4, Appli
Sequence 5, Appli
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26805, A
4, Appli
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 June 3, 2004, 11:36:47 , Search time 11.7333 Seconds
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6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 US-09-697-367-24
US-09-394-272-10
US-08-718-777-7
US-09-051-341-7
US-09-394-272-8
US-09-394-272-4
US-09-394-272-11
US-09-394-272-11
US-09-394-272-9
US-09-394-272-9
US-09-369-147-76
US-08-569-147-76
US-08-569-147-76
US-08-569-147-76
US-08-569-147-76
US-09-569-147-82
 US-09-408-020-4
US-08-963-851-14
US-09-540-236-2677
US-09-134-000C-4318
US-08-070-165F-8
 US-08-885-418-8
US-09-252-991A-26805
US-09-819-989-4
 US-09-134-000C-4848
US-08-853-948B-4
US-08-853-948B-5
 Potal number of hits satisfying chosen parameters:
 389414 seqs, 51625971 residues
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 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Issued Patents AA:*
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 US-09-909-164-12
54
 1 EEVVPXGMDYS 11
 Query
Match Length
 140
140
1065
3472
59
 1049
1068
1068
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1068
1083
1083
 litle:
Perfect score:
 scoring table:
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 Result
No.
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Sequence 4848, Application US/09134000C

| Patent No. 6617156
| Patent Patent No. 6617166

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 Sequence 20, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 21, Appl
Sequence 21, Appl
 Gaps
Sequence 4, A Patent No. 517 Sequence 23,
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Sequence
Sequence
Sequence
Sequence
Sequence
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 Score 36; DB 4; Length 181;
Pred. No. 11;
0; Mismatches 3; Indels
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RESULT 6
US-08-429-054A-11
 SOFTWARE:
 US-09-394-272-10
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 Sequence 5, Application US/08853948B

Sequence 5, Application US/08853948B

Patent No. 6210943

GENERAL INFORMATION:
APPLICANT: ANTHAMA, TOYOTA

TITLE OF INVENTION: THE SAME
TITLE OF INVENTION: THE SAME
TITLE OF INVENTION: THE SAME
TITLE OF INVENTION: UN98/853,948B
CURRENT FILING DATE: 1997-05-09

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5

LENGTH: 348
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 0; Gaps
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 Score 36; DB 3; Length 348;
Pred. No. 22;
Mismatches 1; Indels
 Score 36; DB 4; Length 368;
Pred. No. 24;
2; Mismatches 1; Indels
 Length 341;
 1; Indels
 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Calmi, Perry G.
APPLICANT: Calmi, Perry G.
APPLICANT: Tarczynski, Mitchell
APPLICANT: Tarczynski, Mitchell
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE
FILE REFREENCE: BB1166 US NA
CURRENT APPLICATION NUMBER: US/09/697,367
CURRENT FILING DATE: 2000-10-26
PRIOR PRIOR PELING DATE: 1998-WAY-07
PRIOR FILING DATE: 1998-WAY-07
PRIOR FILING DATE: 1999-WAY-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
SEQ ID NO 24
LENTH: 368
; OTHER INFORMATION: Pro, Ser, Thr, Trp, Tyr, or Val
US-08-853-948B-4
 Score 36; DB 3;
Pred. No. 22;
2; Mismatches
 US-09-697-367-24
Sequence 24, Application US/09697367
Patent No. 6323015
 66.7%;
 Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
 Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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217 VIPPGMDFS 225
 ; TYPE: PRT
; ORGANISM: Citrus unshiu
US-08-853-948B-5
 228 VIPPGMDFS 236
 234 VIPPGMDFS 242
 3 VVPXGMDYS 11
 3 VVPXGMDYS 11
 3 VVPXGMDYS 11
), TYPE: PRT
; ORGANISM: Zea mays
US-09-697-367-24
 RESULT 3
US-08-853-948B-5
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Sequence 11, Application US/08429054A

Patent No. 5917126

GENERAL INFORMATION:
APPLICANT: VAN ASSCHE, CHARLES; LANDO, DANIELLE; BRUNEAU,
APPLICANT: VAN ASSCHE, TONI; GERVALS, MONICA
TITLE OF INVENTION: SUCRENCES PHOSPHATE SYNTHEFASE (SPS),
TITLE OF INVENTION: CDNA FOR MODIFYING SPS EXPRESSION IN PLANT CELLS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN AND MUSERLIAN
 ö
Sequence 10, Application US/09394272

Sequence 10, Application US/09394272

Patent No. 6472588

GENERAL INFORMATION: Candace H.
APPLICANT: Holaday, A. Scott

TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

TITLE OF INVENTION: EXPRESSION OF SUCROSE PROPUCING PLANTS WITH INCREASED

TITLE REPERRACE: 201304/1000

CURRENT APPLICANT: H999-09-10

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 10

IRNGTH: 1049

IRNGTH: 1049

TYPE: RR

CRANIGM: Oryza sativa

US-09-394-272-10
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 Score 36, DB 4, Length 1049;
Pred. No. 80;
2; Mismatches 1, Indels
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,054A
FILING DATE: 26-APR.1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 842,337
FILING DATE: 20-March-1992
APPLICATION NUMBER: PCT/FR 91/00593
FILING DATE: 18-July-1991
CLASSIFICATION: 800
PRIOR APPLICATION: 800
PRIOR APPLICATION DATA:
FILING DATE: 20-July-1990
FILING DATE: 20-July-1990
FILING DATE: 20-July-1990
FILING DATE: 20-July-1990
 JT ANDRESS:

JEET BEENMAN AND MUSERLIAN
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
TIP: 100'
TIP: 100'
 ATTORNEY AGENT INFORMATION:
NAME: Charles A. Muserlian
REGISTRATION NUMBER: 19,683
REPERENCE DOCKET NUMBER: 146.1137
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 661-8000
 E: FLOPPY DISK
IBM PC COMPATIBLE
SYSTEM: PC-DOS/MS-DOS
WORDPERFECT 5.1
 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
 ZIP: 10016
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DI
COMPUTER: IBM PC COMPU
 436 VIPPGMDFS 444
 3 VVPXGMDYS 11
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435 VIPPGMDPS 443

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 66.7%; Score 36; DB 2; Length 1068; 66.7%; Pred. No. 81; tive 2; Mismatches 1; Indels
 Score 36; DB 2; Length 1068;
Pred. No. 81;
2; Mismatches 1; Indels
 COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,777
FILING DATE: UNT YET ASSIGNED
CLASSIFICATION NUMBER: US 08/175,471
FILING DATE: 27-DEC-1993
ATTONEY/AGENT INFORMATION:
NAME: Barbara Rae-Venter
REGISTRATION NUMBER: 32,750
REBERROCE/MONINGER: CGNE.072.02US
TELECOMMUNICATION INFORMATION:
 GENERAL INFORMATION:

APPLICANT: Lando, D.
APPLICANT: Lando, D.
APPLICANT: Bruneau, J. M.
APPLICANT: Bruneau, J. M.
APPLICANT: Gervais, M.
TITLE OF INVENTION: MODIFICATION OF SUCROSE TITLE OF INVENTION: PHOSPHATE
TITLE OF INVENTION: SYNTHASE IN PLANTS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Law Offices of Barbara Rae-Venter STRET: 260 Sheridan Avenue, Suite 440
CITY: Palo Alto
CITY: USA
 Sequence 7, Application US/08718777
Patent No. 5981852
 11:
 TELEFAX: (415)328-4477
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1068
TYPE: Amino acid
STRANDENESS: Single
TOPOLOGY: Unknown
HOLECULE TYPE: Peptide
JS-08-429-054A-11
 66.7%;
 : 1068 amino acids
amino acid
 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
 TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-718-777-7
 435 VIPPGMDFS 443
 3 VVPXGMDYS 11
 US-08-718-777-7
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RESULT 8

105-051-141-7

105-051-141-7

Sequence 7, Application US/09051341

SEQUENCE MUNMER OF SEQUENCES 14

CONDERGYNEE READINES 14

CONDERGYNEE 14

CONDERGYNEE 15

CONDERGYNEE 17

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3 UVPXGMDYS 11

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453 VIPPGMDFS 461
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; ORGANISM: Oryza sativa
US-09-394-272-9
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COUNTRY: U.S
-7. 19103
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US-09-394-272-4

US-09-394-272-4

Sequence 4, Application US/09394272

Sequence 4, Application US/09394272

Sequence 4, Application US/09394272

Sequence 4, Application US/09394272

GENERAL INFORMATION:

APPLICANT: Haigler, Candace H.

APPLICANT: Haigler, Candacy H.

APPLICANT: Haigler, Societ

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

TITLE OF INVENTION: US/09/394,272

CURRENT APPLICATION NUMBER: US/09/394,272

CURRENT FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENGTH: 1081

TYPE: PRT

TYPE: PRT

CRACINISM: Craterostigma plantagineum

US-09-394-272-4
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Sequence 11, Application US/09394272;
Patent No. 6472588;
GENERAL INFORMATION:
APPLICANT: Haigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
TITLE OF INVENTION WUMBER: US/09/394,272
CURRENT FILING DATE: 1999-09-10
CURRENT FILING DATE: 1999-09-10
SEQ ID NO: 11
SEQ ID NO: 11
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                                                                                                                                                                                                                                                                   Query Match 66.7%; Score 36; DB 4; Length 1068; Best Local Similarity 66.7%; Pred. No. 81; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 4; Length 1081;
Pred. No. 83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGIH: 1068
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| 445 VIPPGMDFS 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         435 VIPPGMDFS 443
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                                                                                                           ; TYPE: PRT
; ORGANISM: Zea mays
US-09-394-272-8
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US-09-394-272-11
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Sequence 31637, Application US/09252991A

Sequence 31637, Application US/09252991A

Sequence 31637, Application US/09252991A

Sequence 31637, Application US/09252991A

PAPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERRNCE: 107196.136

CURRENT PAPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR RILING DATE: 1998-07-18

PRIOR FILING DATE: 1998-07-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 1065
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                                                                                                                       RESULT 14

Sequence 82, Application US/08569147

Sequence 82, Application US/08569147

Patent No. 6180377

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: HUMANISED ANTIBODIES

NUMBER OF SEQUENCES: 95

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 61803771s, LLP

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia Place - 46th Floor

CITY: Philadelphia Place - 46th Floor

STREET: Done Liberty Place - 46th Floor

CITY: Philadelphia Place - 46th Floor

STREET: Done Liberty Place - 46th Floor

COMPUTER: PAD COMPACTION AS.A.

STREET: DONE LIBERTY PRESSEE NOW STREET: STREET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 140 amino acids TYPE: amino acid
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TOPOLOGY:
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                                                                   63.0%; Score 34; DB 4; Length 1065; 85.7%; Pred. No. 2e+02; 1ive 0; Mismatches 1; Indels
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31637
                                                                       Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                             324 PQGMDYS 330
                                                                                                                                            5 PXGMDYS 11
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Page 1

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June 3, 2004, 11:57:42; Search time 33.7333 Seconds (without alignments) 91.741 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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SUMMARIES

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45,	46,	47,	48,	49,	50,	57,	52,		11,	17,	18,	19,	20,	23,	24,	21,	25,	28,	29,	33,	36,	37,	43,	30,	34,	38,	96,	42,	44,	
Sequence	Sequence	ø	a)					Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	
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16	17	18	19	70	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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Sequence 8, Application US/09909164
; Sequence 8, Application US/09909164
; Publication No. US20020068702A1
; Publication No. US20020068702A1
; GENERAL INFORMATION:
    APPLICANT: Lim-Wilby, Marguerita
    APPLICANT: Lim-Wilby, Marguerita
    APPLICANT: Lim-Wilby, Marguerita
    APPLICANT: Law, odile E
    APPLICANT: Brunck, Terence K
    TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
    TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
    TITLE OF INTERNACE: 1001-92-US
    CURRENT APPLICATION NUMBER: 60/220,101
    PRIOR PILING DATE: 2000-07-21
    NUMBER OF SEQ ID NOS: 62
    SOFTWARE: Patentin version 3.1
    LENGTH: 11

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: artificial sequence
PERATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
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NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FRAURE:
NAME/KEY: MISC_FEMTURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: MISC FEATURE
LOCATION: (9). (9)
OTHER INFORMATION: D-amino acid
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NAME/KEY: MOD RES
LOCATION: (11)..(11)
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US-09-909-164-22

Sequence 22, Application US/0909164

Sequence 22, Application WS/0909164

Sequence 22, Application No. US2020068702A1

GENERAL INFORMATION:
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: NO.192-US
CURRENT APPLICATION WHERE: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62

SOFTHAMER: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 96.3%; Score 52; DB 12; Length 11; 1 Similarity 100.0%; Pred. No. 0.00097; 11; Conservative 0; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
LENGTHARI: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (8)...(9)
CTHER INFORMATION: D-amino acids
US-09-909-164-13
                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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OTHER INFORMATION: ACETYLATION
PEATURE:
                                                                                                                                                                                           TYPE: PRT
ORGANISM: artificial sequence
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ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
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NAME/KEY: MISC FEATURE
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LOCATION: (6)..(6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                         NAME/KEY: MOD_RES
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NAME/KEY: MOD_RES
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LENGTH: 11
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                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/09909164

Sequence 12, Application No. US20020068702A1

Sequence 12, Application No. US20020068702A1

Sequence 12, Application No. US20020068702A1

SEQUENCE 12, Marguerita

APPLICANT: Corvas International, Inc.

APPLICANT: Law, Odile B

APPLICANT: Law, Odile B

APPLICANT: Brunck, Terence K

ITLE OF INVENTY DEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

URRENT APPLICATION NUMBER: US/09/909,164

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

LENGTH: 11

LENGTH: 11
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APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
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                                                                                                                              Gaps
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                                                                       Query Match 96.3%; Score 52; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.00097; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 96.3%; Score 52; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.00097; Matches 11; Conservative 0; Mismatches 0; Indels
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US-09-909-164-13
US-09-909-164-13
Sequence 13, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: MISC FEATURE
LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MISC_FEATURE
LOCATION: (8) ...(8)
CTHER INFORMATION: D-amino acid
US-09-909-164-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: MOD RES
LOCATION: (1) ...(1)
OTHER INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
; OTHER INFORMATION: AMIDATION
US-09-909-164-8
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                      1 EEVVPXGMDYS 11
                                                                                                                                                                                                                   1 BEVVPXGMDYS 11
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Page 3

APPLICANT: Levy, Odile E

APPLICANT: Brunck, Terence K

TITE OF INTERIOR DATE: 2009-509,164

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT APPLICATION NUMBER: 0003-03-25

PRIOR PELING DATE: 2000-07-21

PRIOR PILING DATE: 2000-07-21

PRIOR PILING DATE: 2000-07-21

SOFTWARE: Patentin version 3.1

SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

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| US-09-164-5 |
| US-09-164-5 |
| US-09-164-5 |
| US-09-164-5 |
| Publication No. US2020068702A1 |
| GENERAL INFORMATION:
| APPLICANT: Lim-Wilby, Marguerita |
| APPLICANT: Levy, Odile B. |
| TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C CURRENT FILING DATE: 2003-03-25 |
| PRIOR PPLICATION NUMBER: 60/220,101 |
| PRIOR PILING DATE: 2000-07-21 |
| NUMBER OF SEQ ID NOS: 62 |
| SOFTWARE: PATENTIN VERSION 3.1 |
| LENGTH: L1
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NAME/KRY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTHER INFORMATION: D-amino acids US-09-909-164-27
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NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: artificial sequence
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ORGANISM: artificial sequence
FEATURE:
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OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.9
Matches 10; Conservative
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NAME/KEY: MISC FEATURE
LOCATION: (8)...(9)
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NAME/KEY: MOD_RES
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US-09-909-164-26

US-09-909-164-26

Sequence 26, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: INTO NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: INTO NOVEL SO 13-25

FRICK APPLICATION NUMBER: 60/220,101

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SEQ ID NO 26

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OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                Query Match

87.0%; Score 47; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 1; Indels
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Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corves International, Inc.
APPLICANT: Lim-Wilby, Marguerita
                                                                                                                                                   OTHER INFORMATION: norvaline-(CO)
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                       FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (9). 7(9)

OTHER INFORMATION: D-amino acid
US-09-909-164-22
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SQUENCE 10. Application US/09909164

FUBLICATION NO. US20020068702A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Corves International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile B
APPLICANT: Levy, Odile B
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOPTWARE: PATENTIN Version 3.1
APPLICANT: Levy, odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN version 3.1
SEQ ID NO 9
LENGTH: 11
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85.2%; Score 46; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 1; Indels
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OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: NOD_RES
LOCATION: (1)...(1)
COTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: NOD FRES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
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! LOCATION: (8)..(8)

OTHER INFORMATION: D-amino acid

US-09-909-164-9
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LOCATION: (1)..(1)
CTHER INFORMATION: ACETYLATION
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LENGTH: 11
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GENERAL INFORMATION:
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: 06/225
PRIOR APPLICATION NUMBER: 06/225
PRIOR APPLICATION NUMBER: 06/225
PRIOR APPLICATION NUMBER: 06/226,101
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENT IN Version 3.1
SEQ ID NO S
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SEQ ID NO S
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ORGANISM: artificial sequence
PEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
PEATURE:
NAME/KEY: MOD_RES
1.0CATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
PEATURE:
NAME/KEY: MISC_FEATURE
1.0CATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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Pred. No. 0.015;
0; Mismatches 1; Indels
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Pred. No. 0.015;
0; Mismatches 1; Indels
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Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, IT
APPLICANT: Lim-Wilby, Marguerita
   OTHER INFORMATION: norvaline-(CO) FEATURE:
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NAME/KRY: MISC. PEATURE
LOCATION: (9) ...(9)
OTHER INFORMATION: D-amino acid
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Best Local Similarity 90.9%;
Matches 10; Conservative
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LOCATION: (11) .. (11)
CTHER INFORMATION: AMIDATION
US-09-909-164-6
                                                                        ; NAME/KEY: MOD RES;
; LOCATION: (11)..(11)
; OTHER INFORMATION: AMIDATION
US-09-900-164-5
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Best Local Similarity 90.9
Matches 10; Conservative
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US-09-909-164-9
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APELICANT: Levy, Odile B

APELICANT: Levy, Odile B

APELICANT: Brunck, Terence K

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT PILING DATE: 2003-03-25

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 32

LENGTH: 11

TYPE
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Sequence 35, Application US/0990164
Sequence 35, Application US/0990164
Sequence 35, Application No. US20020068702A1
GRNERAL INFORMATION:
APPLICANT: Lim-wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: NOUSE, PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: 105/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
FRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 35
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OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , cotation: (9)...(9); OTHER INFORMATION: D-amino acid US-09-909-164-32
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
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ORGANISM: artificial sequence
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NAME/KEY: MOD_RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.9
Matches 10; Conservative
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NAME/KEY: MOD RES
LOCATION: (11)..(11)
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Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-wilby, Marguerita

APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILER REFERENCE: IN01192-03-03-05

PRIOR FILING DATE: 2003-03-25

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

LENGTH: 11
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Pred. No. 0.015;
0; Mismatches 1; Indels
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                                                                                                                                                                               FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                          ; LOCATION: (8). (9)
; OTHER INFORMATION: D-amino acids JS-09-909-164-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                       85.2%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: artificial sequence
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LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                        OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EEVVEXGMSYS 11
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                                                                                                                                                                                                                                                                                                NAME/KEY: MISC_FEATURE
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Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas international, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lavy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: 1001192-US
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEQ ID NO 41
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
NAME/KEY: MOD_RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
PEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
PEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
PEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
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Job time: 34.7333 secs
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; OTHER INFORMATION: D-amino acids
US-09-909-164-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: artificial sequence
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Sequence 40, Application US/09909164

Sequence 40, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Cirvas International, Inc.

APPLICANT: Lim-whiby, Marguerita

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT APPLICATION NUMBER: 6/220,101

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQ ID NO 40

LENGTH: Lim-whip application 3.1

AND APPLICATION NUMBER: Lim-whip application 3.1

AND APPLICANT: Lim-whip application and applicati
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ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)...(11)
OTHER INFORMATION: AMIDATION
FEATURE:
FEATURE:
FEATURE:
FEATURE:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                           85.2%; Score 46; DB 12; Length 11; 90.9%; Pred. No. 0.015; tive 0; Mismatches 1; Indels
                                                         FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
NAME/KEY: MISC_FEATURE
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NAME CAST.

LOCATION: (6)...(6)

OTHER INFORMATION: norvaline-(CO)
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NAME/KEY: NISC FEATURE
LOCATION: (8)..(8)
OTHER INFORMATION: D-amino acid
US-09-909-164-40
                                                                                                                                                                                                                                                                      ; LOCATION: (9). (9)
; OTHER INFORMATION: D-amino acid
US-09-909-164-35
                              OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.5
Matches 10; Conservative
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RESULT 15 US-09-909-164-41 ; Sequence 41, Application US/09909164

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June Run on:

3, 2004; 11:35:47 ; Search time 9 Seconds (without alignments) 117.567 Million cell updates/sec

US-09-909-164-12 54 1 EEVVPXGMDYS 11 Title: Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched: Total number of hits satisfying chosen parameters:

Winimum DB seq length: 0 Waximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	hypothetical prote	conserved hypothet	V1 protein - tobac	sucrose-phosphate	sucrose-phosphate	unknown protein F2	sucrose-phosphate	sucrose-phosphate	sucrose-phosphate	sucrose-phosphate	sucrose-phosphate	hypothetical prote	peptidoglycan-bind	probable alkaline	hypothetical prote	probable membrane	af)	plastocyanin b - L	plastocyanin precu	plastocyanin b pre	6-0-methylguanine-		hypothetical prote	probable hexosyltr	lehydı	ABC transporter AT	phenylalanine-tRNA	3	disease resistance
SUMMARIES	ID	S54619	D69551	A42452	872649	872650	G96764	JC4783	JQ1329	T09837	T04062	T04103	T24111	H87660	H72784	T20173	F69009	B49132	800210	538255	858208	AG3104	D98182	F72745	G69290	35	E86665	7016	113	488
	DB	~	~	7	N	N	N	~	Н	N	N	N	N	~	7	0	0	7	7	7	7	~	7	7	Н	7	7	7	~	7
	Length	ເຜ	9	102	4	4	460	1049	1068	1081	1083	1084	425	433	440	1150	1474	2747	<u>გ</u>	155	168	290	290	296	357	366	565	566	587	906
dł	Query Match	74.1	70.4	66.7	66.7	66.7	66.7	66.7	ú	Ġ	66.7	Ġ	4	4	4.	4.	4.	4.	'n	e.	e.	ë.	'n	e,	ë.	۳.	63.0	ς.	φ,	٠
	Score	40	38	36	36	36	36	36	36	36	36	36	35	35	35	35	35	35	34	34	34	34	34	34	34	34	34	34	34	34
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disease resistance RND multidrug effl hypothetical prote hypothetical 367K partial transposas hypothetical prote fibroblast growth hypothetical prote hypothetical prote conserved hypothet unknown protein [i transposase 1861165 transposase 1861165 transposase 1861105	hypothetical prote pantoate-beta-alan transposase ISC105
744899 F63335 T130830 T130830 A99427 A99471 E90335 S57810 A96546 F90598	C64417 G83055 E90487
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ALIGNMENTS

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	yeast (Sa	2
	3.4	1
	YOR013W	
	protein	Trames: II
ULT 1	othetical protein YOR013w -	ייי רעד זיים רע

hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein C2612; hypothetical protein YOL303.3
C; Species Saccharomyces cerevisiae
C; Date: 08-Jul-1995 #sequence_revisiae
C; Date: 08-Jul-1995 #sequence_revisiae
C; Date: 08-Jul-1995 #sequence_revisiae
C; Accession: S54619; S66879
R; de Haan, M.; Maarse, A.C.; Grivell, L.A.
submitted to the EMBL Data Library, May 1995
A; Recession: S54617
A; Recession: S54617
A; Recession: S54617
A; Recession: S54617
A; Recession: S6407
A; Residues: 1-156 ADBL
A; Recession: S66879
A; Rocession: S66879
A; Rocession: S66879
A; Rocession: S66879
A; Rocession: S66879
A; Residues: 1-156 ADBN
A; Res

A; Cross-references: SGD:S0005539 A; Map position: 15R

C, Superfamily: hypothetical protein YOR013w

Gaps . 0 74.1%; Score 40; DB 2; Length 156; 77.8%; Pred. No. 1; tive 1; Mismatches 1; Indels Query Match 74.1 Best Local Similarity 77.8 Matches 7; Conservative

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2 EVVPXGMDY 10 58 ò

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RESULT 2

Conserved hypothetical protein AF2411 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Accession: D6551
B;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O; Nelson, K.E.; Ketchum, K.A.; Dodson
B;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O; Nelson, K.E.; Ketchum, K.A.; Dodson
G;Accession: D6551
B;Klenk, H.D.; Clayton, R.A.; Tomb, J.F.; White, O.; Neidman, J.F.; Ketchum, K.A.; Dodson
J; Fleischmann, R.D.; Quackenbush, J; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.P.; Kaine, B.P.; Sykes, S.
A;Autterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Shith, H.O.; Woese, C.R.; Venter, J.C.
Shith, H.O.; Woese, C.R.; Venter, J.C.
A;Autle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69551
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

Length 363; Indels

Score 38; DB 2; Pred. No. 6.8; 3; Mismatches

Query Match Best Local Similarity 54.5%; Matches 6; Conservative

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Cjaces (1976) And the sequence of the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Description; catalyzes formation of sucrose-6-phosphate from UDPglucose and D-fructos A, Pathway: sucrose blosynthesis C, Superifamily: sucrose-phosphate synthase; sucrose-phosphate synthase; ckeywords: glycosyltransferase; hexosyltransferase; sucrose blosynthesis F;1-348/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <SSPS>
                                                                                                                                                                                                         \(\text{XComatsu}, A.; Takanokura, Y.; Omura, M.; Akihama, T.
\(\text{Aol. Gen. Genet. 252, 346-351, 1996}\)
\(\text{Yritle: Cloning and molecular analysis of CDNAs encoding three sucrose phosphate synth \(\text{IREFERENCE number: $72648, MUID:96439842; PMID:8842155}\)
\(\text{YAccession: $72650}\)
\(\text{YREFERENCE number: $72650}\)
\(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Cross-references: EMBL:AB006660; NID:g2351059; PIDN:BAA22071.1; PID:g2351060; BECOSTINE SOURCE: fruit, cv. Miyagawa-Wase, BABE Data Library, August 1997; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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C;Genetics:
                         sucrose-phosphate synthase (EC 2.4.1.14) isoform 3 - Citrus unshiu (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown protein F25P22.17 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                 C;Species: Citrus unshiu
C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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23;
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Pred, No. 23;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 VIPPGMDFS 242
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: mRNA; Residues: 1-348 < KOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                            C;Accession: S72650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetica:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
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JC4783
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C;Species: Citrus unshiu
C;Species: Citrus unshiu
C;Daces 24.0Ct.1998 #sequence_revision 24-Oct.1998 #text_change 21-Jul-2000
C;Accession: S72649
R;Komatsu, A.; Takanokura, Y.; Omura, M.; Akihama, T.
Mol. Genet. 252, 346-351, 1996
A;Title: Cloning and molecular analysis of cDNAs encoding three sucrose phosphate syntha
A;Reference number: S72648; MUID:96439842; PMID:8842155
A;Molecule type: DNA
A;Residues: 1-363 <KLE>
A;Cross-references: GB:AE001109; GB:AE000782; NID:g2689432; PIDN:AAB91255.1; PID:g265068
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C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
C;Reywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
P;1-341/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Experimental source: fruit, cv. Miyagawa-Wase
Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
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Status: nucleic acid sequence not shown
Molecule type: mRNA;
Residues: 1-341 < KCM>,
Cross-references: EMBL: AB006319; NID: 92588891; PIDN: BAA23215.1; PID: 92588892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VI protein - tobacco yellow dwarf virus (strain Australia)
C;Species: tobacco yellow dwarf virus
C;Species: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Accession: A42422
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
R;Morlogy 187, 633-642, 1992
A;Title: The nucleotide sequence of the infectious cloned DNA component of the A;Reference number: A42452; MUID:92188538; PMID:1546488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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A;Residues: 1-102 <MOR>
A;Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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Score 36; DB 2; Length 102; Pred. No. 4.3; 3; Mismatches 1; Indels

66.7%; illarity 60.0%; Conservative

Query Match Best Local Similarity

A; Accession: A42452

2 EVVPXGMDYS 11

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sucrose-phosphate synthase (EC 2.4.1.14) 1 - rice
C;Species: Oryza sativa (rice)
C;Species: Oryza sativa (rice)
C;Date: 32.Apr-1999 #sequence_revision 23.Apr-1999 #text_change 20.Jun-2000
C;Accession: T04103
R;Sakamoto, M.; Satozawa, T.; Kishimoto, N.; Higo, K.; Shimada, H.; Fujimura, T.
A;Title: Structure and RFLP mapping of a rice sucrose phosphate synthase (SPS) gene that
A;Reference number: 215212
                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1081 <1NG>
A;Residues: 1-1081 <1NG
A;Genetics: pps2
C;Genetics: pps2
C;Function: A;Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fruc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 4
A; Introns: 86/3; 116/3; 255/3; 322/2; 482/3; 526/3; 570/3; 629/3; 647/3; 668/3; 949/3; 9
A; Note: PSSM11.40
C; Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase homology
F; 230-714/Domain: sucrose/sucrose-phosphate synthase homology <85PS>
   lant Physiol. 115, 113-121, 1997
;ittle: Analysis of cDNA clones encoding sucrose-phosphate synthase in relation to suga
Reference number: 216874; MUID:97451773; PMID:9306694
;Accession: T09837
                                                                                                                                                                                                                                                                                                                                                                                                                                A Pathway: sucrose biosynthesis
C; Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase homology
C; Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F;176-674/Pomain: sucrose/sucrose-phosphate synthase homology <8SS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 2; Length 1081;
Pred. No. 60;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reaidues: 1-1084 <SAK>
A;Cross-references: EMBL:D45890; PIDN:BAA08304.1
A;Experimental source: subsp. Japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.7%;
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Best Local Similarity 66.7
Matches 6; Conservative
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ses 6; Conservative
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445 VIPPGMDFS 453
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Matches
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                                                                                                                                                                                                                                     Wolecule type: mRNA
1,Residues: 1-1049 <NbL>
1,Residues: 1-1049 <NbL>
1,Residues: 1-1049 <NbL>
1,Note: UDPJucose-fructose-phosphate glucosyltransferase; Sucrosephosphate-UDPglucosylt
1,Comment: This enzyme catalyzes the formation of sucrose-phosphate form UDP-glucose and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;;Species: Zea mays (maize)
;;Date: 10-Sep-1999
**Sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
;;Accession: JQ1329; PQ0260
;;Morrell, A.C.; Bruneau, J.M.; Summerfelt, K.; Boersig, M.; Voelker, T.A.
**Jant Cell 3, 1121-1130, 1991
**Jant Cell 3, 1121-1130, 1991
**Yritle: Expression of a maize sucrose phosphate synthase in tomato alters leaf carbohyd
';Reference number: JQ1329; MJID:92333837; PMID:1840396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nyolecule type: protein
1,Residues: 71-74,206-212,471-481,872-892 <WORL>
1,Residues: This enzyme transfers the glucosyl group from UDPglucose to fructose-6-phosph
3,Comment: This enzyme is involved in the regulation of carbon partitioning in the leave
                                                                     \'valdez-Alarcon, J.J.; Ferrando, M.; Salerno, G.; Jimenez-Moraila, B.; Herrera-Estrella
sene 170, 217-222, 1996
\'varacterization of a rice sucrose-phosphate synthase-encoding gene.
\'varacterization of a rice sucrose-phosphate synthase-encoding gene.
\'xReference number: JC4783; MJID:96235138; PMID:8666248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           () Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fruc () Pathway: sucrose biosynthesis () Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase, sucrose-phosphate synthase homology (); Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis (); 180-663/Domain: sucrose/sucrose-phosphate synthase homology <85PS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fru
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.)Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
.)Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
?;178-666/Domain: sucrose/sucrose-phosphate synthase homology <8SPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                    ı,Gene: Spsl
ı,İntrons: 24/1; 103/3; 183/3; 205/3; 435/3; 475/3; 519/3; 578/3; 596/3; 617/3; 931/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    iucrose-phosphate synthase (EC 2.4.1.14) isoform 2 - Craterostigma plantagineum
);Species: Craterostigma plantagineum
);Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
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;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 18-Jun-1999;Accession: JC4783
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i, Molecule type: mENA
i, Residues: 1-1068 «WOR»
i, Cross-references: GB: M97550; NID: g168625; PIDN: AAA33513.1; PID: g168626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 66.7%; Score 36; DB 2; Length 1049; Best Local Similarity 66.7%; Pred. No. 58; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 1; Length 1068;
Pred. No. 59;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ucrose-phosphate synthase (EC 2.4.1.14) - maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           436 VIPPGMDFS 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       435 VIPPGMDPS 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 VVPXGMDYS 11
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                                                                                                                                                                                                            ;Accession: JC4783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: T09837
                                                                                                                                                                                                                                                                                                                                                                                                            Genetics:
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C,Genetics: A,Gene: Sps1

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probable alkaline proteinase APB0263 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: H72784
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaiawa, H.; Takaniya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 5
A;Introns: 33/3; 63/3; 132/3; 169/3; 221/3; 299/3; 379/2; 423/2; 438/2; 471/1; 513/2; 6
                                                                                                                                                                                                                                                                                                                                                                                                                       AjStatus: preliminary
AjMolecule Yype: DNA
AjResidues: 1-440 «KAW»
AjRossa-references: DDBJ:APO00058; NID:g5103388; PIDN:BAA79178.1; PID:g5103657
AjExperimental source: strain Kl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-1150 <WIL>
A; Cross-references: EMBL: 281486; PIDN: CAB03994.1; GSPDB: GN00023; CESP: C53A5.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1150 WA
A;Residues: 1-1150 WBBJ:Z78015; PIDN:CAB01437.1; GSPDB:GN00023; CESP:C53A5.2
A;Experimental source: clone R02D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein C53A5.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T20173; T23857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 64.8%; Score 35; DB 2; Length 440; Best Local Similarity 66.7%; Pred. No. 35; Matches 6; Conservative 2; Mismatches 1; Indels
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submitted to the EMBL Data Library, August 1996
A;Aeference number: Z19808
A;Accession: T23857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Gene: APE0263
C, Superfamily: subtilisin; subtilisin homology
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: H87660
C;Accession: H87660
E; Killerman, W.C.; Feldblynm, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ernolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A;Reference number: Ascession: H87660
A;Accession: H87660
A Map position: 1
A.Introns: 120/2; 221/3; 452/3; 492/3; 536/3; 595/3; 613/3; 634/3; 946/3; 989/2
A.Introns: 120/3; 200/2; 221/3; 452/3; 492/3; 536/3; 595/3; 613/3; 634/3; 946/3; 989/2
C.Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
C.Keywords: glycosyltransferase; hexosyltransferase
F:196-680/Domain: sucrose/sucrose-phosphate synthase homology <85PS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: EMBL: Z81109; PIDN: CAB03241.1; GSPDB: GN00023; CESP: R10D12.10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein R10D12.10 - Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C.Accession: T24111 submitted to the EMBL Data Library, October 1996 A;Reference number: Z19842 A;Accession: T24111
                                                                                                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                                                                           Query Match 66.7%; Score 36; DB 2; Length 1084; Best Local Similarity 66.7%; Pred. No. 60; Matches 6; Conservative 2; Mismatches 1; Indels
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64.8%; Score 35; DB 2; Length 425;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 5; Conservative 3; Mismatches 2; Indels
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A;Residues: 1-425 <WIL>
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A;Introns: 23/3; 56/3; 113/3; 257/2
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Matches 6; Conservative
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-433 < STO>
A; Cross-references: C; Generia
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RESULT 13

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ALIGNMENTS
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InterPro; IPR006275; CarA_L glu.
InterPro; IPR006343; CPase_L D2.
InterPro; IPR0054849; CPase_L D2.
InterPro; IPR005480; CPase_L D3.
InterPro; IPR005481; CPase_L D3.
InterPro; IPR004362; MGS_IIRe.
Pfam; PP002089; CPSase_L Chain; 2.
Pfam; PF02786; CPSase_L D2; 2.
Pfam; PF02786; CPSase_L D3; 1.
                                                                                                                                                                                                                                       STANDARD;
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vibrio chol
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xenopus lae
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                                                                           June 3, 2004, 11:32:06; Search time 4.86667 Seconds (without alignments) 117.693 Million cell updates/sec
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P31819

P343802

P3822

P06423

P080424

P18283

P18485

P1848
GenCore version 5.1.6
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                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                         141681 seqs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
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RPP8_ARATH
RP8H_ARATH
Y939_METJA
PANC_PSEAE
HMPA_VIBCH
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Y11K_TYDVA
SPS_ORYSA
SPS_MAIZE
SPSZ_CRAPL
FAF_DROME
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Maximum Match 100%
Listing first 45 summaries
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HALEL
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SCHPO
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                                                   OM protein - protein search, using sw model
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LISMO
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                               finimum DB seq length: 0
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54
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1401
2717
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Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          litle:
Perfect score:
                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                         Sequence:
                                                                                                                                                                                                                         Searched:
                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
No.
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P08203 escherichia P06190 salmonella Q9wz1 thermotoga Q04827 rattus norv P30219 homo sapien P30280 mus musculu Q90459 brachydanio P50755 xenopus lae P49706 gallus gall P53782 xenopus lae P55169 gallus gall P30281 homo sapien
ARAD BCOLI ARAD SALIY HISS THEMA CGD2 RAT CGD2 HUMAN CGD2 HUMAN CGD1 BRARE CGD1 BRARE CGD2 CGT1 CK CGD2 CGT1 CK CGD2 CGT1 CK CGD1 CGT1 CK CGD1 CGT1 CK CGD1 CGT1 CK CGD1 CGT1 CK CGD1 CGT1 CK CGD1 CGT1 CK
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=ATCC 25586;

WEALINE=21886394; PubMed=11889109;

Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., Nagarieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N., Overbeek R., Genome sequence and analysis of the oral bacterium Fusobacterium rucleatum strain ATCC 25586.";

"Genome sequence and analysis of the oral bacterium Fusobacterium propleatum strain ATCC 25586.";

"Genome sequence and analysis of the oral bacterium Fusobacterium propleatum strain ATCC 25586.";

"Genome sequence and analysis of the oral bacterium Fusobacterium phosphate + i-glutamathe + carbamoyl phosphate.

"I SATHWAY: Arginine biosynthesis."

"I PATHWAY: Pyrimidine biosynthesis."

"I PATHWAY: Pyrimidine biosynthesis."

"I SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamcyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamcyl-phosphate synthetase ammonia chain)
                                                                                                                                                                                                                                                                                                                                               CARB OR FN0422.
Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
PRT; 1058 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
-!- SIMILARITY: Belongs to the carB family
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a

QVVPSGINYS 16

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                                                                                                                                                                                                                                                                                                                                                                                                                       ö
R PFam; PF02142; MGS; 1.

DR PRINTS; PR00099; CPSASE.

DR TIGREPMS; TIGROJ369; CPSASE.

DR PROSITE; PS00866; CPSASE.

DR PROSITE; PS00867; CPSASE.

ENGINE; PS00867; CPSASE.

CARBOXPHOSPHATE SYNTHETIC DOMAIN.

CARBAMONI PHOSPHATE SYNTHETIC DOMAIN.

**CARBAMONI PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92188538; PubMed=1546458;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
"The nuclectide sequence of the infectious cloned DNA component of
tobacco yellow dwarf virus reveals features of geminiviruses
                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                          52 ATP (POTENTIAL).
84 MANGANESE 1 (BY SIMILARITY).
86 MANGANESE 1 AND 2 (BY SIMILARITY).
80 MANGANESE 2 (BY SIMILARITY).
80 MANGANESE 3 (BY SIMILARITY).
82 MANGANESE 3 (BY SIMILARITY).
83 MANGANESE 3 (BY SIMILARITY).
84 MANGANESE 3 (BY SIMILARITY).
85 MANGANESE 3 (BY SIMILARITY).
86 MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 1; Length 1058;
Pred. No. 9.4;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 1; Length 102;
Pred. No. 2.2;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A42452; A42452.
InterPro; IPR006221; Gemini_mov.
Pfam; PF01708; Gemini_mov; I.
Hypothetical protein.
SEQUENCE 102 AA; 11178 MW; A40ECFIE0AF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
NCBI_TaxID=31599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infecting monocotyledonous plants.";
Virology 187:633-642(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last seq
01-GCT-1993 (Rel. 27, Last ann
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.7%;
                                                                                                                                                                                                                                                                                                                                                                                        70.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 EIVPNGLNYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EVVPXGMDYS 11
                                                                                                                                                                                                                                              153
302
302
284
284
298
300
30
820
832
1058 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y11K TYDVA
P31619;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                             DOMAIN
REPEAT
REPEAT
NP_BIND
NP_BIND
METAL
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                                                                                                                                                                                                                                                                                                                                                                                      Jene 170:217-222(1996).

-!- FUNCTION: Involved in the regulation of carbon partitioning in the leaves of plants. May regulate the synthesis of sucrose and therefore play a major role as a limiting factor in the export of photoassimilates out of the leaf.
-!- CAPALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP + sucrose 6-phosphate.
-!- ENZYME REGULATION: Activity regulated by phosphorylation and moderated by concentration of metabolites and light.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PATHWAY: Sucrose synthesis.
-!- SUBINIT: Homodimer or homotetramer (By similarity).
-!- PTW: Phosphorylated. However, phosphorylation is not essential for enzyme function (By similarity).
-!- SIMILARITY: Belongs to the glycosyltransferase family 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                  (UDP-glucose-fructose-phosphare glucosyltransferase).
Oryza sativa (Rice)
Oryza sativa (Rice)
Subaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatcophyta, Magnoliophyta; Lillopsida, Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                         Herrera-Estrella L.; "Characterization of a rice sucrose-phosphate synthase-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 1; Length 1049;
Pred. No. 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1049 AA; 116455 MW; ED862E2819AA4B04 CRC64;
                                                                                                                                                                                                                                                                           STEAIN-cv. Indica-IR36; TISSUE-Leaf;
MEDLINE-96235138; PubMed-8666248;
Valdez-Alarcon J.J., Ferrando M., Ulmenez-Moraila B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001296; Glyco_trans_1.
Pfam; PF00534; Glycos_transf_1, 1.
Transferase; Glycosyltransferase; Jhosphorylation.
20. 29. 29. Poly-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
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                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1068 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@igb-sib.ch)
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POLY-ARG.
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P31927;
01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U33175; AAC49379.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 66.7
                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               436 VIPPGMDFS 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; JC4783; JC4783.
Gramene; Q43802; -.
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                               NCBI_TaxID=4530;
                                ORYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
SEQUENCE
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                                SPS ORY
Q43802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
SPS_MAIZE
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RESULT 3
SPS_ORYSA
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Gaps

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EVVPXGMDYS 11

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                              -i- PATHWAY: Sucrose synthesis.
-i- SUBDNIT: Homodimer or homocetramer (By similarity).
-i- PTM: Phosphorylated. However, phosphorylation is not essential for enzyme function (By similarity).
-i- SIMILARITY: Belongs to the glycosyltransferase family 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSEB24; Q999T6; Q970Z7;
01-NOV-1997 (Rel. 35, Created)
28-FSEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Probable ubiquitin carboxyl-terminal hydrolase FAF (EC 3.1.2.15)
Probable ubiquitin thiolesterase FAF) (Ubiquitin-specific processing protease FAF) (Ubiquitin thiolesterase FAF) (Ubiquitin-specific processing protease FAF) (Recent facets protein).
PAF) OR BCDNA:LD2582 OR CG1945.
Drosophila melanogaster (Fruit fly).
Buxaryota, Arthropoda; Haxapoda; Insecta; Pterygota;
Bobydroidea; Drosophilidae; Drosophila.
NUBL TaxID=7227;
                                                                                                                              MEDINE=97451773; PubMed=9306694; Ingram J., Salamini F., Bartels D., Ingram J., Chandler J.W., Gallagher L., Salamini F., Bartels D., Amanlysis of cDNA clones encoding sucrose-phosphate synthase in "Amalysis of cDNA clones encoding sucrose-phosphate synthase in relation to sugar interconversions associated with dehydration in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, Y11795, CAA72491.1; -.
EMBL, Y109837, TO8A72401.1; -.
InterPro, IPR001296; Glyco_trans_1.
Pfam; PF00534; Glycos transf_1; 1.
Transferase; Glycosyltransferase; Phosphorylation; Multigene family.
Transferase; Glycosyltransferase; Polyly SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 1; Length 1081;
Pred. No. 25;
2; Mismatches 1; Indels
Lamiales, Lamiales incertae sedis; Lindernieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1081 AA; 120933 MW; DD142DC2F1A72900 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 2778 AA.
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MEDLINE=93202020; PubMed=1295747;
Fischer-Vize J.A., Rubin G.M., Lehmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7
Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                     SEQUENCE FROM N.A.
                            Craterostigma.
NCBI_TaxID=4153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAF DROME
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  셤
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                                                                                                                                                                                                                                                                                                                                    STRAINE-CV. PIONEER 3184; TISSUE=Leaf;

MEDLINE=9238837; PubMed=1840396;

MEDLINE=9238837; PubMed=1840396;

MEDLINE=9238837; PubMed=1840396;

MEDLINE=9238837; PubMed=1840396;

MEDLINE=9238837; PubMed=1840396;

MEDLINE=0 a maize sucrose Hosphate synthase in tomato alters

leaf carbohydrate partitioning.";

Plant Cell 3:1121-1130(1991).

I. Plant Cell 3:1121-1130(1991).

I. PUNCTION: Involved in the regulation of carbon partitioning in the leaves of plants. May regulate the synthesis of sucrose and therefore play a major role as a limiting factor in the export of photosesimilates out of the leaf.

CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP + sucrose 6-phosphate.

CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate and and moderated by concentration of metabolites and light.

CHOMEN AND ACTIVITY CONCENTRATION: ACTIVITY regulated by phosphorylation and moderated by concentration of metabolites and light.

CHOMEN AND ACTIVITY CONCENTRATION: ACTIVITY PROGRAMMAN: Sucrose Synthesis.

CHOMEN AND ACTIVITY ACTIVITY PROGRAMMAN: Sucrose Synthesis.

CHOMEN AND ACTIVITY ACTIVITY PROGRAMMAN: Sucrose Synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- DEVELOPMENTAL STAGE: Germinating seeds or mature leaves.
-!- PTM: Phosphorylated. However, phosphorylation is not essential for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craterostigma plantagineum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sucrose-phosphate synthase 2 (EC 2.4.1.14) (UDP-glucose-fructose-phosphate synthase 2)
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 71-74; 206-212; 471-481 AND
872-892.
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14) (UDP-glucose-fructose-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the glycosyltransferase family 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.7%; Score 36; DB 1; Length 1068; 66.7%; Pred. No. 25; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 1068 AA; 118575 MW; 074679B5E9A1D282 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Malerbo, 2023,

InterPro; IPR001296; Glyco_trans 1.

Pfam; Pr00534; Glycos transf_1, T.

Transferase; Glycosyltransferase; Phosphorylation.

DOMAIN

25

31
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                                                                            phosphate glucosyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M97550; AAA33513.1; -. PIR; JQ1329; JQ1329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.7
Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          435 VIPPGMDFS 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              function.
                                                                                                                                                                                                                                       NCBI TaxID=4577;
                                                                                                                                 Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MaizeDB; 25294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPS2 CRAPL
004933,
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SPS2_CRAPL RESULT 5

OCCUPATION

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Gaps

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R. STRAIN-BEEKRALAN, N. A.

R. ARGUENEZE FROM N. A.

RA Adams M. D., Celniker S.E., Li P. W., Hoskins R.A., Galle R.F.,
Adams M. D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M. D., Celniker S.E., Holt R.W., Hoskins R.A., Galle R.F.,
Adams M. D., Celniker S.E., Holt R.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Hedderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Raker E.G., Helt G., Walson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayaktarold, D. Bolahako S.
RA Beckon K.Y. Benos P.V., Barman B.P., Bhandari D., Belasley E.M.,
Ballew R.M., Cawley S., Dallker J., Bayraktarold L., Beasley E.M.,
RA Burtis K.C., Buaem D.A., Baller H. J., Cadlew E., Center A., Candra I.
RA Burtis K.C., Buaem D.A., Baller H. C., Garenport L.B., Davies P.,
RA Gerbalos B., Delchan M.R., Bouck J., Baromoport L.B., Davies P.,
RA Gerbalos B., Delchar A., Deng Z., Mays A.D., Dew I., Diez S.M.,
B. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Gerty J.M., Cawley S., Dallker C., Terract C., Ferriera S., Fleischman W.,
RA Bartis N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., I Degram C.,
Adali M., Kalush F., Karefte G., Kraft C., Kravitz S., Kulp D., Lai Z.,
List Y., Latteris B., McInteon G.H., McLeod M.P., McHesen D.L.,
RA Martilov G. Milshina N.V., Modesod M.P., McPherson D.L.
RA Martilov G. Milshina N.V., Modesod M.P., McPherson D.L.
RA Bartis N.W., Mother M. W., McLeod M.P., McHebel J.M., Nandron S.M., Moy W., Murthy B., Murphy L., Mazay D.M., Welfers M. B., McInteon G.F., Polas G., Mozis S., Woodser T., Walsenbach J., Was Rainer T. K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shier E., Spradiling A.C., Stapleton M., Strong R., Sun B.,
RA Strakas R., Mers R., Pong P.N., Zhong Y., Zhu S., Zhu X., Smith H.O.,
RA Jang Z.-Y., Wassarman D.A., Welley K.C., Wu D., Yang S., Zhu X., Smith H.O.,
RA Jang Z.-Y., Wassarman 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Serkeley;

WEDLINE-20196012; PubMed=10731138;

Rubin G.M., Hong L., Brokstein P., Evans-Holm M., Frise B.,

Stapleton M., Harvey D.A.;

Stapleton M., Harvey D.A.;

Stapleton M., Harvey D.A.;

To be compound every and embryo development, and plays a role in compound eye assembly and cogenesis respectively. In the role in compound eye assembly and cogenesis respectively. In the raval eye disks, cells outside the assembling facets require this protein for short-range cell interactions that prevent the mystery cells from becoming photoreceptors. It is also required for muclear migration and cellularization in early embryogenests and could play a role in pole cell determination, development or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22426069; PubMed=12337572; Matthews B.B., Campbell K.S., Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.I Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lewis S.E.; "Annotation of the Drosophila melanogaster euchromatic genome: a
  "The fat facets gene is required for Drosophila eye and embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Biol. 3: RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1089-2778 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISIONS, AND ALTERNATIVE SPLICING.
                                                  Development 116:985-1000(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 review.";
                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0007349; P:cellularization; IMP.
GO; GO:0007456; P:cellularization; IMP.
GO; GO:0007456; P:cytoplasm; Gensu Drosophila); IMP.
GO; GO:0008583; P:mystery cell fate differentiation (sensu Dr. .; IMP.
GO; GO:0008583; P:mystery margration; IMP.
GO; GO:0006519; P:prortein deubiquitination; IDA.
GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IGI.
InterPro; IPR001394; Peptidase_C19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                ISOId=P55824-3; Sequence=VSP_005269;
-!- TISSUE SPECIFICITY: Eye disks and ovaries.
-!- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
-!- SIMILARITY: Belongs to peptidase family C19.
            -!- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)0 = ubiquitin + a thiol.
-!- ALTERNATIVE PRODUCTS:
                                                      Event-Alternative splicing, Named isoforms=3; Comment=Experimental confirmation may be lacking for some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35; DB 1; Length 2778; Pred. No. 1.1e+02; 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                       [sold=P55824-2; Sequence=VSP_005270;
                                                                                                             IsoId=P55824-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                     EMBL; L04959; AAF01345.1; -.
EMBL; L04960; AAF01347.1; -.
EMBL; L04960; AAF01347.1; -.
EMBL; L04960; AAF01348.1; -.
EMBL; AE003779; AAF57198.1; -.
EMBL; AE003779; AAF57198.1; -.
EMBL; AE0003779; AAN14291.1; -.
EMBL; AE000779; AAN14291.1; -.
MEROPS; C19.007; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFam, PF00443, UCH; 1.
PROSITE, PS00972, UCH 2.1; 1.
PROSITE; PS00973; UCH 2.2; 1.
PROSITE; PS50235; UCH 2.3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.8%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 54.5°,
G; Conservative
                                                                                   isoforms;
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RESULT 7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF222283; AAF81719.1; -.

REMBL; AF232283; AAF81719.1; -.

REMBL; AB40923; BA496014.1; ALT_INIT.

EMBL; AB40923; BA496014.1; ALT_INIT.

REMBL; AB40923; CAC16128.1; -.

REMBL; AL33378; CAC16128.1; -.

REMBL; AC33273; CAC16128.1; -.

REMBL; AC3327; CAC16128.1; -.

RIM; 605322; -.

ROJ, GO:0003779; F:actin binding; NAS.

ROJ, GO:0003779; F:actin binding; Relch_rep.

REAMRT; SM00625; Relch_rep.

REAMRT; SM00625; Relch_rep.

REAMRT; Relch; 6.

REART; Relch; Actin-binding; Relch repeat; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Nagase T., Kikuno R., Ishikawa K. I., Hirosawa M., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XVII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                          MEDLINE=20347694; PubMed=10888605; Koob M.D., Nemes J.P., Benzow K.A.; The SCAB transcript is an antisense RNA to a brain-specific transcript encoding a novel actin-binding protein (KLHLI)."; Hum. Mol. Genet. 9:1543-1551(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KELCH 1.
KELCH 2.
KELCH 3.
KELCH 4.
KELCH 5.
KELCH 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kelch repeat; Repeat.
SER-RICH.
              ONNE4; OPHAX4; OPHAX65; OPP238;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Kelch-like protein 1.
    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20277482; PubMed=10819331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [3]
SEQUENCE OF 179-409 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82680 MW;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Res. 7:143-150(2000)
                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         649 7
701 7
748 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
    KHL1 HUMAN
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REPEAT
SEQUENCE
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee J. -S.; "Molecular cloning and characterization of plastocyanin precursor in
                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD001235; Copper blue; 1.
PROSITE; PS00196; COPPER BLUE; 1.
Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
63.9%; Score 34.5; DB 1; Length 748; 80.0%; Pred. No. 35; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
E45725D25B5F400D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Contains 1 plastocyanin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLASTOCYANIN.
PLASTOCYANIN-LIKE.
COPPER (BY SIMILARITY)
COPPER (BY SIMILARITY)
                                                                                                                                                                                                                   154 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000923; BlueCu 1.
InterPro; IPR001235; Copper_blue.
InterPro; IPR008972; Cupredoxin.
Pfam; PF00127; copper-bind; 1.
pRINTS; PR00156; COPPERBLUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Ilpoom; TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF093636; AAC78108.1; -. HSSP; P00289; 2PCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15577 MW;
Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                       STANDARD;
                                                                                                            127 EEVVP-GMDF 135
                                                                       1 EEVVPXGMDY 10
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1154
1142
147
                                                                                                                                                                                                                                                                                                                                    Oryza sativa (Rice).
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94 1
139 1
142 1
154 AA; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 58-154.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4530;
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RANSIT
                                                                                                                                                                                                       ORYSA
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SEQUENCE
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DOMAIN
METAL
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PLAS_ORYSA
ID _PLAS_O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nielsen P., Gausing K.;
"In vitro binding of nuclear proteins to the barley plastocyanin gene
promoter region.";
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hordeum vulgare (Barley).
Bukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae;
Triticeae, Hordeum.
NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product taylor. 277:97-104 (1993).

-1. FUNCTION: Participates in electron transfer between P700 and the cytochrome bef complex in photosystem I.

-1. SUBCELLULAR LOCATION: Loosely bound to the inner thylakoid membrane surface in chloroplasts.

-1. SIMILARITY: Contains 1 plastocyanin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1] — SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=CA. Bomi;
Nielsen O.S., Gausing K.;
"The precursor of barley plastocyanin: sequence of cDNA clones and gene expression in different tissues.";
FEBS Lett. 225:159-162(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DR EMBL; Y00704; CAA66696.1; -
DR EMBL; 223347; CAA68696.1; -
DR PIR; S38255, S38255.

BR HSSP; P00289; 2PCF.

InterPro; IPR000923; BlueCu 1.

BR InterPro; IPR000922; Cupredoxin.

R InterPro; PR001235; Copper_blue.

R PRINTS; PR00125; Copper_blue; I.

R PROSITE; PS00196; COPPER_BLUE; I.

R CALOroplast; Electron transport; Copper; Thylakoid; Membrane; I.

TRANSIT 1. 58 CHINDARYANI.
                                                            ô
63.0%; Score 34; DB 1; Length 154; 54.5%; Pred. No. 8.7; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLASTOCYANIN.
PLASTOCYANIN-LIKE.
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence
28-FEB-2003 (Rel. 41, Last annotatio
Plastocyanin, chloroplast precursor.
                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE FROM N.A.
STRAIN=cv. NK 1558;
MEDLINE=94039091; PubMed=8223592;
                                                            6; Conservative
                                                                                                                                                                       100 EDAVPSGVDVS 110
                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                   1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58
155
155
140
143
143
   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                PLAS HORVU
P08248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
DOMAIN
METAL
                           Best Loca
                                                                                                                                                                                                                                                                                       PLAS_HORVU
                                                                                                                                                                                                                                                            RESULT
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                                                                                  ö
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=cv. Italica,
Dimitrov M.I., Egorov C.A., Donchev A.A., Atanasov B.P.,
Dimitrov M.I., Egorov C.A., Donchev A.A., Atanasov B.P.,
"Complete amino acid sequence of poplar plastocyanin b.",
FEBS Lett. 226:17-22(1987).
-I. FUNCTION: Participates in electron transfer between P700 and the
                                                                                                                                                                                                                                                                                                                                            Populus nigra (Lombardy poplar).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Malpighiales; Sallcaceae; Saliceae; Populus.

NCBI_TaxID=3691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, Z50186; CAA90565.1; -.

REBL, Z50186; CAA90565.1; -.

RIR, SS8208; S8208.

RIRSP, P00299; 1PLC.

InterPro; IPR000923; BlueCu.1.

InterPro; IPR001235; Cupredoxin.

R Pfan, Pf00127; copper-bind; 1.

R PRINTS; PR00156; COPPERBLUE.

R PROSTIE; PS00196; COPPER BLUE; 1.

R PROSTIE; PS00196; COPPER BLUE; 1.

R TANNSIT | 1. 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytochrome b6-f complex in photosystem I.

-!- SUBCELLULAR LOCATION: Loosely bound to the inner thylakoid membrane surface in chloroplasts.
-!- SIMILARITY: THESE ARE 12 DIFFERENCES BETWEEN THE SEQUENCE OF FORLAR PLASTOCYANINS A AND B.
-!- SIMILARITY: Contains 1 plastocyanin-like domain.
                                                                                  ö
                                                63.0%; Score 34; DB 1; Length 155; 54.5%; Pred. No. 8.7;
                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRALM-ev. Italia, IISSUB-Leaf;
Reichert J., Jenzelewski V., Haehnel W.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
120 120 T -> N (IN CV, NK 1558).
155 AA; 15709 MW; DAA7EABESF6F4F91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLASTOCYANIN B.
PLASTOCYANIN B.
PLASTOCYANIN-LIKE.
COPPER.
COPPER.
                                                                                                                                                                                                                                                               01-0cT-1989 (Rel. 12, Created)
01-0cT-1986 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Plastocyanin B, chloroplast precursor.
                                                                                  2; Mismatches
                                Query Match
Best Local Similarity 54...
6; Conservative
                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                 101 EDAVPSGVDVS 111
                                                                                                                 1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 70-168.
                                                                                                                                                                                                                                    PLAT POPNI
VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the phenylalanyl-tRNA synthetase beta chain family. Subfamily 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ATCC 35210 / B31;
MEDLINE=9805544; PubMed-9403685;
Frager C. M., Casjens S., Hanng W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fledschmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Flyli C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Veneer J.C.;
                                                                                                                                                                                                                                                    PIR; A70164; A70164.
TIGR; BB0514; -.
HAMAP, ME_00284; -.; 1.
InterPro; IPR005147; B5.
InterPro; IPR004531; PheT_arch.
Pfam; PF03484; B5; 1.
TIGRPAMs; TIGR00471; pheT_arch; 1.
Aminoacy1-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Complete protecome.
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=ATCC 35210 / B31;
Barbour A.G., Hinnebusch J.;
"Phenylalanyl-trNA synthetase genes (alpha and beta subunits) and thioredoxin reductase gene of Borrelia burgdorferi.";
thioredoxin reductase gene of Borrelia burgdorferi.";
submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                           Borrelia burgdorferi (Lyme disease spirochete).
Bacteria, Spirochaetes, Spirochaetales, Spirochaetaceae, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP diphosphate + L-phenylalanyl-tRNA(Phe).
                                                                ö
                             63.0%; Score 34; DB 1; Length 168; 54.5%; Pred, No. 9.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                3; Indels
168 AA; 16981 MW; F20DA6EA2038AEEA CRC64;
                                                                                                                                                                                                                      566 AA.
                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U82978; AAB41019.1; -. EMBL; AE001153; AAC66870.1; -.
              Query Match
Best Local Similarity 54.2
Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 390:580-586(1997).
                                                                                                                     |: || |: | | 112 EDAVPSGVDVS 122
                                                                                                                                                                                                                      STANDARD;
                                                                                                 1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CV. Columbia;
A Seki M., Iida K., Saturai T., Akiyama K., Ishida J.,
A Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
A Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
A Hayashizaki Y., Shinozaki K.;
T "Arabidopsis thaliana full-length CDNA.";
I. Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
-: FUNCTION: Potential disease resistance protein.
-: DOMAIN: The LRR repeats probably act as specificity determinant of pathogen recognition (By similarity).
-: SIMILARITY: Belongs to the disease resistance NB-LRR family.
-: SIMILARITY: Contains 1 NB-ARC domain.
-: DATABASE: NAME=NIB-LRRS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE=Functional and comparative genomics of disease resistance gene
                                                                           Gaps
                                                                                                                                                                                                                                                      10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
Probable disease resistance RPP8-like protein 4.
RPP8L4 OR AT5G48620 OR KISNIS.9.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv. Columbia;
MEDLINE-99087489; PubMed-9872454;
Nakamura Y., Sato S., Asamizu B., Kaneko T., Kotani H., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned Pl and TAC clones.";
DNA Res. 5:297-308(1998).
                                                                           ;
0
                                     63.0%; Score 34; DB 1; Length 566; 85.7%; Pred. No. 33;
                                                                           1; Indels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00364; DISEASERSIST.
Plant defense; ATP-binding; Repeat; Leucine-rich repeat.
DOMAIN 10 45 LEUCINE-ZIPPER.
566 AA; 65173 MW; 9D48C8B5D6D3B74B CRC64;
                                                          Pred. No. 33;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB015468; BAB10695.1; -.
EMBL; AK117163; BAC41841.1; -.
Interpro; IPR000767; Disease_resist.
Interpro; IPR001611; LRR.
Interpro; IPR00181; NB-ARC.
Pfam; PF00560; LRR; 2.
Pfam; PF00991; NB-ARC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WWW="http://niblrrs.ucdavis.edu".
                                                                               6; Conservative
                                                                                                                                                        169 VPFGMDY 175
                                                                                                                  4 VPXGMDY 10
                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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      SEQUENCE
                                                                                                                                                                                                              RESULT 12
RBL4_ARATH
ID _RBL4_A
                                                                             Matches
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"Intragent's recombination and diversifying selection contribute to the volution of downy mildew resistance at the RPP8 locus of Arabidopsis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cooley M.B., Pathirana S., Wu H.-J., Kachroo P., Klessig D.F.; "Members of the Arabidopsis HRT/RPP8 family of resistance genes confer resistance to both viral and oomycete pathogens."; plant Cell 12:653-676(2008)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=cv Columbia,
MEDLINE=2259850; PubMed=14593172;
MEDLINE=22598850; PubMed=14593172;
Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
Karlin-Newmann G., Liu S.K., Lam B., Sakano H., Wu T., Yu G.,
Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
Chao Q., Choy N., Edju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8W4_09; Q8GWG5; Q9M5A1; Q9ZSY3; Q9ZSY4;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Disease resistance protein RPP8 (Resistance to Peronospora parasitica protein 8).
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPDB OR HRI OR ATSG43470 OR WWF20.19.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis virializanae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Columbia;
MEDDINDE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISOFORM 1), FUNCTION, MUTANTS RPP8-1; RPP8-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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STRAIN-scv. COlumbia, and cv. Landsberg erecta;
STRAIN-scy. COlumbia, and cv. Landsberg erecta;
MEDLINE-99030133; PubMed-9811794;
MCDOWell_J.M., Dhandaydham M., Long T.A., Aarts M.G.M., Goff;
                                                                                                                                                                                                                             Length 908;
                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                          3111991B17239693 CRC64;
                                                                                                                                                                                                                     Score 34; DB 1;
Pred. No. 54;
?, Mismatches
                            LRR 1.
LRR 2.
LRR 3.
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS.
   NB-ARC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. Di-17;
MEDLINE=20271766; Pubmed=10810142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                             104448 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant Cell 10:1861-1874(1998).
                                                                                                                                                                                                                             63.0%;
                                                                                                                                                                                                                                                     60.0%;
                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                             883 EKLVPGGEDY 892
                                                                                                                                                                                                                                                                                                                                                           1 EEVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Res. 7:31-63(2000)
                                                                                                                                                          908 AA;
                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conser
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pathogen recognition.

-! MISCELLANDOUS: In cv. Columbia and cv. Landsberg erecta, RPPB specifically recognizes the Emcos avirulence protein from Peronospora parasitica, while it is not the case in cv. Di-17, where it confers resistance to Turnip Crinkle Virus uppon recognition of the viral capsid protein.
-! SIMILARITY: Bongs to the disease resistance NB-LRR family. RPPB/HRT subfamily.
-! SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
-! SIMILARITY: Contains 1 NB-ARC domain.
-! DATABASE: NAME-NIB-LRRS,
NOTE-Functional and comparative genomics of disease resistance gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20496823; PubMed=11041886;
Ren T., Qu F., Morris T.J.;
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Note=Has been shown to exist only in cv. Columbia so far;
Note=Has been shown to exist only in cv. Columbia so far;
DOMAIN: The LRR repeats probably act as specificity determinant of
pathogen recognition.

POLYMORPHISM: The strong polymorphisms present in cv. Di-17 and
cv. Columbia are probably due to an unequal crossing-over between
the highly related RPBs and RPHBA genes present in cv. Landsberg
erecta. Such variations probably modify the specificity of
Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T., Satou M., Tames R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y. Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R., "Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                       STRAIN=CV. Columbia;
Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Seki M., Iida K., Kamnya A., Narusaka M., Carninci P., Kawai J.,
Hayashizaki Y., Shinozaki K.;
"Arabidopsis thaliana [ull-length cDNA.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    defense response.
SUBUNIT: Interacts with the NAC protein TIP.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q8W4J9-1; Sequence=Displayed;
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WWW="http://niblrrs.ucdavis.edu".
                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 2)
                                                                                                                                                               Science 302:842-846(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTION WITH TIP.
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EMBL, AY062514; AAL32592.1; -. EMBL; AK118862; BAC43449.1; -. InterPro; IPR000767; Disease_resist.

EMBL; AF089710; AAC83165.1; -. EMBL; AF089711; AAC78631.1; -.

EMBL; AF234174; AAF36987.1; EMBL; AB025638; BAA97426.1;

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GKGV -> EKGI (in cv. Landaberg erecta).

C -> R (in cv. Landaberg erecta).

C -> R (in cv. Landaberg erecta).

F -> L (in cv. Landaberg erecta).

C -> Q (in cv. Di-17).

G -> Q (in cv. Di-17).

Y -> S (in cv. Di-17).

R -> P (in cv. Di-17).

R -> P (in cv. Di-17).

R -> P (in cv. Di-17).

R -> F (in cv. Di-17).

R -> F (in cv. Di-17).

R -> F (in cv. Di-17).

R -> K (in cv. Di-17).

A -> V (in cv. Di-17).

A -> V (in cv. Di-17).

A -> V (in cv. Di-17).

A -> V (in cv. Di-17).

C -> S (in cv. Di-17) and cv. Landaberg erecta).

C -> R (in cv. Di-17 and cv. Landaberg erecta).

C -> R (in cv. Di-17 and cv. Landaberg erecta).

C -> R (in cv. Di-17 and cv. Landaberg erecta).

C -> R (in cv. Di-17 and cv. Landaberg erecta).

C -> R (in cv. Di-17 and cv. Landaberg erecta).
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T -> I (in cv. Di-17).
S -> R (in cv. Di-17).
S -> R (in cv. Di-17).
H -> Q (in cv. Di-17).
I -> L (in cv. Landsberg erecta).
X -> N (in cv. Landsberg erecta).
X -> N (in cv. Landsberg erecta).
PRFEEDYW -> WDBDFG (in cv. Landsberg
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WRMLLTSRNEGVGIH -> BLLWYIHEALFLLNS (in
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I -> K (in cv. Di-17 and cv. Landsberg
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Y -> P (in cv. Di-17).

S -> Y (in cv. Landsberg erecta).

C -> S (in cv. Di-17 and cv. Landsberg
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A -y ( in cv. Landsberg erecta).

E -> Q (in cv. Landsberg erecta).

DATLSWQ -> NKYLRYH (in cv. Di-17).

NKLSWQ -> NKYLRYH (in cv. Landsberg erecta).

WQ -> SH (in cv. Landsberg erecta).
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And Control 10:1861-1874(1998).

1. Plant Cell 10:1861-1874(1998).

2. I PROCITION: Disease resistance protein. Resistance proteins guard the plant against pathogens that contain an appropriate avirulence protein via an indirect interaction with this avirulence protein. That triggers a defense system including the hypersenative response, which restricts the pathogen growth. In contrast to RPPB, it does not specifically recognize the Emco5 avirulence protein from Peronospora parasitica.

2. INSTRILANBOUS: In cv. Columbia and cv. Di-17, this protein is not present due to an unequal crossing over between the RPPB and RPBHA genes that creates a unique RPPB gene.

3. INILANITY: Belongs to the disease resistance NB-LRR family.

3. SIMILANITY: Contains 2 leucine-rich (LRR) repeats.

4. SIMILANITY: Contains 1 NB-ARC domain.

5. INILANESE: NAME=NIB-LRRS;

6. III DATABASE: NAME=NIB-LRRS;

6. II DATABASE: NAME=NIB-LRRS;

6. III NDATABASE: NAME=NIB-LRRS;

6. III NDATABASE: NAME=NIB-LRRS;
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STRAIN=cv. Landsberg erects;
MEDLINES99030193; Pubmed=9811794;
MCDOWell J.M., Dhandsycham M., Long T.A., Aarts M.G.M., Goff S.,
Holub B.B., Dangl J.L.,
Holub B.B., ceombination and diversifying selection contribute to the evolution of downy mildew resistance at the RPP8 locus of Arabidopsis.";
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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63.0%; Score 34; DB 1; Length 908; 60.0%; Pred. No. 54; ive 2; Mismatches 2; Indels
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InterPro; IPR000767; Disease_resist.
InterPro; IPR001611; LRR.
InterPro; IPR001611; LRR.
Ffam; PF00560; LRR; 2.
Pfam; PF00560; LRR; 2.
Pfam; PF00511; NB-RR; 1.
PRINTS; PR00364; DISEASERSIST.
Plant defense; ATP-binding; Repeat; Leucine-rich repeat.
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146 459 NB-ARC.
602 625 LRR 1.
844 669 LRR 2.
192 199 ATP (POTENTIAL).
910 AA, 105263 MW, 5BIB9F65A19A12EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-8003 (Rel. 42, Last annotation update)
RPH8A.
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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
SUTRAIN=JAL-1 / DSM 2661 / ATCC 43067;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake O.A., FitzGerald L.M., Clayton R.A., Goodyne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kellley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borrodovsky M.,
Klerk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
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InterPro; IPR01163; SDRNP Sm.
InterPro; IRR05358; UPF0153.
Pfam, PF03692; UPF0153; ...
Hypothetical protein; Complete proteome.
SEQUENCE 276 AA; 33454 MM; 97BD69D392BC8FDF CRC64;
                                                                                                                                                                                                                                                                                   Methanococcus jannaschii.
Archaea; Buryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
NCBI_TaxID=2190;
                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-COT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ0939.
276 AA
    PRT;
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STANDARD;
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Search completed: June 3, 2004, 11:49:53 Job time : 4.86667 secs

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SEQUENCE FROM N.A.
STRAIN=FY1679;
MEDLINE=94169519; PubMed=7764548;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 EEVVPXGMDYS 11
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Q88cc0 Q8k143 1 Q9kv42 (Q9x382 Q9y813	083192 083192 08x215 08x215 09x617 09x617 017704 052673		088733 0807,0 09yet8 07uf95 02950 029920
Q88CC0 Q8KL43 Q9XVK4 Q9A382 Q9YFI3	Q83L92 Q52680 Q8XZL5 Q946J7 Q95P46 Q9U6A3 Q17704	052666 027146 027146 08TBJT 08TBJT 08E5L9 08DZW9 07V6Q4	Q8GP33 Q8U7U0 Q9YET8 Q7UF95 Q815A7 Q29920
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ALIGNMENTS

MEDLINE=94019318; PubMed=8413243; Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlendy G., Saccharomyces cerevisiae (Baker's yeast). Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces. "CYC2 encodes a factor involved in mitochondrial import of yeast De haan M., Grivell L.A., Maarse A.C.; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases SEQUENCE FROM N.A. STRAIN=FY1679; De haan M., Maarse A.C., Grivell L.A.; Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases MIPS; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases Last sequence update) Last annotation update) 156 AA Created) Mol. Cell. Biol. 13:6442-6451(1993). PRT;

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SEQUENCE FROM N.A.
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STRAINS-HTB831 / DSM 14371 / JCM 11309;
MEDLINE=22220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
"Molecular cloning of a gene, DHS1, which complements a drug-hypersensitive mutation of the yeast Saccharomyces cerevisiae.";
Biosci. Biotechnol. Blochem. 58:391-395 (1994).
EMBL; Z74920; CAA99201.1; -.
EMBL; X74319; CAA60762.1; -.
PIRS; S54619; S54619.
SGD; S0005539; YOR013W.
SEQUENCE 156 AA; 17881 MW; 380442B74C272B41 CRC64;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
NCBI_TaxID=182710;
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STRAINS-VC-16 / DSM 4304 / ATCC 49558;
MEDINE-8049343; PubMed-9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.4%; Score 38; DB 16; Length 319; 60.0%; Pred. No. 18; tive 3; Mismatches 1; Indels
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74.1%; Score 40; DB 3; Length 156;
Best Local Similarity 77.8%; Pred. No. 3;
Matches 7; Conservative 1; Mismatches 1; Indels
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InterPro; IPR001279; Blactmase-like.
Pfan, PF00753; lactamase_B; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 319 AA; 35617 MW; 3BDAE4BF13E79E37 CRC64;
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Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein AF2411.
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1-MAR-2003 (TrEWBLrel. 23, Last sequence update)
01-JUN-2003 (TrEWBLrel. 24, Last annotation update)
Hypothetical conserved protein.
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Best Local Similarity 60.0°
Best Conservative
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189 EQLVPHGIDY 198
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WEDLINE=222214; PubMed=12240834;

WEDLINE=222214; PubMed=12240834;

WARAMURA Y., Kaneko T., Saco S., Ikeuchi M., Katoh H., Sasamoto S.,

WA tanabe A., Iriguchi M., Kawashina K., Kimura T., Kishida Y.,

Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N.,

Kiyokawa C., Kohara M., Takeuchi C., Yamada M., Tabata S.;

Kiyokawa C., Kohara M., Takeuchi C., Yamada M., Tabata S.;

"Complete genome structure of the thermophilic cyanobacterium

Thermosynechococcus elongatus BP-1.";

DNA Res. 9:123-130 (1002).

RMBL; AP005374; BAC09170.1; -.

GO; GO:0005215; Fitransporter activity; IEA.

GO; GO:0005115; Fitransporter activity; IEA.

GO; GO:0005115; Fitransporter activity; IEA.

GO; GO:00051215; Fitransporter activity; IEA.

RO; GO:000510; Pitransporter activity.

RD; RD; PRO01036; Acrflvin_res.

Pfam; PR00873; ACR tran; I.

Pfam; PR00873; ACR tran; I.

PR PRINTS; PR00702; ACRIFLAVINRP.
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Karlavage A.K., Graham D.B., Kyrpides N.C.,
Peterson S., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McKeil L.K., Badger T.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Wencer J.C.,
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                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.4%; Score 38; DB 17; Length 363; 54.5%; Pred. No. 20; 2; Indels tive 3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002103; Bac_luciferase.
Pfam; PR00296; bac luciferase; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 363 AA; 41736 MW; 05976BAE788F4803 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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PIR; D69551; D69551.
TIGR; AF2411; -.
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les 6; Conservative
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843 EEVLPNGIGYS 853
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Q8W568;
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STRAIR=V883 (AFCC 700802;
STRAIR=22550857; PubMed=12663927;
Paulsen IT., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R.,
Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Daugherty S., Dedson R.T., Umayam L., Brinkac L., Beanan M.,
Daugherty S., Dedson R.T., Durkin S., Kolonay J., Madugu R., Nelson W.,
Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
Enterococcus faecalis."
                                                                                                                                                                                                                      Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBL_TaxID=1351;
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Pepermatophyta; Magnoliophyta; eudicoryledons; core eudicots; rosids;
eurosids II; Sapindales; Rutaceae; Citrus.
NCBL_TaxID=55188;
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                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Large conductance mechanosensitive channel protein.
MSCL OR EF3152.
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Last annotation update)
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GO; GO:0016020; C:membrane; IEA.

GO; GO:0005216; F:non channel activity; IEA.

GO; GO:0006810; P:transport; IEA.

GO:0006810; P:transport; IEA.

InterPro; IPR001185; MS_channel.

Pfam; PF01741; MsCL; 1.
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01-JAN-1998 (TrEMBLrel. 05, Last seque)
01-JUN-2003 (TrEMBLrel. 24, Last annot
Sucrose-phosphate synthase (Fragment)
                                                                   PRT;
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ProDom; PD007253; MS_channel; 1.
TIGRFAMS; TIGR00220; mscL; 1.
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Best Local Similarity 70.0
Matches 7; Conservative
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                                                                PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                Q82ZB4
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                   RESULT 5
                                          282ZB4
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STRAIN=cv. Miyagawa-Wase; TISSUE-Juice sacs and segment epidermis; Komatsu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.; "Differential expression of three sucrose-phosphate synthase isoforms during sucrose accumulation in citrus fruits (Citrus unshiu Marc.)."; EMBL; AB006319; BAA23215.1; -. PIR: $72649; $72649.

NOW TER 1 1 1

NOW TER 341 341

SEQÜENCE 341 AA; 38136 MW; 61417A69C4560777 CRC64;
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Komatsu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.;

Komatsu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.;

"Differential expression of three sucrose-phosphate synthase isoforms during sucrose accumulation in citrus fruits (Citrus unshiu Marc.).";

BMBL; AB006660; BAA22071.1;

PIR, $72650; $72650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Citrus unshiu (Satsuma orange).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids;
eurosids II; Sapindales; Rutaceae; Citrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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TISSUE-Juice sacs and segment epidermis;
MEDLINE=96439842; PubMed=8842155;
KOMATSU A., Takanokur Y., Omura M., Akihama T.;
"Cloning and molecular analysis of cDNA encoding three sucrose phosphate synthase isoforms from a citrus fruit (Citrus unshiu
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                                                                                                                                                                                                                                                                                                     Length 341;
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348 AA; 38556 MW; EEIC21EBA6FF5C5E CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Sucrose-phosphate synthase (Fragment).
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Last annotation update)
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66.7%; Pred. No. 51;
trive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                   66.7%; Score 36; DB 10;
66.7%; Pred. No. 50;
ative 2; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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234 VIPPGMDFS 242
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Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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VIPPGMDFS 422
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                                                                                                                                                                                                                                                                                                        Kim C.J., Chen H., Cheuk R., Shinn P., Banh J., Bowser L.,
Kim C.J., Chen H., Cheuk R., Shinn P., Banh J., Bowser L.,
Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Lin J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
Palm C.J., Quach H.L., Sakurai T., Sacou M., Seki M., Southwick A.,
A Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
Shinozaki R., Davis R.W., Theologis A., Ecker J.R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
Brail, A419806; AA131981.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RBL, A4419806; AA131981.;
RBL, A4419806; AA131981.;
RBL, A7411904; AAM47552.;
RBL, A741104; Pept Sale.
RGO; GO:000558; P:prolyl oligopeptidase activity; IEA.
RGO; GO:000558; P:proclysis and peptidolysis; IEA.
RICEPPO; IPRO02471; Pept Sale.
                                                                                                   SEQUENCE FROM N.A.

Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,

Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,

Bowser L., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,

Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,

Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,

Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,

Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAINSCY. Columbia, MEDIATIZ; Federspiel N.A., Kaul S., MEDLINE=210(719); PubMed=11130712; Federspiel N.A., Kaul S., MEDLINE=210(6719); Palm C.J., Federspiel N.A., Kaul S., White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., Buehler E., Chan A., Chao Q., Chen H., Chauk R.F., Chin C.W., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujil C.Y., Gill J.E., Goldmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L., Khunter J.L., Jenkins J., Johnson C., Khan S., Khan S., Khan B., Kwan A., Lam B.,
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta,
Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots; rosids;
eurosids II, Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryoča; Viridiplantee; Strepcophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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                                                                                                                                                                                                                                    Ecker J.R.;
"Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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49682 MW; A159955B21742C4A CRC64;
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Last sequence update)
Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2003 (TrEMBLrel. 25,
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es 7; Conservative
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Q9C9T7;
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Q9C9T7
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Sugiharto B., Sakakibara H., Sugiyama T.,
Sugiharto B., Sakakibara H., Sugiyama T.,

"Differential Expression of Two Genes for Sucrose-Phosphate Synthase
RT is Sugarcane: Nolecular Cloning of the cDNAs and Comparative Analysis
of Gene Expression.",

"Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

"REML, PAR01337) P. Lansferase activity, transferring glycosyl. ., IEA.

"OG GO:00046524; F: Sucrose-phosphate synthase activity, IEA.

"OG GO:00046524; F: Sucrose-phosphate synthase activity, IEA.

"OG GO:0009058; P: Sucrose-phosphate synthase activity, IEA.

"OR GO:0009058; P: Sucrose-phosphate synthase activity, IEA.

"Refam, PR00534; Glycos transferase."

"Refam, PR00534; Glycos transferase."

"Mycosyltransferase; Transferase."

"Mycosyltransferase; Transferase."

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"SEQÜENCE 1047 AA, 116379 MW, DOEDB34961BIDB3D CRC64;
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Saccharum.
Langin-Hooper S., Lee A., Lee J.W., Lenz C.A., Li J.H., Li Y.-P., Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A., Miltscher J., Miranda M., Niguyen M., Nierman W.C., Osborne B.I., Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley B. Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M., Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysotskala V.S., Walker M., Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.7%; Score 36; DB 10; Length 460; 70.0%; Pred. No. 70; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                   Mature 408 a16-820 (2000).

EMBL, AC012679; AAG52073.1; -.

DI, G96764; G96764.

G0, G0:003824; F:catalytic activity; IEA.

G0; G0:0003828; F:prolyl oligopeptidase activity; IEA.

G0; G0:006598; F:prolyl oligopeptidase activity; IEA.

G1; G0:006598; F:procelysis and peptidolysis; IEA.

InterPro; IPR00377; Pept S9 AS.

PROSITE; PS00708; PRO ENDOPEP_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein. -
SEQUENCE 460 AA; 50564 MW; B94B27B5C4B249EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14) (Fragment)
SOSPS1.
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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les 7; Conserv
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01-UUN-2002 (TrEMBLrel. 21, Created)
01-UUN-2002 (TrEMBLrel. 21, Last sequ
01-UUN-2003 (TrEMBLrel. 24, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Putative sucrose-phosphate synthase.
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                                                                                                                                                                                              66.7%;
                                                                                                                                                                      Query Match Best Local Similarity 60...
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453 VIPPGMDFS 461
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Q9GQ04;
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Q8S064
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BU Arabidopsis sequencing project;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AL049487; CAB39764.1;

EMBL; AL049487; CAB39764.1;

PIR, T04062; T04062.

PIR, T04062; Fructose-phosphate synthase activity; IEA.

GO; GO:0046575; Fructose-phosphate synthase activity; IEA.

GO; GO:00106757; Fructose-phosphate synthase activity; IEA.

GO; GO:0010757; Fructose
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                                                                            01-MAY-2000 (TEMBLrel. 13, Created)
01-MAY-2000 (TEMBLrel. 13, Last sequence update)
01-MNY-2000 (TEMBLrel. 24, Last sequence update)
01-MN-2003 (TEMBLrel. 24, Last annotation update)
Sucrose-phosphate synthase-like protein (EC 2.4.1.14).
F28M11.40 OR AT4G10120.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
Mayer K.F.X., Lemcke K., Schueller C.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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GO; GO:0004459; F:L-lactate dehydrogenase activity; IEA.
GO; GO:0009058; P:biosynthesis; IEA.
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EU Arabidopsis sequencing project;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
Sucrose phosphate synthase.
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66.7%; Pred. No. 1.8e+02;
tive 2; Mismatches 1;
                           PRT; 1083 AA.
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Best Local Similarity 66.77
6; Conservative
                           PRELIMINARY;
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NCBI_TaxID=3702;
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243010
08N36
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatochyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enthartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                      Score 36; DB 10; Length 1084;
Pred. No. 1.8e+02;
2; Mismatches 1; Indels 0
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Sasaki I., Matsumoto T., Yamamoto K.;
"Orrya sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0678F11.";
Submitted (MAR-201) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003437; BAB86107.1; -
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Na+/K+/201-cocransporter (Fragment).
Eriocheir sinensis (Chinese mitten crab).
Eriocheir sinensis (Chinese mitten crab).
Bukaryoca; Meazoa; Arthropoda; Crustaceas; Malacostraca;
Bubracchyura; Bucarida; Decapoda; Pleocyemata; Brachyura;
Bubrachyura; Grapsoidea; Varunidae; Eriocheir.
GO, GO:0006096; P:glycolysis; IEA.
InterPro; IPR001296; Glyco_trans_1.
InterPro; IPR001557; L.LDH.
Pfam; PF00534; Glycos_transf_1; 1.
PROSITE; PS00644; L.LDH; 1.
SEQUENCE 1084 AA; 119417 MW; 4D0D79AFEDD2F92B CRC64;
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GO; GO: 0004459; F:L-lactate dehydrogenase activity; IEA.
GO; GO: 0009058; P: biosynthesis; IEA.
GO; GO: 0006096; P:glycolyais; IEA.
InterPro; IPR001296; Glyco_trans_1.
InterPro; IPR001297; L_LDH.
Pfam; PF0054; Glycos transf_1; 1.
PROSITE; PS00064; L_LDH; 1.
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SEQUENCE FROM N.A.
MEDLINE=21664373; PubMed=11792842;
Shimizu T., Ohteni K., Hirakawa H., Ohthima K., Yamashita A.,
Shimizu T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic flesh-eater."
Weihrauch D., Towle D.W.; Mark/Marker are expressed in Mark/Hi-exchanger and Nark/K+/2Cl- -cotransporter are expressed in gills of the euryhaline Chinese crab Eriocheir sinensis."; Comp. Biochem. Physiol. 126:S158-S158(2000).
MEBL; AR301160; ARG39938.1; -. NON TER.
                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium perfringens.
Bacteria, Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium:
NCBI_TaxID=1502;
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                                                                                                                                                Query Match 64.8%; Score 35; DB 5; Length 219; Best Local Similarity 75.0%; Pred. No. 49; Matches 6; Conservative 1; Mismatches 1; Indels
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EMBL; AP003185; BAB79763.1; -
GO; GO:0003824; F:carelytic activity; IEA.

InterPro; IPR000205; MoeB.
InterPro; IPR00025; NAD BS.
InterPro; IPR000594; ThiF_domain.

Pfam, PF00899; ThiF; Complete protecome.

SEQUENCE 253 AA; 27714 MW; 814DF79D3B0D7486 CRC64;
                                                                                                219 219 219 219 219 AM; 599442DA26F0D3F1 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                     253 AA
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CPE0057.
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Search completed: June 3, 2004, 11:57:33 Job time: 29.8667 secs

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Claim 17; Page 65; 69pp; English
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Maximum Match 100%
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1 EEVVPXGMDYS 11
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ALIGNMENTS

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Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                               Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41
                                                                                                                                                                                                                                                                                                                                                                               'note= "N-terminal acetyl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "D-form residue"
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ABB80561 standard; peptide; 11
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                                                                                                  (first entry)
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Sequence 11 AA;

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence represents a peptide compound of the invention having hepatitis C virus (HCW) protease inhibitory activity. The peptides of the invention are alpha-ketcomide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCW protease. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4
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                                                                                                                                                   96.3%; Score 52; DB 5; Length 11; 100.0%; Pred. No. 0.0024; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "N-terminal acetyl"
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                                                                                                                                                                                    11; Conservative
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                                                                                                                                                                                                                                               EEVVPXGMDYS
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                                                                                                                                                                     Local Similarity
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                                                                                                                         Sequence 11 AA;
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pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus

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                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9.
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DB 5; Le...
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Pred. No. 0.0024;
0; Mismatches 0; Indels
       Score 52; DB Pred. No. 0.00; Mismatches
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                                                                                                                                        ABB80529 standard; peptide; 11 AA.
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100.0%; Pre
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      96.3%;
ilarity 100.0%;
Conservative 0
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                                                       1 EEVVPXGMDYS 11
                                                                            EEVVPXGMDYS 11
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Best Local Similarity
Matches 11; Conserv
                    Similarity
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Modified-site
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ABB80529
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to breat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "N-terminal acetyl"
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EEVVPXGMDYS 11
                                              EEVVPXGMDYS 11
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protease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                virus
                                                                           Hepatitis C virus, HCV, serine protease; inhibitor; alpha-ketoamide;
virucide.
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                                                          Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #42
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                                                                                                                                                                         'note= "N-terminal acetyl"
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                                    (first entry)
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Best Local Similarity
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                                                                                                                                                  Key
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                                                                                                                        Synthetic.
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          ABB80562;
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Gaps

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ABB80562 standard; peptide; 11 AA.

RESULT 5 ABB80562 ID ABB8

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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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Pred. No. 0.023;
0; Mismatches
                              'note= "N-terminal acetyl"
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Location/Qualifiers
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ilarity 90.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                         (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-361643/39.
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                Misc-difference 9
                                                                                                Misc-difference
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                                                                                                                                                                                       /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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                                               Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
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virucide.
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                Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #22
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                                                                                                                                    Location/Qualifiers
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90.9%;
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Matches 10
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ABB80543;

ABB80543 RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                             ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
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                                 /note= "C-terminal amide"
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          'note= "D-form residue"
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                                                                                                                                                      (CORV-) CORVAS INT INC
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es 10; Conserv
Misc-difference 9
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Matches
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                                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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                                                                                                                                                                                                                                                                                                                                          Score 46; DB 5; Length 11;
Pred. No. 0.036;
0; Mismatches 1; Indels
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                                                                                    Brunck TK;
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                                                                                                                                                                                      Claim 17; Page 64; 69pp; English
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          19-JUL-2001; 2001WO-US023169.
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Best Local Similarity 90.5
Matches 10; Conservative
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                                                                                    Lim-Wilby M, Levy OE,
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                                                             (CORV-) CORVAS INT INC
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                 peptide compound having hepatitis C virus protease inhibitory ity useful for treating disorders associated with hepatitis C virus
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                                                                                   Claim 17; Page 65; 69pp; English
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          WPI; 2002-361643/39
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les 10; Conser
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(first entry)

carbonyl forming keto-amide linkage with

note= "N-terminal acetyl"

/note= "Norvalyl residue 7"

Location/Qualifiers

'note= "C-terminal amide"

The sequence represents a peptide compound of the invention having

Brunck

Levy OE,

2000US-0220101P.

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hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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Pred. No. 0.036;
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90.9%;
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Best Local Similarity 90.9
Matches 10; Conservative
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Length 11;

Score 46; DB 5; Pred. No. 0.036; Mismatches

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ABB80547;

RESULT 13

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virucide.

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have viruside activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                    /note= "2-aminoisobutyry1 carbony1 residue forming a keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
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                                                                                                                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46
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Pred. No. 0.036;
0; Mismatches
                                                                                                                                                                                                                                                                        'note= "N-terminal acetyl"
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                               ABB80566 standard; peptide; 11 AA.
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Norvalyl carbonyl forming keto-amide linkage with residue ?"
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                   Length 11;
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                 Score 46; DB 5;
Pred. No. 0.036;
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90.9%;
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Matches 10; Conservative
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                                                                                 1 EEVVPXGMDYS 11
                                                                                                              EEVVPXGMSYS 11
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activity usefu
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                           /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                     Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
Hepatitis C virus, HCV, serine protease, inhibitor, alpha-ketoamide, virucide.
                                                                                            'note= "N-terminal acetyl"
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                                                                 Location/Qualifiers
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                                                                                                                                                   Misc-difference
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., Score 46; DB 5; Length 11; Pred. No. 0.036; 0; Mismatches 1; Indels 85.2%; 90.9%; Query Match
Best Local Similarity 90.9
Matches 10; Conservative ð

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Search completed: June 3, 2004, 11:48:24 Job time: 46.9333 secs

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TYPE: PRT; ORGANISM: Enterococcus faecalis US-09-134-000C-4848
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Sequence 4, Appli
Sequence 24, Appli
Sequence 10, Appl
Sequence 11, Appl
Sequence 7, Appli
Sequence 7, Appli
Sequence 1, Appli
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Sequence 82
Sequence 31
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Sequence 1
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-853-948B-4

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US-09-697-367-24

US-09-394-272-10

US-08-429-054A-11

US-08-129-12-28

US-09-051-341-7

US-09-394-272-8

US-09-394-272-9

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Maximum Match 100%
Listing first 45 summaries
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No.
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Sequence 4848, Application US/09134000C
; Fatent No. 6617156
; General No. 6617156
; General No. 6617156
; General No. 6617156
; General No. 6617156
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; FRIOR APPLICATION NUMBER: US 60/055,778
; FRIOR APPLICATION NUMBER: US 60/055,778
; FRIOR PILING DATE: 1997-08-15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4848
; LINGTH: 181
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Sequence 4, Application US/08853948B
Parent No. 6210943
GENERAL INFORMATION:
APPLICANT: AKIHAMA: TOYOTA
TITLE OF INVENTION: THE SAME
TITLE OF INVENTION: THE SAME
TITLE OF INVENTION: THE SAME
TITLE OF INVENTION: THE SAME
TITLE OF INVENTION: THE SAME
TITLE OF INVENTION: THE SAME
TITLE OF INVENTION: THE SAME
TITLE OF INVENTION: THE SAME
TITLE OF INVENTION: THE SAME
TITLE OF INVENTION: THE SAME
TITLE OF INVENTION: THE SAME
THE SEPREMENT FILING DATE: 1997-05-09
NUMBER OF SEC ID NOS: 10
SECTION A
LENGTHARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 341
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                              Sequence 4, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 21, Appli
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 21, Appl
Sequence 21, Appl
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Sequence 2
Sequence 2
         Sequence
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OCGANISM: Citrus unshiu

FEATURE:
OTHER INFORMATION: Xaa at position 109 is one of Ala, Arg, OTHER INFORMATION: Cys, Gln, Glu, Gly, His, Ile, Leu, Lys,
US-06-580-988A-23
US-08-460-694-4
US-08-460-644-4
US-08-193-977-7
US-08-193-977-7
US-08-246-361A-21
US-08-246-361A-21
US-08-246-361A-21
US-08-464-517-22
US-08-464-517-22
US-08-464-31A-22
US-08-464-31A-22
US-08-463-772-22
US-08-926-8458-21
US-08-926-8458-21
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Patent No. 621043

Patent No. 621043

GENERAL INFORMATION:

APPLICANT: AKKHAMA, Toyota

TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE FROM CITRUS AND DNA ENCODING

TITLE OF INVENTION: THE SAME

FILE REFERENCE: 0049-0235-0

CURRENT FILING DATE: 1997-05-09

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5

LENGTH: 348

TYPE: PRT

CORRANISM: CITLUS UNShiu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 3; Length 348;
Pred. No. 22;
                                                 Length 341;
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                                                                                  1; Indels
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APPLICANT: Claim, Perry G.
APPLICANT: Claim, Perry G.
APPLICANT: Tarczynaki, Mitchell
TITLE OF INVENTION: SUGGOSE PHOSPHATE SYNTHASE
TITLE OF INVENTION: SUGGOSE PHOSPHATE SYNTHASE
TITLE OF INVENTION: SUGGOSE PHOSPHATE SYNTHASE
TITLE OF INVENTION: BULD ON 10-10-26
CURRENT FILING DATE: 200-10-26
PRIOR FILING DATE: 1998-MAY-07
PRIOR FILING DATE: 1999-MAY-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: MICROSOFT OFFICE 97
SEQ ID NOS: 24
SEQ ID NO 24
LENGTH: 368
; OTHER INFORMATION: Pro, Ser, Thr, Trp, Tyr, or Val
US-08-853-948B-4
                                                 DB 3;
22;
                                               Score 36; DB 3
Pred. No. 22;
2; Mismatches
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Patent No. 6323015
GENERAL INFORMATION:
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                                              h 66.7%;
Similarity 66.7%;
6; Conservative ;
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Best Local Similarity 66.7
Matches 6; Conservative
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234 VIPPGMDFS 242
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Best Local Similarity
Matches 6; Conserv
                                               Query Match
Best Local Similarity
Matches 6; Conserv
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ORGANISM: Zea mays
                                                                                                                                                                                                        RESULT 3
US-08-853-948B-5
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US-08-429-054A-11

Sequence 11, Application US/08429054A

Patent No. 5917126

GENERAL INFORMATION:
APPLICANT: VAN ASSCHE, CHARLES; LANDO, DANIELLE; BRUNEAU,
APPLICANT: VAN ASSCHE, CHARLES; LANDO, DANIELLE; BRUNEAU,
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHETASE (SPS),
TITLE OF INVENTION: A PREPARATION METHOD AND CDNA THEREFOR, AND USE OF THE
TITLE OF INVENTION: CDNA FOR MODIFYING SPS EXPRESSION IN PLANT CELLS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN AND MUSERLIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
Sequence 10, Application US/09394272

Sequence 10, Application US/09394272

Patent No. 6472588

GENERAL INFORMATION:
APPLICANT: Halagler, Candace H.
APPLICANT: Halagler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED FILE REPERENCE: 201304/1.000

CURRENT APPLICATION NUMBER: US/09/394,272

CURRENT PILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 10.
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FILING DATE: 26-APR-1995
CIASSIFCATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 842,337
FILING DATE: 20-March-1992
APPLICATION NUMBER: PCT/FR 91/00593
FILING DATE: 18-UALY-1991
CIASSIFICATION DATA:
APPLICATION NUMBER: French 90402094.9
FILING DATE: 20-UALY-1990
CIASSIFICATION NUMBER: French 90402094.9
FILING DATE: 20-UALY-1990
ATTORNEY/AGENT INFORTATION: 800
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NAME: Charles A. Muserlian
REGISTRATION NUMBER: 19,683
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FELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 600 THIRD AVENUE CITY: NEW YORK STATE: NEW YORK
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Matches 6, Conservative
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ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY 1
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ORGANISM: Oryza sativa
US-09-394-272-10
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435 VIPPGMDFS 443
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66.7%; Score 36; DB 2; Length 1068;
Best Local Similarity 66.7%; Pred. No. 81;
Matches 6; Conservative 2; Mismatches 1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
COMPUTER: IEB PC compatible
OPERATURG SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,777
FILING DATE: NOT YET ASSIGNED
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/175,471
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BATDATA RAB-VENCET
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 32,750
REJERHONE: (415)328,4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Law Offices of Barbara Rae-Venter STREET: 260 Sheridan Avenue, Suite 440 CITY: Palo Alto STATE: California COUNTRY: USA ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08718777
Patent No. 5981852
GENERAL INFORMATION:
APPLICANT: Van Assche, C.
APPLICANT: Lando, D.
APPLICANT: Brancau, J. M.
APPLICANT: Gervais, M.
TITLE OF INVENTION: PHOSPHATE
TITLE OF INVENTION: PHOSPHATE
TITLE OF INVENTION: SYNTHASE IN PLANTS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Barbara Rae-Venter
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1068 amino acids TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                      TYPE: Amino acid
STRANDEDNESS: Single
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-429-054A-11
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3 VVPXGMDYS 11

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Sequence 7, Application US/09051341

Patent No. 6124528

GENERAL INFORMATION:

TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING

TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE:

TUTLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE:

MUMBER OF SEQUENCE: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE:

ADDRESSEE:

CORRESPONDENCE: 1200 STATEM:

COUNTRY: USA

ZIP: 94306

CONTYRY: USA

ZIP: 94306

COMPUTER READALE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

COMPATIBLE

COMPATIBLE

COMPATIBLE

COMPATIBLE

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US-09-394-272-8

Sequence 8, Application US/09394272

Sequence 8, Application US/09394272

Sequence 8, Application US/09394272

Sequence 8, Application US/09394272

APPLICANT: Haigler, Candace H.

APPLICANT: Haigler, Scott

TITLE OF INVENTION: TRANSENIC FIBER PRODUCING PLANTS WITH INCREASED

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

FILE REFERRINCE: 201344/1000

CURRENT APPLICATION NUMBER: US/09/394,272

CURRENT FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 14
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/051,341

FILING DATE:

CLASSIFICATION NUMBER: US/09/051,341

FILING DATE:

APPLICATION NUMBER: US/09/051,341

FILING DATE: 25-0CT-1996

APPLICATION NUMBER: US 08/549,016

FILING DATE: 27-0CT-1996

APPLICATION NUMBER: US 08/549,016

FILING DATE: 12-0AN-1995

ATTORNEY/AGENT INFORMATION:

NAME: BATDATA Rae-Venter: Ph.D.,

REGISTRATION NUMBER: 32,750

REGISTRATION NUMBER: 32,750

REGISTRATION NUMBER: GGNE.110.02US

TELEPHONE: (415)328-4400
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 66.7
Matches 6; Conservative
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roPOLOGY: linear
rowwcoll TYPE: protein
US-09-051-341-7
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453 VIPPGMDFS 461
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US-09-394-272-9
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ZIP: 19103
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TYPE: PRT
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| Sequence 11, Application US/09394272
| Patent No. 6472586
| GENERAL INFORMATION:
| APPLICANT: Haigler, Candace H. APPLICANT: Haigler, Candace H. APPLICANT: Holdady, A. SCENCE PRODUCING PLANTS WITH INCREASED TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE FILE REPERENCE: 201304/1000
| CURRENT APPLICANTON NUMBER: US/09/394,272
| CURRENT PILING DATE: 1999-09-10
| NUMBER OF SEQ ID NOS: 14
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 11
| LENGTH: 1083
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Sequence 4, Application US/09394272

Sequence 4, Application US/09394272

Sequence 4, Application US/09394272

Sequence 4, Application US. 647258

Sequence 4, Application

APPLICANT: Haigler, Candace H.

APPLICANT: Haigler, Candacy A. Scott

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

CURRENT APPLICATION NUMBER: US/09/394,272

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENGTH: 1081
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                                                                                                                                    Query Match 66.7%; Score 36; DB 4; Length 1068; Best Local Similarity 66.7%; Pred. No. 81; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 1081;
83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 66.7%; Score 36; DB Best Local Similarity 66.7%; Pred. No. 83; Matches 6; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Craterostigma plantagineum
US-09-394-272-4
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Best Local Similarity 66.7-
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 1068
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483 VIPPGMDFS 491
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435 VIPPGMDFS 443
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                                  ; LENGTH: 1068
; TYPE: PRT
; ORGANISM: Zea mays
US-09-394-272-8
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US-09-394-272-11
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Seguence 5, Application US/0334172

Seguence 6, Application US/0334172

Seguence 7, Application US/0334173

Seguence 7, Application US/035417

Seguence 7, Application US/0355147

Seguence 7, Application US/035147

Seguence 7, Application US/035147

Seguence 7, Application US/035147

Seguence 7, Application US/0351447

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 WESULT 14
US-08-560-147-82
Sequence 82, Application US/08569147
Sequence 82, Application US/08569147
Setent No. 6180377
TITLE OF INVENTION:
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NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Woodcock Washburn Kurtz Palace - 46th Floor
STREET: One Liberty Place - 46th Floor
STRATE: PA
COUNTY: U.S.A.
ZIP: 19103
COMPUTER: IBM PC compatible
OCHETRER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
OCHETRE: IBM PC compatible
OCHETRE: PALCATION DATA:
MEDIUM TYPE: Patentin Release #1.0, Version #1.25 (EPO)
CURSTENTY STREET FORM:
MADE: TLAING DATE: S36
ATTORNEY/AGENT INFORMATION:
TELEBHONE: (215) 568-3100
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TYPE: amino acid
TYPE: amino acid
TOPOLLOGY: linear
MOLECULE TYPE: protein
US-08-569-147-82
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 122 VVPTGFDY 129
 3 VVPXGMDY 10
3 VVPXGMDY 10
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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31637
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Page

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Sequence 13,
Sequence 22,
Sequence 26,
Sequence 27,
 Sequence 6, A Sequence 9, A Sequence 10, Sequence 31, Sequence 32, Sequence 46, Sequence 40, Sequence 41,
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 Published Applications AA:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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 Pitle:
Perfect score:
 Score
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Sequence 8, Application US/09909164
; Publication No. US2020068702A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
ITILE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IND1192-US
FILE REFERENCE: 1001192-US
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTING DATE: 1000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTING DATE: 1000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTING DATE: 1000-07-21
NUMBER OF SEQ ID NOS: 62
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SOFTWARE: PATENTING DATE: 1000-07-21
SOFTWARE: PATENTING DATE: 1000-07-21
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SOFTWARE: PATENTING DATE: 2000-07-21
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SOFTWARE: PATENTING DATE: 2000-07-21
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
ALIGNMENTS
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NAME/KEY: MISC FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
 NAME/KBY: MISC FEATURE LOCATION: (9). . . (9) OTHER INFORMATION: D-amino acid
 TYPE: PRT ORGANISM: artificial sequence
 NAME/KEY: MOD_RES
LOCATION: (11)..(11)
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US-09-909-164-8
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US-09-164-22

JS Sequence 22, Application US/09909164

Publication No. US2020068702A1

J SHERAL INFORMATION:

APPLICANT: Orrvas International, Inc.

APPLICANT: Lim-Wilby, Marguerita

FILE REFERENCE: INOUEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: LO09-09-25

FILE REFERENCE: LO09-09-21

FRIOR PAPLICATION NUMBER: 60/220,101

PRIOR PAPLICATION NUMBER: 60/220,101

PRIOR PLING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SEQ ID NO 22

LENGTH: 11

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LENGTH: 11

MARGUERITE PAPENTITIS C

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 OTHER INFORMATION: 11-mer synthesized according to example 1
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96.3%; Score 52; DB 12; L
Best Local Similarity 100.0%; Pred. No. 0.00097;
Matches 11; Conservative 0; Mismatches 0;
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CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
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SEQ ID NO 13
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; LOCATION: (8)..(9)
; OTHER INFORMATION: D-amino acids
US-09-909-164-13
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LOCATION: (1) .. (1)
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 TYPE: PRT
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 LOCATION: (11)..(11)
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OTHER INFORMATION: AMIDATION
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LOCATION: (6)..(6)
 NAME/KEY: MOD_RES
 임
 Sequence 13, Application US/0909164

Sequence 13, Application No. US20020068702A1

GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Colle E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: NoveL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
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 OTHER INFORMATION: 11-mer synthesized according to example 1
 Query Match 96.3%; Score 52; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.00097; Matches 11; Conservative 0; Mismatches 0; Indels
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FRATURE:
NAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
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 NAME/KEY: MISC_FEATURE

LOCATION: (8) ...(8)

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OTHER INFORMATION: ACETYLATION
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 TYPE: PRT
ORGANISM: artificial sequence
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 US-09-909-164-13
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Sequence 5, Application US/09909164
; Bedication No. US20020068702A1
; Publication No. US20020068702A1
; GENERAL INFORMATION:
; APPLICANT: Cim-whiby, Marguerita
; APPLICANT: Lim-whiby, Marguerita
; APPLICANT: REFERENCE: IN01192-US
; FILE REFERENCE: IN01192-US
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5.
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
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OTHER INFORMATION: D-amino acids
US-09-909-164-27
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NAME/KEY: MOD RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
FRATURE:
 NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
 TYPE: PRT
ORGANISM: artificial sequence
PEATURE:
 TYPE: PRT
ORGANISM: artificial sequence
 NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 Query Match
Best Local Similarity 90.9
Matches 10; Conservative
 1 EEVVPXGMDYS 11
 1 EEVVPXGQDYS 11
 PEATURE:
NAME/KEY: MISC_FEATURE
 FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (6). 7(6)
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 FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
 Score 47; DB 12; Length 11; Pred. No. 0.0097; 0; Mismatches 1; Indels
 Length 11;
 1; Indels
 Score 47; DB 12;
Pred. No. 0.0097;
0; Mismatches
 Sequence 27, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corves International, Inc.
APPLICANT: Lim-Wilby, Marguerita
 OTHER INFORMATION: norvaline-(CO)
 NAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
 NAME/KEY: MISC_FEATURE

LOCATION: (9)...(9)

OTHER INFORMATION: D-amino acid
US-09-909-164-22
 FEATURE:
NAME/KEY: MOD RES
LOCATION: (1) - (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11) - (11)
OTHER INFORMATION: AMIDATION
 LOCATION: (8). . . (8)
CTHER INFORMATION: D-amino acid
US-09-909-164-26
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
 TYPE: PRT ORGANISM: artificial sequence
 1 REVVPXGMDYS 11
 1 EEVVPXGQDYS 11
 1 EEVVPXGMDYS 11
 1 EEVVPXGODYS 11
 NAME/KEY: MISC FEATURE
 US-09-909-164-27
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US-09-909-164-10

US-09-909-164-10

i Sequence 10. Application US/09909164

j Publication No. US20020068702A1

general INFORMATION:
 APPLICANT: Corvas International, Inc.
 APPLICANT: Lim-Wilby, Marguerita
 APPLICANT: Lim-Wilby
 TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEDATITIS C
 FILE REPRENCE: INO192-US
 CURRENT APPLICATION NUMBER: US/09/909,164
 CURRENT PILING DATE: 2000-07-21
 NUMBER OF SEQ ID NOS: 62
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 10
 LENTH: III
APPLICANT: Levy, odile E
APPLICANT: Levy, odile E
APPLICANT: Brunck, Terence K
APPLICANT: Brunck, Terence K
FILE REPERENCE: INO192-08
CURRENT APPLICATION NUMBER: 10/609/909,164
CURRENT APPLICATION NUMBER: 2003-03-25
FRICK APPLICATION NUMBER: 60/220,101
FRICK APPLICATION NUMBER: 60/220,101
FRICK APPLICATION NUMBER: 60/220,101
FRICK FILING DATE: 2000-07-21
STORM FILING DATE: 2000-07-21
STORM FILING DATE: 2000-07-21
STORM FILING DATE: 2000-07-21
STORM FILING DATE: 2000-07-21
STORM FILING DATE: 2000-07-21
 FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
 OTHER INFORMATION: 11-mer synthesized according to example 1
 85.2%; Score 46; DB 12; Length 11; 90.9%; Pred. No. 0.015;
 FEATURE:
NAME/KEX
LOCATION: (6). (6)
OTHER INFORMATION: norvaline- (CO)
 NAME/KEY: MISC_FRATURE
COCATION: (8)...(8)
OTHER INFORMATION: D-amino acid
US-09-909-164-9
 NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 TYPE: PRT
ORGANISM: artificial sequence
 TYPE: PRT
ORGANISM: artificial sequence
 FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 Best Local Similarity 90.9
Matches 10; Conservative
 1 EEVVPXGMDYS 11
 1 EEVVPXCMSYS 11
 (11)..(11)
 NAME/KEY: MOD_RES
LOCATION: (11)..(:
 Query Match
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 APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TICRENT APPLICANTON NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR PRILING DATE: 2003-03-25
RRIOR PRILING DATE: 2003-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO S: 62
LENGTH: 11
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0
 OTHER INFORMATION: 11-mer synthesized according to example 1
 Score 46; DB 12; Length 11;
Pred. No. 0.015;
0; Mismatches 1; Indels
 DB 12; Length 11;
 1; Indels
 Score 46; DB 1
Pred. No. 0.019
0; Mismatches
 S-09-909-164-9
Sequence 9, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
 Sequence 6, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
 NAME/KEY: MISC FEATURE
LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
 OTHER INFORMATION: norvaline-(CO)
 FEATURE:
NAMEN/KEY: 91.C. (9)
LOCATION: (9)... (9)
OTHER INFORMATION: D-amino acid
 NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 TYPE: PRT
ORGANISM: artificial sequence
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
 NAME/KEY: MOD RES
LOCATION: (11)..(11)
COTHER INFORMATION: AMIDATION
US-09-909-164-6
 (11) (THER INFORMATION: AMIDATION US-09-909-164-5
 1 EEVVPXGMDYS 11
 EEVVPXGMSYS 11
 1 EEVVPXGMDYS 11
 1 EEVVPXGMSYS 11
 FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)..(1
 EATURE
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LEVY, Odile B

AFFLICANT: Brunck, Terence K

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: IN01192-US

CURRENT PEPLICATION NUMBER: US/09/909,164

CURRENT FILING DATE: 2003-03-25

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR PEPLIOR

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQ ID NO 32

LENGTH: 11
 Sequence 35, Application US/09909164

| Sequence 35, Application US/0909164
| Publication No. US20020068702A1
| Publication No. US20020068702A1
| Publication No. US20020068702A1
| APPLICANT: Lin-Wilby, Marguerita
| APPLICANT: Lin-Wilby, Marguerita
| APPLICANT: Lin-Wilby, Marguerita
| APPLICANT: Brunck, Terence K | TITLE OF INVENTION: NOVEE PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C | TITLE OF INVENTION: NUMBER: US/09/909,164 | CURRENT APPLICATION NUMBER: 60/220,101 | PRIOR FILING DATE: 2000-07-21 | NUMBER OF SEQ ID NOS: 62 | SEQ ID NOS: 62 | SEQ ID NOS: 62 | SEQ ID NOS: 62 | SEQ ID NOS: 62 | SEQ ID NOS: 62 | LENGTH: 11
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 Gaps
 TYPE: PRT
ORGANISM: artificial sequence
ERATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
 ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
 Length 11;
 1; Indels
 DB 12;
 Score 46; DB 1
Pred. No. 0.015
0; Mismatches
 LOCATION: (6). (6) OTHER INFORMATION: norvaline-(CO)
 LOCATION: (9). (9)
OTHER INFORMATION: D-amino acid
 NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 FEATURE:
NAME/FEX: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 85.2%;
 FRATURE:
NAME/KRY: MOD RES
NOCATION: (11).
OTHER INFORMATION: AMIDATION
 Query Match
Best Local Similarity 90.5
Matches 10; Conservative
 1 EEVVPXGMDYS 11
 1 REVVPXGTDYS 11
 NAME/KEY: MISC FEATURE LOCATION: (9)..(9)
 NAME/KEY: MISC_FEATURE
 US-09-909-164-32
 TYPE: PRT
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 Sequence 31, Application US/09909164

Publication No. US20020068702A1
GENERAL INFORMATION:

SPPLICANT: Corvas International, Inc.

APPLICANT: Lim.Wilby, Marguerita

APPLICANT: Lim.Wilby, Marguerita

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Brunck, Terence K

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: INO192-US

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT PILING DATE: 2003-03-25

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1
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 Gaps
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 OTHER INFORMATION: 11-mer synthesized according to example 1
 Query Match 85.2%; Score 46; DB 12; Length 11; Best Local Similarity 90.9%; Pred. No. 0.015; Matches 10; Conservative 0; Mismatches 1; Indels
 85.2%; Score 46; DB 12; Length 11; 90.9%; Pred. No. 0.015; tive 0; Mismatches 1; Indels
 APPLICANT: Corvas International, Inc. APPLICANT: Lim-Wilby, Marguerita
 Sequence 32, Application US/09909164 publication No. US20020068702A1 GENERAL INFORMATION:
 NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
 ; LOCATION: (6). (6)
; OTHER INFORMATION: norvaline-(CO)
US-09-909-164-31
 NAME/KEY: MISC_FEATURE
1.OCATION: (8)...(9)
2.09-909-164-10
 NAME/KEY: MOD_RES
LOCATION: (1) ...(1)
OTHER INFORMATION: ACETYLATION
FRATURE:
 ORGANISM: artificial sequence
 LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 OTHER INFORMATION: AMIDATION
 Query Match
Best Local Similarity 90.9
Matches 10; Conservative
 1 EEVVPXGMDYS 11
 1 EEVVPXGMSYS 11
 1 EEVVPXGTDYS 11
 1 REVVPXGMDYS 11
 NAME/KEY: MISC FEATURE
 NAME/KEY: MOD_RES
 RESULT 12
US-09-909-164-32
 RESULT 11
US-09-909-164-31
 SEQ ID NO 31
LENGTH: 11
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Publication No. US20020068702A1
 1 EEVVPXGMDYS 11
 NAME/KEY: MISC FEATURE
 Sequence 40, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: NOUNE, PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT FILING DATE: 2003-03-25
PRIOR FILING DATE: 2003-03-25
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEQ ID NOS: 62
SEQ ID NO 40
LENGTH: 11
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 FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
 Score 46; DB 12; Length 11;
Pred. No. 0.015;
0; Mismatches 1; Indels
 Score 46, DB 12; Length 11;
Pred. No. 0.015;
0; Mismatches 1; Indels
 FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
 NAME/KEY: MISC FEATURE
LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
 FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (9)...(9)
OTHER INFORMATION: D-amino acid
US-09-909-164-35
 NAME/KEY: MISC_FEATURE
LOCATION: (8)..(8)
OTHER INFORMATION: D-amino acid
US-09-909-164-40
 NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative (
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
 TYPE: PRT
ORGANISM: artificial sequence
 NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 OTHER INFORMATION: AMIDATION
 1 EEVVPXGMDYS 11
 1 EEVVPXGSDYS 11
 1 EEVVPXGMDYS 11
 EEVVPXGSDYS 11
 RESULT 14
US-09-909-164-40
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RESULT 15 US-09-909-164-41 ; Sequence 41, Application US/09909164

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GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-wilby, Marguerita
APPLICANT: Lim-wilby, Odile B
APPLICANT: Law, Odile B
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT PILING DATE: 2003-03-25
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
SEQ ID NO 41
SEQ ID NO 41
SEQ ID NO 41
SEQ ID NO 41
TYPE: PT
ORGANISM: artificial sequence
SEATURE: PRIOR MARGINE SEQUENCE
CREATER TAPE: PT
ORGANISM: artificial sequence
 0
 OTHER INFORMATION: 11-mer synthesized according to example 1 PEATURE:
 Query Match 85.2%; Score 46; DB 12; Length 11; Best Local Similarity 90.9%; Pred. No. 0.015; Matches 10; Conservative 0; Mismatches 1; Indels
 Search completed: June 3, 2004, 12:57:16
Job time: 33.7333 secs
 NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
PEATURE:
 LOCATION: (8). (9)
CTHER INFORMATION: D-amino acids
US-09-909-164-41
 NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
 FEATURE:
NAMES/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
FEATURE:
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(without alignments)
117.567 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 June 3, 2004, 11:35:47 ; Search time 9 Seconds
 283366
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 283366 seqs, 96191526 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 US-09-909-164-13
54
1 EEVVPXGMDYS 11
 PIR 78: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *
 Title:
Perfect score:
Sequence:
 Scoring table:
 OM protein
 Searched:
 Database
 Run on:
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hypothetical prote Description \$54619 D69551 A42452 \$72649 \$72664 G96764 JC4783 TQ9337 TO4062 TO4103 T24111 H87660 T20173 F69009 B49132 800210 H72784 Query Match Length DB 348 460 1049 1068 1081 1083 Score Result

probable alkaline hypothetical prote probable membrane fat facets (faf) s plastocyanin b - L plastocyanin precu plastocyanin b pre 6-0-methylguanineconserved hypothet V1 protein - tobac sucrose-phosphate phenylalanine-tRNA succinate dehydrog disease resistance sucrose-phosphate unknown protein F2 sucrose-phosphate hypothetical prote peptidoglycan-bind 06-methylguanine-D hypothetical prote probable hexosyltr i-lactate dehydrog ABC transporter AT sucrose-phosphate sucrose-phosphate sucrose-phosphate sucrose-phosphate S38255 S58208 AG3104 D98182 F72745 G69290 0000 

| no tra           | hypothetical 367K<br>partial transposas | hypothetical prote<br>fibroblast growth | hypothetical prote hypothetical prote | conserved hypothet unknown protein [i | transposase ISC105<br>transposase ISC105 | hypothetical prote<br>pantoate-beta-alan | transposase ISC105 |
|------------------|-----------------------------------------|-----------------------------------------|---------------------------------------|---------------------------------------|------------------------------------------|------------------------------------------|--------------------|
| T48899<br>F83335 | 130830<br>T31308<br>A99427              | A90471<br>S27021                        | E90335<br>S57810                      | A96001<br>A96546                      | F90298<br>C90307                         | C64417<br>G83055                         | E90487             |
| 000              | N 10 10                                 | 0 0                                     | 0 0                                   | 0 0                                   | 04 03                                    | 0.0                                      | 101                |
| 908              | 3472<br>97                              | 128                                     | 184                                   | 247                                   | 262                                      | 276                                      | 299                |
| 0.00             | . 0. 4                                  | <del>-</del> ! -:                       | -: -:                                 | 44                                    | <u> </u>                                 | 4.5                                      | id.                |
| 63               | 63.0<br>61.1                            | 61                                      | 61                                    | 61                                    | 61                                       | 61                                       | 61                 |
| 444              | 4 4 6                                   | ღ ღ<br>ღ ღ                              | e e                                   | M M                                   | e e<br>e e                               | 333                                      | 9 6                |
| 0 1 0            | и ш ш<br>и ш д                          | 32<br>36                                | 37                                    | 9.0                                   | 4 4                                      | <b>4.</b> 4                              | . 4.<br>           |

## ALIGNMENTS

RESULT 1

| hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)                            |
|--------------------------------------------------------------------------------------------|
| N'Alternate names: hypothetical protein 02612; hypothetical protein YOL303.3               |
| C. Species: Saccharomyces cerevisiae                                                       |
| C)Date: 08-011-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002                |
| C.A.CCEBLUM: SJELT); Seev./<br>St.de Haan, M.; Maarse, A.C.; Grivell, L.A.                 |
| submitted to the EMBL Data Library, May 1995                                               |
| A;Reference number: S54617                                                                 |
| A,Accession: S54619                                                                        |
| A; Molecule type: DNA                                                                      |
| A;Residues: 1-156 <deh></deh>                                                              |
| A; Cross-references: EMBL:X87331; NID:G1041652; PIDN:CAA60762.1; PID:9829123               |
| R;de Haan, M.; Grivell, L.A.; Maarse, A.C.                                                 |
| submitted to the Protein Sequence Database, July 1996                                      |
| A;Reference number: S66877                                                                 |
| A;Accession: S66879                                                                        |
| A; Molecule type: DNA                                                                      |
| A; Residues: 1-156 < DEW>                                                                  |
| A, Cross-references: EMBL: 274920; NID: g1420109; PIDN: CAA99201.1; PID: g1420111; MIPS: X |
| AjExperimental source: strain S288C                                                        |
| C;Genetics:                                                                                |
| A;Cross-references: SGD:S0005539                                                           |
| A, Map position: 15R                                                                       |
| C, Superfamily: hypothetical protein YOR013w                                               |
|                                                                                            |
| Best Local Similarity 77.8%; Pred. No. 1;                                                  |
|                                                                                            |
| Qy 2 EVVPXGMDY 10                                                                          |

YOR01

||:| ||| EVMPLGMDY 58 20

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Conserved hypothetical protein AF2411 - Archaeoglobus fulgidus conserved hypothetical protein AF2411 - Archaeoglobus fulgidus (Species: Archaeoglobus fulgidus C; Species: Archaeoglobus fulgidus C; Date: 05-Dec.1997 #sequence\_revision 05-Dec.1997 #text\_change 22-Oct-1999 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accession: 069551 (Accessi

70.4%;

Query Match
Best Local Similarity 54.5
Matches 6; Conservative

| :|| |:|:| 120 ENIVPYGIDFS 130 1 EEVVPXGMDYS 11

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Cybecies: Arabidopsis thaliana (mouse-ear crees)
Cybecies: Arabidopsis thaliana (mouse-ear crees)
Cybecies: Arabidopsis thaliana (mouse-ear crees)
Cybecies: Ochar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
CyAccession: G96764
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Chung, C.; Khan, S.; Khaykin, E.; Kim, C.; A; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.W.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Wenter, J.C.; Davis, R.W.
A;Attle: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A;Accession: G96764
A;Status: praliminary
A;Molecule chunger: Affall; MUD:21016719; PMID:11130712
Sucrose-phosphate synthase (EC 2.4.1.14) isoform 3 - Citrus unshiu (fragment)
C;Species: Citrus unshiu
C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
C;Accession: S72650
R;Komatsu, A.; Ta2650
R;Komatsu, A.; Ta26, 346-351, 1996
A;Title: Cloning and molecular analysis of cDNAs encoding three sucrose phosphate synth A;Aceference number: S72648; MUID:96439842; PMID:8842155
A;Accession: S72650
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
 A; Description: catalyzes formation of sucrose-6-phosphate from UDPglucose and D-fructos A; Pathway: sucrose biosynthesis
C; Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase homology C; Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis P;1-348/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <SSPS>
 A)Residues: 1-348 «KOM»
A)Cross-references: EMBL:AB006660; NID:g2351059; PIDN:BAA22071.1; PID:g2351060
A)Experimental source: fruit, cv. Miyagawa-Wase
A,Ryte: the nucleotide sequence was submitted to the EMBL Data Library, August 1997
 A;Cross-references: GB:AE005173; NID:g6692750; PIDN:AAF24856.1; GSPDB:GN00141
C;Genetics:
 Gaps
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 66.7%; Score 36; DB 2; Length 348; 66.7%; Pred. No. 17; 17; artive 2; Mismatches 1; Indels
 Length 460;
 Indels
 5
 DB 23;
 66.7%; Score 36; DB 70.0%; Pred. No. 23; ive 0; Mismatches
 sucrose-phosphate synthase (EC 2.4.1.14) - rice C, Species: Oryza sativa (rice)
 Query Match
Best Local Similarity 66.
 Conservative
 218 EEDVPSAMDY 227
 10
 234 VIPPGMDFS 242
 3 VVPXGMDYS 11
 1 REVVPXGMDY
 Local Similarity
tes 7; Conserv
 A; Gene: F25P22.17
 A; Map position: 1
 Query Match
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 A42452

A42452
V1 protein - tobacco yellow dwarf virus (strain Australia)
C;Species: tobacco yellow dwarf virus
C;Species: tobacco yellow dwarf virus
C;Species: tobacco yellow dwarf virus
C;Accession: A42452
C;Accession: A42452
C;Accession: A42452
C;Accession: A42452
A;Aitle: The nucleotide sequence of the infectious cloned DNA component of tobacco yelld
A;Pitle: The nucleotide sequence of the infectious cloned DNA component of tobacco yelld
A;Reference number: A42452; MUID:92188538; PMID:1546458
 A;Molecule type: DNA
A;Residues: 1-363 <KLE>
A;Cross-references: GB:AE001109; GB:AE000782; NID:g2689432; PIDN:AAB91255.1; PID:g265068
 R;Komatsu, A.; Takanokura, Y.; Omura, M.; Akihama, T.
Mol. Gen. Genet. 252, 346-351, 1996
A;Title: Cloning and molecular analysis of cDNAs encoding three sucrose phosphate syntha
A;Reference number: S72648; MUID:96439842; PMID:8842155
 Description: catalyzes formation of sucrose-6-phosphate from UDPglucose and D-fructose
 A; Pathway: sucrose biosynthesis
C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
C;Keywords: glycosyltranaferase; hexosyltranaferase; sucrose biosynthesis
F;1-341/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <SSPS>
 ; Molecule type: mEMA;
Residues: 1-341 < KCM>
; Cross-references: EMBL:AB006319; NID:g2588891; PIDN:BAA23215.1; PID:g2588892
; Sxperimental source: fruit, cv. Miyagawa-Wase
; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1997
; Genetics:
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 sucrose-phosphate synthase (EC 2.4.1.14) isoform 2 - Citrus unshiu (fragment)
 C.Species: Citrus unshiu
C.Species: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
C,Accession: S72649
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 A, Accession: A42452
A, Molacule type: DNA
A, Residues: 1-102 KNOR>
A, Cross-references: GB:M81103; NID: g335283; PIDN: AAA47947.1; PID: g335284
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 Score 36; DB 2; Length 341;
Pred. No. 16;
2; Mismatches 1; Indels
 Length 102;
 Length 363;
 1; Indels
 2; Indels
 DB 2;
6.8;
 DB 2;
 Score 38; DB 2
Pred. No. 6.8;
3; Mismatches
 Score 36; DB;
Pred. No. 4.3;
3; Mismatches
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60.08;

Query Match
Best Local Similarity 60.0
Matches 6; Conservative

2 EVVPXGMDYS 11

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Status: nucleic acid sequence not shown

66.7%; ilarity 66.7%; Conservative

Query Match Best Local Similarity Matches 6; Conserv

228 VIPPGMDFS 236

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3 VVPXGMDYS 11

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C;Accession: T04103
R;Sakamoto, M.; Satozawa, T.; Kishimoto, N.; Higo, K.; Shimada, H.; Fujimura, T.
Bath Sci. 112, 207-217, 1995
A;Title: Structure and RFLP mapping of a rice sucrose phosphate synthase (SPS) gene that A;Reference number: 215212
 C;Accession: T04062
R;Bevan, M; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X
submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15184
Plant Physiol. 115, 113-121, 1997
A;Title: Analysis of cDNA clones encoding sucrose-phosphate synthase in relation to sug?
A;Areference number: Z16874; MUID:97451773; PMID:9306694
A;Accession: T09837
A;Status: preliminary; translated from GB/EMBL/DDBJ
 A,Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fruc
A,Pathway: sucrose biosynthesis
 A;Map position: 4
A;Introns: 86/3; 116/3; 255/3; 322/2; 482/3; 526/3; 570/3; 629/3; 647/3; 668/3; 949/3;
 C;Superfēmily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology C;Superfēmily: sucrose-phosphate synthase; c;Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis P;176-674/Domain: sucrose/sucrose-phosphate synthase homology <855>
 synthase homology
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 A;Molecule type: mRNA
A;Residues: 1-1081 cING>
A;Residues: 1-1081 cING>
A;Cross-references: EMBL:Y11795; NID:g2190349; PIDN:CAA72491.1; PID:g2190350
A;Experimental source: ABA-treated callus
C;Genetics:
A;Gene: sps2
C;Function:
 sucrose-phosphate synthase homolog F28M11.40 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 16-Jul-1999
 C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
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 C:Superfemily: sucrose-phosphate synthase; sucrose/sucrose-phosphate F;230-714/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
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 Score 36; DB 2; Length 1083;
Pred. No. 60;
2; Mismatches 1; Indels
 Score 36; DB 2; Length 1081;
Pred. No. 60;
 1; Indels
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A;Experimental source: cultivar Columbia; BAC clone F28M11
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
 sucrose-phosphate synthase (EC 2.4.1.14) 1 - rice
 A;Cross-references: EMBL:D45890; PIDN:BAA08304.1
 2; Mismatches
 A, Experimental source: subsp. Japonica
 Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
 Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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445 VIPPGMDFS 453
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VIPPGMDFS 491
 3 VVPXGMDYS 11
 3 VVPXGMDYS 11
 A;Residues: 1-1084 <SAK>
 A; Accession: T04103
 A, Accession: T04062
 A; Note: F28M11.40
 Genetics:
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 A;Molecule type: mRNA
A;Residues: 1-1049 <VAL>
A;Cross-references: GB-U33175; NID:g1449931; PIDN:AAC49379.1; PID:g988270
A)Anote: UDPglucose-fructose-phosphate glucosyltransferase; Sucrosephosphate-UDPglucosylt
C;Comment: This enzyme catalyzes the formation of sucrose-phosphate form UDP-glucose and
 Description: catalyzes the formation of sucrose-6-phosphate from UDFglucose and D-fruct Pathway: sucrose biosynthesis processes are sucrose-phosphate synthase; sucrose-phosphate synthase; sucrose-phosphate synthase; sucrose-phosphate synthase; sucrose-phosphate synthase; sucrose-phosphate synthase; sucrose-phosphate; pathways sucrose-phosphate synthase homology sometimes and pathways sucrose-sucrose-phosphate synthase homology sometimes.
 C;Species: Zea mays (maize)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JQ1329; PQ0260
R;Worrell, A.C.; Bruneau, J.M.; Summerfelt, K.; Boersig, M.; Voelker, T.A.
Plant Cell 3, 1121-1130, 1991
A;Title: Expression of a maize sucrose phosphate synthase in tomato alters leaf carbohyd
A;Reference number: JQ1329; MUID:92338937; PMID:1840396
 A,Molecule type: protein
A,Molecule type: protein
A,Residues: 71-74,206-212,471-481,872-892 <MOR1>
A,Coment: This enzyme transfers the glucosyl group from UDPglucose to fructose-6-phosph
C,Comment: This enzyme is involved in the regulation of carbon partitioning in the leave
 A,Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-frud A,Pathway: sucrose biosynthesis
C,Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase; sucrose-phosphate synthase; sucrose biosynthesis
C,Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F;180-663/Domain: sucrose/sucrose-phosphate synthase homology <8SPS>
)Accession: JC4783
;/Valdez-Alarcon, J.J.; Ferrando, M.; Salerno, G.; Jimenez-Moraila, B.; Herrera-Estrella
 A;Gene: Sps1
A;Introns: 24/1; 103/3; 183/3; 205/3; 435/3; 475/3; 519/3; 578/3; 596/3; 617/3; 931/3;
C;Function:
 sucrose-phosphate synthase (EC 2.4.1.14) isoform 2 - Craterostigma plantagineum C;Species: Craterostigma plantagineum C;Species: Craterostigma plantagineum C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000 C;Accession: T09937 R;Ingram, J; Chandler, J.W.; Gallagher, L.; Salamini, F.; Bartels, D.
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 Gene 170, 217-222, 1996
A/Title: Characterization of a rice sucrose-phosphate synthase-encoding gene.
A/Reference number: JC4783; MUID:96235138; PMID:8666248
 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 18-Jun-1999
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 A;Accession: JQ1329
A;Molecule type: mRNA
A;Residues: 1-1668 <WOR>
A;Cross-teferences: GB:M97550; NID:g168625; PIDN:AAA33513.1; PID:g168626
A;Accession: PQ0260
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 Query Match
66.7%; Score 36; DB 2; Length 1049;
Best Local Similarity 66.7%; Pred. No. 58;
Matches 6; Conservative 2; Mismatches 1; Indels
 Score 36; DB 1; Length 1068;
Pred. No. 59;
2; Mismatches 1; Indels
 sucrose-phosphate synthase (EC 2.4.1.14) - maize
 66.7%;
 6; Conservative
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436 VIPPGMDFS 444
 VVPXGMDYS 11
 3 VVPXGMDYS 11
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 Query Match
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Matches 6; Conserv
 A; Accession: JC4783
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66.7%; 66.7%;

Query Match
Best Local Similarity 66.7
Matches 6; Conservative

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A;Gene: CESP:C53A5.2
A;Map position: 5
A;Introns: 33/3; 63/3; 132/3; 169/3; 221/3; 299/3; 379/2; 423/2; 438/2; 471/1; 513/2; 6
 probable alkaline proteinase APB0263 - Aeropyrum pernix (strain KI)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: H7284
B;Aavarabayaai, Y;Hino, Y;Horikawa, H;Yamazaki, S;Haikawa, Y;Jin-no, K;Takama, H;Takamiya, M;Masuda, S;Funahashi, T;Tanaka, T;Kudoh, Y;Jamazaki, J;DNA Res; Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy A;Accession: H7284
A;Reference number: A72450;MUD:99310339;PMID:10382966
A;Catus: preliminary
A;Molecule type: DNA
A;Residues: 1-440 cxAm>
A;Residues: 1-440 cxAm>
A;Cross-references: DDB0:Ap000058;NID:g5103388;PIDN:BAA79178.1;PID:g5103657
A;Experimental source: strain Kl
 hypotherical protein C53A5.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caecosion: T20173; T23857
R;Mortimore, B.
S;Mortimore, B.
S;Status: preliminary; translated from GB/EMBL/DDBJ
A;Roference number: Z19232
A;Roference number: Z19232
A;Molecule type: DNA
A;Roference number: Clone C53A5
S;Matthews, L.
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 64.8%; Score 35; DB 2; Length 1150; 66.7%; Pred. No. 1e+02; tive 2; Mismatches 1; Indels
 2; Length 440;
 1; Indels
 Query Match.
64.8%; Score 35; DB
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches
 A,Gene: APE0263
C,Superfamily: subtilisin; subtilisin homology
 completed: June 3, 2004, 12:00:01
ne : 9 secs
 Query Match.

Best Local Similarity 66.7

Matches 6; Conservative
 120 EVLPWGVDY 128
 3 VVPXGMDYS 11
 2 EVVPXGMDY 10
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562 VLPVGIDYS
 Gene: APE0263
 C; Genetics:
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 peptidoglycan-binding protein, probable [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: H87660
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
C;Genetics:
A;Genes Spai
A;Gene: Spai
A;Map position: 1
A;Introns: 120/3; 200/2; 221/3; 452/3; 492/3; 536/3; 595/3; 613/3; 634/3; 946/3; 989/2
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C;Superfamily: sucrose-phosphate synthase, sucrose-phosphate synthase homology
C;Keywords: glycosyltransferase; hexosyltransferase
F;196-680/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
 A;Reference number: Z19842
A;Accession: T24111
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-425 <WIL>
A;Cross-references: EMBL;Z81109; PIDN:CAB03241.1; GSPDB:GN00023; CESP:R10D12.10
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 A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-433 <STO>
A/Cross-references: GB:AE005673; NID:g13425020; PIDN:AAK25284.1; GSPDB:GN00148
C/Genetics:
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 hypochetical protein R10D12.10 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 (S, Accession: T24111 R; Percy, C. submitted to the EMBL Data Library, October 1996
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 Length 1084;
 Score 35; DB 2; Length 433;
Pred. No. 35;
2; Mismatches 3; Indels
 Length 425;
 2; Indels
 Query Match
64.8%; Score 35; DB 2;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 5; Conservative 3; Mismatches
 Score 36; DB 2;
Pred. No. 60;
2; Mismatches
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A;Map position: 5 A;Introns: 23/3; 56/3; 113/3; 257/2

RESULT 13

64.8%; 54.5%;

Local Similarity nes 6; Conserva

Query Match Best Local S: Matches 6

1 EEVVPXGMDYS 11

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A; Experimental source: clone R10D12

C;Genetics: A;Gene: CESP:R10D12.10

xenopus lae gallus gall xenopus lae gallus gall homo sapien

009wzr1 0004827 730279 730280 7200459 720755 720755 720755 720755 720755

thermotoga rattus norv homo sapien mus musculu brachydanio

escherichia

P08203

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 RECURRER FROW N.A.

SEQUENCE FROW N.A.

STAIN=21886394; PubMed=11889109;

K Apptral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Asptral V., Anderson I., Ivanova N., Grachkin G., Zhu L., Asptral V., Chaga O., Goltsman E., Bernal A., Bartanan M., Cardner W., Grachkin G., Zhu L., Nasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., Narpides M., Wallunas T., Pusch G., Haselkorn R., Larsen N., Voverbeek R., Ingenome sequence and analysis of the oral bacterium Fusobacterium nuclearum strain ATCC 2586.";

I. Genome sequence and analysis of the oral bacterium Fusobacterium nuclearum ATCC 2586.";

I. Bacteriol. 184:2005-2018(2002).

I. CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + phosphate + L-glutamate + carbamoyl phosphate.

I. CATALYTIC ACTIVITY: 2 ATP + L-glutamine to similarity).

I. PATHMAY: Arginine biosynthesis.

I. PATHMAY: Pyrimidine biosynthesis, first step.

I. PATHMAY: Pyrimidine biosynthesis, first step.

I. PATHMAY: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chains to synthesize carbamoyl phosphate (By similarity).
 28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate syntheres ammonia chain)
Carbamoyl-phosphate synthetase ammonia chain)
CARB ON FN0422.
Fusobacterium nucleatum (subsp. nucleatum).
Bacteria, Fusobacteria; Fusobacterales; Fusobacteriaceae;
 PRT; 1058 AA
 ALIGNMENTS
 ARAD_SALTY
HIS9_THEMA
GGD2_RAT
GGD2_MOUSE
GGD1_BRARE
GGD1_XENLA
GGD2_XENLA
GGD2_XENLA
 EMBL; AE010554; AAL94625.1; ALT_INIT.
 HAMAP; MF 01210; -; 1.
InterPro; IPR006275; CarA L glu.
InterPro; IPR006493; CPase L.
InterPro; IPR005499; CPase L. D2.
InterPro; IPR005480; CPase L. D3.
InterPro; IPR004362; MGS IIKe.
InterPro; IPR004362; MGS IIKe.
IPR004362; CPSase L. Chain; 2.
IPR0; IPR064362; MGS IIRe.
IPR0, IPR064362; MGS IIRe.
IPR0, IPR064362; CPSase L. Chain; 2.
IPR0; IPR064363; CPSase L. Chain; 2.
IPR0; IPR064363; CPSase L. Chain; 2.
IPR0; IPR064363; CPSase L. D3; 1.
 08RGB6;
28-FEB-2003 (Rel. 41, Created)
 STANDARD;
Fusobacterium.
NCBI_TaxID=76856;
FUSIN
RESULT 1
halomonas e
halomonas e
homo sapien
mus musculu
 homo sapien
oryza sativ
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 simian foam
vibrio chol
 oryza sativ
 zea mays (m
craterostig
 populus nig
 arabidopsis
 methanococc
 pseudomonas
 vibrio chol
rattus norv
 gallus gall
schizosacch
 homo sapien
xenopus lae
 daucus caro
 listeria in
listeria mo
 Q8rg86 fusobacteri
 borrelia bu
 rattus norv
 hordeum vul
 drosophila
 (without alignments)
117.693 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 June 3, 2004, 11:32:06 ; Search time 4.86667 Seconds
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 P20422
Q88cg0
Q92bc5
Q8y6u8
Q04667
 Q9kv29
P15822
 P27399
 141681
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Fotal number of hits satisfying chosen parameters:
 141681 seqs, 52070155 residues
 SUMMARIES
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METUA
PSEAE
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 CARB_FUSNN
Y11K_TYDVA
SPS_ORYSA
SPS_MAIZE
SPSZ_CRAPL
 HALEL
HUMAN
MOUSE
CHICK
SCHPO
SFV3L
 DAUCA
 OM protein - protein search, using sw model
 DROME
 ORYSA
HORVU
POPNI
BORBU
 XENLA
 REL4_ARATH
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 PANC
HMPA
ACDM
 CEK2
SULH
ENV S
RPOC
ZEP1
 PLAS
 RP8H
 ECB1
 Winimum DB seq length: 0 Waximum DB seq length: 2000000000
 US-09-909-164-13
54
 1 EEVVPXGMDYS 11
 Query
Match Length DB
 SwissProt_42:*
 982
1401
2717
472
97
150
165
165
 !itle:
Perfect score:
Sequence:
 Scoring table:
 Score
 Database :
 Searched:
 Result
No.
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7 QVVPSGINYS 16

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Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=4530;
 SPS_ORYSA
Q43802;
 SEQUENCE
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Matches
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 ö
AR PFam; PF02142; MGS; 1.

DR PRINTS; PR00098; CPSASE.

DR PROSITE: PS00866; CPSASE.1 1.

DR PROSITE: PS00866; CPSASE.2; 2.

DR PROSITE: PS00867; CPSASE.2; 2.

KM Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

KM Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

KM Arginine biosynthesis; Complete proteome.

- APP-binding; Manganese; Complete proteome.

- APP-binding; Manganese; Complete proteome.

- APP-binding; Manganese; Complete proteome.

- AREANOYL PHOSPHATE SYNTHETIC DOMAIN.

- AREANOYL PHOSPHATE SYNTHETIC DOMAIN.
 Gaps
 SQUENCE FROM N.A. Dubwed=1546458;
MDTINE=92188538; Pubwed=1546458;
MORTIS B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
Mortis B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
The mucleotide sequence of the infectious cloned DNA component of tobacco yellow dwarf virus reveals features of geminiviruses infecting monococyledonous plants.";
Virology 187:633-642(1992).
 ATP (POTENTIAL).

ATP (POTENTIAL).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).
 ;
0
 DB 1; Length 1058; 9.4;
 66.7%; Score 36; DB 1; Length 102; 60.0%; Pred. No. 2.2;
 1; Indels
 1 protein. 1102 AA; A40ECFIE0AF55B67 CRC64;
 Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses, ssDNA viruses, Geminiviridae, Mastrevirus.
 01-JUL-1993 (Rel. 26, Created)
01-ZUL-1993 (Rel. 26, Last sequence update)
01-CTT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
 Score 38; DB Pred. No. 9.4; 3; Mismatches
 EMBL; M81103; AAA47947.1; -.
PIR; A42452; A42452.
IDRO2521; JER02521; Gemini mov.
Pfam; PF01708; Gemini mov; I.
Hypothetical protein.
 70.4%;
 117451
 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
 Query Match
Best Local Similarity 60.0
6; Conservative
 STANDARD;
 |:|| |::||
190 EIVPNGLNYS 199
 1058
546
1058
210
 2 EVVPXGMDYS 11
 153
302
284
284
298
300
300
820
832
1058 AA;
 NCBI_TaxID=31599;
 TYDVA
 YIIK TYDVA
ID YIIK TYDV
AC P31619;
 SEQUENCE
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3; Mismatches

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 ö
 General 170:217-222(1996).

-I- FUNCTION: Involved in the regulation of carbon partitioning in the leaves of plants. May regulate the synthesis of sucrose and therefore play a major role as a limiting factor in the export of photoassimilates out of the leaf.
-I- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
 Gaps
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14)
(UDP-glucose-fructose-phosphate glucosyltransferase).
Oryza sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryzea.
 sucrose 6-phosphate.
-!- ENZYME REGULATION: Activity regulated by phosphorylation and
moderated by concentration of metabolites and light.
 Herrera-Estrella L.; "(Characterization of a rice sucrose-phosphate synthase-encoding
 ö
 DB 1; Length 1049; 24;
 Indels
 1049 AA; 116455 MW; ED862E2819AA4B04 CRC64;
 STRAINE_cv. Indica-IR36; TISSUE=Leaf;
MEDLINE=96235138; PubMed=8666248;
Valdez-Alarcon J.J., Ferrando M., Jimenez-Moraila B.,
 Gramens; Varous, Caramens 1.

From Fron Stransfers, Glyco trans 1.

Fransferses, Glycos transferses, Phosphorylation.

22 29 POLY-GLY.

DOMAIN 695 698 POLY-GLU.

DOMAIN 775 779 POLY-ARG.
 Score 36; DB 1
Pred. No. 24;
2; Mismatches
 PRT; 1068 AA.
 SPS MAIZE STANDARD;
P31927;
01-JUL-1993 (Rel. 26, Created)
 EMBL; U33175; AAC49379.1; -.
 66.78;
 66.78;
 6; Conservative
 436 VIPPGMDFS 444
 3 VVPXGMDYS 11
 PIR; JC4783; JC4783.
Gramene; Q43802; -.
 RESULT 4
SPS MAIZE
ID SPS MA
AC P3192'DT O1-JUJ
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us-09-909-164-13.rsp

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lamiids; Lamiales; Lamiales incertae sedis; Lindernieae;
 DOMAIN
SEQUENCE
 SEQUENCE
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 ö
 -1- FUNCTION: Involved in the regulation of carbon partitioning in the leaves of plants. May regulate the synthesis of sucrose and therefore play a major role as a limiting factor in the export of photoassimilates out of the leaf.
-1- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
 sucrose 6-phosphate.
-!- ENZYME REGULATION: Activity regulated by phosphorylation and moderated by concentration of metabolites and light.
-!- PATHWAX: Sucrose synthesis.
-!- SUBDWIT: Homodimer or homotetramer.
-!- DEVELOPMENTAL STAGE: Germinating seeds or mature leaves.
-!- PTW: Phosphorylated. However, phosphorylation is not essential for
 Worrell A.C., Bruneau J.-M., Summerfelt K., Boersig M., Voelker T.A., "Expression of a maize sucrose phosphate synthase in tomato alters leaf carbohydrate partitioning.";
 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
 Gaps
 Tracheophyta;
 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
50crose-phosphate synthase 2 (EC 2.4.1.14) (UDP-glucose-fructose-phosphate glucosyltransferase 2).
 SEQUENCE FROM N.A., AND SEQUENCE OF 71-74; 206-212; 471-481 AND
 (UDP-glucose-fructose-
 ô
 enzyme function.
 Score 36; DB 1; Length 1068; Pred. No. 25;
 Zea mays (Maize).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Trach
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
 SEQUENCE 1068 AA; 118575 MW; 074679B5E9A1D282 CRC64;
 1; Indels
 Maizeld, 2227, 197001296; Glyco_trans_1.
Pfam; PPF0034; Glycos transf_1; 1.
Transferase; Glycosyltransferase; Phosphorylation.
DOMAIN 25
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14) (UDP
 PRT; 1081 AA.
 2; Mismatches
 STRAIN=CV. PIONEER 3184; TISSUE=Leaf;
MEDLINE=92338837; PubMed=1840396;
 phosphate glucosyltransferase)
 66.7%;
 EMBL; M97550; AAA33513.1; -.
 Craterostigma plantagineum.
 6; Conservative
 STANDARD;
 435 VIPPGMDFS 443
 3 VVPXGMDYS 11
 JQ1329.
 Local Similarity
 MaizeDB; 25294; -
 NCBI_TaxID=4577;
 J01329;
 CRAPL
 ESULT 5
1982_CRAPL
(C 004933, 7
11.5-DEC-1;
)T 15-DEC-1;
)T 15-DEC-1;
)T 15-DEC-1;
)T 15-DEC-1;
)T 15-DEC-1;
)T 16-DEC-1;
)T 18-DEC-1;

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 FAF DROME STANDARD; PRT; 2778 AA.
PS5824, Q9V9T6; Q9V0Z7;
28-2824, Q9V9T6; Q9V0Z7;
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
16-MAR-2004 (Rel. 43, Last annotation procease
16-MAR-2004 (Rel. 43, Last annotation)
16-MAR-2004 (Rel. 43, Last annotation)
17-MAR-2004 (G1946.
18-MAR-2004 (Fruit fly).
 Gaps
 DIR, T09837, T09837.
InterPro, IPR001296; Glyco_trans_l.
Pfam; PP00534; Glycos_transf=1; l.
Transferase; Glycosyltransferase; Phosphorylation; Multigene family.
Transferase; 248
POIY-SER.
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0
 SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), AND TISSUE SPECIFICITY
 Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
 66.7%; Score 36; DB 1; Length 1081; 66.7%; Pred. No. 25;
 787 790 POLY-ARG.
1081 AA; 120933 MW; DD142DC2F1A72900 CRC64;
 Mismatches
 Fischer-Vize J.A., Rubin G.M., Lehmann R.;
 TISSUE=Eye imaginal disk;
MEDLINE=93202020; PubMed=1295747
 ..
 EMBL; Y11795; CAA72491.1; -.
 Conservative
 445 VIPPGMDFS 453
 3 VVPXGMDYS 11
 Local Similarity
Les 6; Conserv
Craterostigma.
NCBI_TaxID=4153;
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The far faces gene is required for Droscphila eye and embryoner Tisses-1000(1992).

By SIGNORIES FROW N.A.

READ TO CALLINES S. HOLL & M. BRAKINS R.A. GCADURG J.D.,

AMARIN M.D., CALLINES S. B. HOLL & M. BRAKINS R.A. GCADURG J.D.,

AMARIN M.D., CALLINES S. B. HOLL & M. BRAKINS R.A. GARGETON S.N.,

READ TO CALLINES S. B. HOLL & M. BRAKINS R.A. GARGETON S.N.,

BRANCH R.A. BRAN A. BRAKER S.G. HALL G. NEBRONC C.R. MIGHER ON S.N.,

BRANCH R.A. BRAN A. BRAKER S.G. HALL G. NEBRONC C.R. MIGHER S.N.,

BRANCH R.A. BRAN A. BRAKER S.G. BRANCH S. GARGETON S.N.,

BRANCH R.A. BRAN A. BRAKER S.G. BRANCH S. GARGETON S. CHORE M. C. CHARLE S. C.

BRANCH R.A. BRANCH S. BRAKER S.G. BRANCH S. CHORE M. C. CHARLE S. M. CHARLE S. S. BRANCH S. G. BRANCH S. C. CHORE M. C. CHARLE S. M. CHARLE S. S. BRANCH S. C. BRANCH S. C. BRANCH S. S.G. BRANCH S. C. CHORE M. C. CHARLE S. M. CHARLE S. S. GARGETON S. CHARLE S. M. C. CHARLE S. M. CHARLE S. S. GARGETON S. CHARLE S. C. CHARLE S. M. CHARLE S. S. GARGETON S. CHARLE S. M. C. BRANCH S. GARGETON
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 ö
 GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0007349; P:cellularization; IMP.
GO; GO:0009745; P:cellularization; IMP.
GO; GO:0000456; P:eye morphogenesis; IMP.
GO; GO:0000583; P:mystery cell fate differentiation (sensu Dr. . .; IMP.
GO; GO:0007097; P:myclear migration; IMP.
GO; GO:0006511; P:unclear migration; IMP.
GO; GO:0006511; P:unclear dependent protein catabolism; IGI.
InterPro; IPR001394; Peptidase_C19.
 Gaps
 Isoid=P55824-3; Sequence=VSP_005269;
-1- TISGUE SPECIFICITY: Bye disks and ovaties.
-1- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
-1- SIMILARITY: Belongs to peptidase family C19.
function.
CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)0
 ubiquitin + a thiol.
ALTERNATUR PRODUCTS:
BVent-Alternative splicing; Named isoforms=3;
Comment-Experimental confirmation may be lacking for some
 ;
0
 Score 35; DB 1; Length 2778;
Pred. No. 1.1e+02;
2; Mismatches 3; Indels
 IsoId=P55824-2; Sequence=VSP_005270;
 IsoId=P55824-1; Sequence=Displayed;
 EMBL, L04959, AAPO1345.1; -. BMBL, L04958, AAPO1346.1; -. BMBL, L04960; AAPO1340.1; -. BMBL, L04960; AAPO1348.1; -. BMBL, AE003779; AAPO1361.1; -. BMBL, AE003779; AAPO1361.1; -. BMBL, AF145677; AAD38652.1; -.
 PROSITE, PS00972; UCH 2_1; 1. PROSITE; PS00973; UCH 2_2; 1. PROSITE; PSS0335; UCH 2_3; 1. Ubl conjugation pathway; Hydr
 64.8%;
54.5%;
 FBgn0005632; faf
 1394 EVIVPDGODFS 1404
 Conservative
 1 EEVVPXGMDYS 11
 Query Match
Best Local Similarity
6; Conserva
 Pfam; PF00443; UCH;
 Developmental
 Name=2
 MEROPS; C1
FlyBase; F
 CONFLICT
CONFLICT
SEQUENCE
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RESULT 7

us-09-909-164-13.rsp

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Query Match
Best Local Similarity
Matches 8; Conserv
 SEQUENCE OF 58-154
 Gramene; P20423;
 NCBI_TaxID=4530;
 Transit peptide.
TRANSIT 1
CHAIN 58
 ORYSA
 METAL
METAL
SEQUENCE
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 DOMAIN
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 TISSUBE Brain;
MEDIUBE 20277482; PubMed=10819331;
MEDIUBE 20277482; PubMed=10819331;
Magase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XVII. The complete sequences of 100 new cDNA clones from brain which code for large process in vitro.";
DNA Res. 7:143-150(2000).
 MIM; 605332; -...
GO; GO: 0005737; C:cytoplasm; NAS.
GO; GO: 0003779; F:actin binding; NAS.
GO; GO: 0003779; F:actin binding; NAS.
InterPro; IRR000210; BTB POZ.
InterPro; IRR00652; Kelch_rep.
Pfam; PF00561; BTB; 1.
Pfam; PF00561; BTB; 1.
Pfam; PF00561; BTB; 1.
SMART; SM00625; BTB; 1.
PROSITE; PS50097; BTB; 1.
Cytoskeleton; Actin-binding; Kelch_rep.
 Kay M.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May play a role in organizing the actin cytoskeleton of the brain cells.
 Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 MEDINE=20347694; Pubmed=10888605; Koob M.D., Nemes J.P., Benzow K.A.; The SCAS transcript is an antisense RNA to a brain-specific transcript encoding a novel actin-binding protein (KLHLI)."; Hum. Mol. Genet. 9:1543-1551(2000).
 C11C43D8282F9FF9 CRC64;
 -!- SUBCELLULAR LOCATION: Cytoplasmic.
-! TISSUS SPECIFICITY: Highly expressed in brain.
-!- SIMILARITY: Contains 1 BTB/POZ domain.
-!- SIMILARITY: Contains 6 Kelch repeats.
KHIL HUMAN STANDARD; PRT; 748 AA. 09A64; 09A84; 09A865; 09P238; 16-0CT-2001 [Rel. 40, Created) 16-0CT-2001 [Rel. 40, Last sequence update) 10-0CT-2003 [Rel. 42, Last annotation update) KEICH-1ike protein 1. As Annotation update) KIHLI OR KIAA1490.
 EMBL; AF252283; AAF81719.1; -.
EMBL; AF552279; AAF81716.1; -.
EMBL, AB040923; BAA96014.1; ALT_INIT.
EMBL; AL553738; CAC16128.1; -.
Genew; HGNC:6352; KLHL1.
 BTB.
KELCH 1.
KELCH 2.
KELCH 3.
KELCH 4.
KELCH 5.
 SER-RICH
 82680 MW;
 [3]
SEQUENCE OF 179-409 FROM N.A.
 748 AA;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 MCBI_TaxID=9606;
 REPEAT
REPEAT
SEQUENCE
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 Gaps
 STRAIN=cv. Japonica;
MEDLINE=8938662; PubMed=2780537;
MEDLINE=8938662; PubMed=2780537;
Yano H., Kamo M., Tsugita A., Aso K., Nozu Y.;
"The amino acid sequence of plastocyanin from rice (Oryza sativa, subspecies japonica).";
Protein Seq. Data Anal. 2:385-389(1989).
-!- FUNCTION: Participates in electron transfer between P700 and the Cytochrome bof. Complex in photosystem I.
-!- SUBCELULAR LOCATION: Locaely bound to the inner thylakoid membrane surface in chloroplasts.
 Molecular cloning and characterization of plastocyanin precursor in
 Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Lillopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
 ij
 InterPro; IRR000923; BlueCu_1.
InterPro; IRR001235; Copper_blue.
InterPro; IRR001235; Copper_blue.
Pran; PR00127; copper-blud; 1.
PRINTS; PR00125; COPPERBLUE.
PROSTIE: PS001255; COPPER BLUE; 1.
Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
 DB 1; Length 748;
 0; Indels
 PLASTOCYANIN.
PLASTOCYANIN-LIKE.
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
A) E45725D25B5F400D CRC64;
 Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
 -1- SIMILARITY: Contains 1 plastocyanin-like domain.
 P20423; Q9SBB8;
01-FEB-1991 (Rel. 17, Created)
28-FEB-2003 (Rel. 41, Last aequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Plastocyanin, chloroplast precursor.
Score 34.5; DB
Pred. No. 35;
1; Mismatches
 CHLOROPLAST
 SEQUENCE FROM N.A.
STRAIN=cv. Ilpoom; TISSUE=Leaf;
 EMBL; AF093636; AAC78108.1; -. HSSP; P00289; 2PCF.
 Ψ.
 63.9%;
80.0%;
 15577
 8; Conservative
 STANDARD;
 127 EEVVP-GMDF 135
 10
 1154
1154
1139
142
142
 1 EEVVPXGMDY
 58
58
139
142
147
154 AA;
 Oryza sativa (Rice)
```

120 120 T -> N (IN CV. NK 1558). 155 AA; 15709 MW; DAA7EABESF6F4F91 CRC64;

VARIANT SEQUENCE

```
-i-SIMILARITY: Concerns 1 plastcocyanin-like domain.

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 ö
 SEQUENCE FROM N.A.
STRATNS-C. NK 1558;
MEDLINE-94039081; PubMed=8223592;
Nielsen P., Gausing K.;
"In vitro binding of nuclear proteins to the barley plastocyanin gene
 Gaps
 product 123.2... 27:97-104(1993).

-1- FUNCTION: Participates in electron transfer between P700 and the cytochrome b6-f complex in photosystem I.

-1- SUBCELLULAR LOCATION: Loosely bound to the inner thylakoid membrane surface in chloroplasts.
 Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum.
NCBL_TaxID=4513;
 STRAIN=cv. Bomi;
Nielsen O.S., Gausing K.;
The precursor of barley plastocyanin: sequence of cDNA clones and
gene expression in different tissues.";
FEBS Lett. 225:159-162(1987).
 R MBL; Y00704; CAA66666.1; -.
R PIR; S38255; S38255.
R HSSP; P00289; 2PCF.
R InterPro; IPR000923; Bluecu_1.
R InterPro; IPR001235; Copper_blue.
R InterPro; IPR008972; Cupredoxin.
R Pfam; PF00127; copper-bind; 1.
R PRINTS; PR00156; COPPERBLUE.
R ProDom; PD001235; Copper blue; 1.
R PROSITE; PS00125; COPPER_BLUE; 1.
R PCD00m; PD001235; COPPER_BLUE; 1.
R PROSITE; PS00126; COPPER_BLUE; 1.
R CALOroplast; Rlectron transport; Copper; Thylakoid; Membrane; Transit peptide.
R TRANSIT
 ö
Score 34; DB 1; Length 154;
Pred. No. 8.7;
 3; Indels
 PLASTOCYANIN.
PLASTOCYANIN-LIKE.
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
 01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnoration update)
Plastocyanin, chloroplast precursor.
 155 AA
 Mismatches
 63.0%;
54.5%;
Query Match
Best Local Similarity 54.5
Matches 6; Conservative
 STANDARD;
 100 EDAVPSGVDVS 110
 1 EEVVPXGMDYS 11
 58
1155
140
143
143
 promoter region.";
 SEQUENCE FROM N.A.
 PLAS HORVU
P08248;
 CHAIN
 METAL
```

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 0
 STRAIN=CV. Italica;
Dimitrov M.I., Egorov C.A., Donchev A.A., Atanasov B.P.;
Promplete amino acid sequence of poplar plastocyanin b.";
FBS Lett. 226:17-22(1987).
I PEBS Lett. 226:17-22(1987).
I PUNCTION: Participates in electron transfer between P700 and the cytochrome b6-f complex in photosystem I.
I SUBCELLULAR LOCATION: Loosely bound to the inner thylakoid membrane surface in chloroplasts.
I SIMILARITY: THERE ARE 12 DIFFERENCES BETWEEN THE SEQUENCE OF POPLAR PLASTOCYANINS A AND B.
I SIMILARITY: Contains 1 plastocyanin-like domain.
 Gaps
 Populus nigra (Lombardy poplar).
Makaryoca; Varidiplancae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicots; rosids; eurosids 1; Malpighiales; Salicaceae; Saliceae; Populus.
 ö
 PERMY PRO0127; copper bind; 1.

PRINTS; PRO01235; COPPERBUE.
PROSTIE; PRO01235; COPPER BLUE; 1.

Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
Transit peptide; Multigene family.
TRANSIT 1 69 PLASTOCYANIN B.

CHAIN 70 168 PLASTOCYANIN B.

PROMAIN 70 168 PLASTOCYANIN E.

PRASTOCYANIN LIKE.
Query Match 63.0%; Score 34; DB 1; Length 155; Best Local Similarity 54.5%; Pred. No. 8.7; Matches 6; Conservative 2; Mismatches 3; Indel8
 SEQUENCE FROM N.A. STRAIN=cv. Italical TISSUE=Leaf; STRAIN=cv. Italical TISSUE=Leaf; Strain=Ly Contaclewski V., Haehnel W.; Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
 01-OCT-1989 (Rel. 12, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
 01-0CT-1996 (Rel. 34, Last sequence upc
28-FBB-2003 (Rel. 41, Last annotation v
Plastocyanin B, chloroplast precursor.
 COPPER.
 COPPER.
 EMBL, Z50186; CAA90565.1; -.
PIR, S00210, S00210.
PIR, S5208, S8208.
HSSP, P00299; 1PLC.
InterPrc; IPR000933; BlueCu 1.
InterPrc; IPR000233; BlueCu 1.
InterPrc; IPR000372; Cupredoxin.
 101 EDAVPSGVDVS 111
 STANDARD;
 1 REVVPXGMDYS 11
 SEQUENCE OF 70-168
 NCBI_TaxID=3691;
 POPNI
 Query Match
 RESULT 10
PLAT POPNI
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566 AA; 65173 MW; 9D48C8B5D6D3B74B CRC64;
 h 63.0%;
Similarity 85.7%;
6; Conservative 0
 STANDARD;
 169 VPFGMDY 175
 4 VPXGMDY 10
 Query Match
Best Local Similarity
 homologs;
 R8L4 ARATH
Q9FJK8;
 SO SEQUENCE
 R8L4_ARATH
 Matches
 ઠે
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 ó
 similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the phenylalanyl-tRNA synthetase beta chain family. Subfamily 2.
 SEQUENCE FROM N.A.
STRAIN=ATCC 35210 / B31;
MEDLINE=9805943; PubMed=9403685;
MEDLINE=98056943; PubMed=9403685;
Lathigra R., Mitte O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M., Dougharty B., Tomb U.F., Flaischmann R.D., Richardson D., Peterson J., Kerlavage A.K., Quackenbush J., Salzberg S., Hanson M., Van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Ariiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B., Smith H.O., Venter J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrelia
 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine---
FRNA ligase beta chain) (PheRS).
 EMBL; U82978; AAB41019.1; -.

EMBL; AE01153; AAC66870.1; -.

PIR; A70164; A70164.

HAMAP; MF_00284; -; 1.

InterPro; IPR006131; PheT_arch.

Pfam; PF03484; B5; 1.

TIGRNAM; TIGR04471; pheT_arch; 1.

TIGRNAM; TIGR04471; pheT_arch; 1.

Complete protecome.
 Gaps
 SEQUENCE FROM N.A.
STRAIN=ATCC 35210 / B31;
Barbour A.G., Hinnebusch J.;
"Phenylalanyl-tRNA synthetaes genes (alpha and beta subunits) and thioredoxin reductaes gene of Borrelia burgdorferi,";
submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
 Borrelia burgdorferi (1yme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia
 Nature 390:586-586(1997).
-!- CARALYIIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP
diphosphate + L-phenylalanyl-tRNA(Phe).
-!- SUBUNI: Tetramer of two alpha and two beta chains (By
 ;
0
 63.0%; Score 34; DB 1; Length 168; 54.5%; Pred. No. 9.5; tive 2; Mismatches 3; Indels
 168 AA; 16981 MW; F20DA6EA2038AEEA CRC64;
 566 AA.
 PRT;
 Conservative
 |: || |: |
112 EDAVPSGVDVS 122
 STANDARD;
 1 EEVVPXGMDYS 11
 Query Match
Best Local Similarity
 NCBI_TaxID=139;
 burgdorferi
 9
 BORBU
 SECUENCE
 SYFB_BORBU
 Matches
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 ö
 10-CCT-2003 (Rel. 42, Created)
10-CCT-2003 (Rel. 42, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
10-CCT-2003 (Rel. 42, Last annotation update)
Probable disease resistance RPP8-like protein 4.
RPP8L4 OR AT5G48620 OR KISN18-9.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta; Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids; euroside II; Brassicales; Brassicaceae, Arabidopsis.
Nibl_TaxID=3702;
 Gaps
 SEQUENCE FROM N.A.
STRATNS-CV. COlumbia,
MEDLINE-99087489; PubMed-9872454;
Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
 "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned Pl and TAC clones.";

NAR Res. 5:297-336(1998).
 ö
Score 34; DB 1; Length 566;
Pred. No. 33;
0; Mismatches 1; Indels.
 InterPro; IPR002182; NB-ARC.
Pfam; PF00560; LRR; 2.
Pfam; PF00931; NB-ARC; 1.
PRINTS; PR00364; DISEASERSIST.
Plant defense; ATP-binding; Repeat; Leucine-rich repeat.
DOMAIN
 908 AA.
 WWW="http://niblrrs.ucdavis.edu".
 EMBL, AB015468; BAB10695.1; -.
EMBL, AK117163; BAC41841.1; -.
InterPro; IPR000767; Disease_resist.
InterPro; IPR01611; LRR.
```

α

us-09-909-164-13.rsp

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ö
 STRAIN=cv. Di-17;
MEDLINE=20271766; PubMed=10810142;
Cooley M.B., Pathirana S., Mu H.-J., Rachroo P., Klessig D.F.;
Cooley M.B., Pathirana S., Mu H.-J., Rachroo P., Klessig D.F.;
"Members of the Arabidopsis HRT/RPP8 family of resistance genes confer
"------ to both viral and comycete pathogens.";
 "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty Pl and TAC
 STRAIN=cv. Columbia, and cv. Landsberg erecta;
MEDLINE=99030193; PubMed=9811794;
MCDowell J.M., Dhandaydham M., Long T.A., Aarts M.G.M., Goff S.,
Holub E.B., Dangl J.L.;
"Intragenic recombination and diversifying selection contribute to the
evolution of downy mildew resistance at the RPP8 locus of
Arabidopsis.";
 SEQUENCE FROM N.A. (ISOFORM 1).

STRAIN=cv. Columbia;

MEDIJIRE=22954850; PubMed=14593172;

MEDIJIRE=22954850; PubMed=14593172;

MEDIJIRE=22954850; PubMed=14593172;

Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F., Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carnindi P.,

Chao O., Choy N., Enju A., Goldsmith A.D., Gurial M., Hansen N.F.,

Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Idda K., Karnes M.,

Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
 Q8W4_0; Q8CWGS; Q9MSA1; Q9ZSY3; Q9ZSY4;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 43, Last sequence update)
115-WAR-2004 (Rel. 43, Last annotation update)
Disease resistance protein RPPB (Resistance to Peronospora parasitica
 Gaps
 protein 8).

RPP8 OR HRT OR AT5G43470 OR MWF20.19.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 STRAIN=cv. Columbia;
MEDLINBE-20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu B., Kotani H.,
Tabata S.;
 SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, MUTANTS RPP8-1; RPP8-2 RPP8-3, AND VARIANTS. STRAIN=cv. Columbia, and cv. Landsberg erecta;
 ..
0
 DB 1, Length 908;
 2; Indels
 559 LRR 1.
223 LRR 2.
867 LRR 3.
199 ATP (POTENTIAL).
104448 MW, 3111991B17239693 CRC64;
 SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS
 Score 34; DB 1; Pred. No. 54; 2; Mismatches
 908 AA
NB-ARC
 PRT;
 SEQUENCE FROM N.A. (ISOFORM 1).
 Plant Cell 10:1861-1874(1998).
 63.08;
 60.08;
 6; Conservative
 STANDARD;
 883 EKLVPGGEDY 892
 1 EEVVPXGMDY 10
 DNA Res. 7:31-63(2000)
 146 4
575 5
600 6
842 8
192 1
 Best Local Similarity
 NCBI_TaxID=3702;
 ARATH
 clones.";
DOMAIN
REPEAT
REPEAT
REPEAT
NP BIND
SEQUENCE
 Query Match
 Matches
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 NTERRACTION WITH TIP.

X MEDLINE-20196823; PubMed=11041886;

Ren T., Qu F., Morris T.J.;

Ren T., Qu F., Morris T.J.;

Ren T., Qu F., Morris T.J.;

THRT gene function requires interaction between a NAC protein and risk gene function requires protein to confer resistance to turning crinkle virus."; yiral capsid protein to confer resistance proteins guard the plant against pathogens that content an appropriate avirulence protein via an indirect interaction with this avirulence protein. That triggers a defense system including the hypersensitive response, which restricts the pathogen growth. The interaction with TIP (TCV-interacting protein) may be essential for the recognition of the avirulence proteins, and the triggering of the defense response.

C.-I. SUBDINIT: Interacts with the NAC protein TIP.
 DATABASE: NAME-NIB-LRRS;
NOTE-Functional and comparative genomics of disease resistance gene
 Isoda-0804439-2; Sequence-VSP 007171, VSP 007172;
Note-Has been shown to exist only in cv.—Columbia so far;
Note-Has been shown to exist only in cv.—Columbia so far;
DOMAIN: The LRR repeats probably act as specificity determinant of pathogen recognition.
POLYMORPHISM: The strong polymorphisms present in cv. Di-17 and cv. Columbia are probably due to an unequal crossing-over between the highly related RPBs and RPHRA genes present in cv. Landsberg erecta. Such variations probably modify the specificity of
Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T., Satou M., Tamse R., Vayaberg M., Wallender E.K., Wong C., Yamamura Y., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; "Empirical analysis of transcriptional activity in the Arabidopsis
 J.,
Kawai J.,
 SEQUENCE FROM N.A. (ISOFORM 2).
STAIN-ECV. COLUMDIA;
SERI M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Imyashizaki Y., Shinozaki K.,
"Arabidopsis thaliana full-length cDNA.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
 Event=Alternative splicing; Named isoforms=2;
 IsoId=Q8W4J9-1; Sequence=Displayed;
 EMBL; AF089710; AAC83165.1; -.
EMBL; AF089711; AAC76631.1; -.
EMBL; AP234174; AAF36597.1; -.
EMBL; AY062918; BAA97426.1; -.
EMBL; AY062914; AAL33592.1; -.
EMBL; AX18862; BAC43449.1; -.
INCEPPO; IPRO00767; Disease_resist.
 homologs;
WWW="http://niblrrs.ucdavis.edu".
 genome.";
Science 302:842-846(2003).
 Name=1;
 Name=2
 +
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RP8H ARATH
 DOMAIN
REPEAT
REPEAT
NP BIND
SEQUENCE
 -
 885
 P59584;
 RESULT 14
RP8H_ARATH
 셤
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 ò
 Landaberg erecta).

GKGV -> EKGI (in cv. Landaberg erecta).

GKGV -> EKGI (in cv. Landaberg erecta).

E -> D (in cv. Landaberg erecta).

F -> L (in cv. Di-17).

G -> Q (in cv. Di-17).

G -> U (in cv. Di-17).

G -> C (in cv. Di-17).

Y -> S (in cv. Di-17).

Y -> S (in cv. Di-17).

Y -> S (in cv. Di-17).

Y -> S (in cv. Di-17).

Y -> S (in cv. Di-17).

Y -> S (in cv. Di-17).

X -> T (in cv. Di-17).

X -> T (in cv. Di-17).

Y -> K (in cv. Di-17).

Y -> K (in cv. Di-17).

Y -> K (in cv. Di-17).

Y -> K (in cv. Di-17).

Y -> K (in cv. Di-17).

Y -> K (in cv. Di-17).

Y -> K (in cv. Di-17).

Y -> K (in cv. Di-17).
 N -> F (in cv. Di-17 and cv. Landsberg erecta)
DEBIGATYSLFY -> YSKISAYDLFN (in cv. Landsberg erecta).
Landsberg erecta).
A -> W (in cv. Landsberg erecta).
E -> Q (in cv. Landsberg erecta).
E -> Q (in cv. Landsberg erecta).
DN -> NR (in cv. Landsberg erecta).
NPVLSWQ -> NKTLENRYH (in cv. Lil).
DN -> NR (in cv. Landsberg erecta).
WQ -> SH (in cv. Landsberg erecta).
 10G0L -> \overline{\rm VDEQ1} (in cv. Landsberg erecta) G -> E (in cv. Di-17) SGK -> RGE (in cv. Di-17 and cv.
 LRR 2.
ATP (POTENTIAL).
WRWLLTSRNEGVGIH -> ELLWYIHEALFILNS (in
 F-> S (in cv. Di-17 and cv. Landsberg erecta).
W -> C (in cv. Di-17 and cv. Landsberg C-> R (in cv. Di-17 and cv. Landsberg C-> R (in cv. Di-17 and cv. Landsberg
 C -> S (in cv. Di-17 and cv. Landsberg
erecta).
 T -> I (in cv. Di-17).
S -> R (in cv. Di-17).
S -> R (in cv. Di-17).
H -> Q (in cv. Di-17).
I -> L (in cv. Landeberg erecta).
KNKT -> RNAR (in cv. Di-17).
K -> N (in cv. Landeberg erecta).
K -> N (in cv. Landeberg erecta).
 erecta).

PRF -> SRFK (in cv. Di-17).

Y -> F (in cv. Di-17).

S -> Y (in cv. Landsberg erecta).

C -> S (in cv. Di-17 and cv. Landsberg
 -> N (in cv. Landsberg erecta).
-> K (in cv. Di-17 and cv. Landsberg
isoform 2).
/FTId=VSP 007171.
Missing (In isoform 2)
/FTId=VSP_007172.
 erecta).
 erecta)
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 erecta)
 4443
44460
4486
4486
514486
 518
 387
 399
 31
29
87
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283
369
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85
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Arabuchesis.;

Plant Cell 10:1861-1874(1998).

-!- PUNCTION: Disease resistance protein. Resistance proteins guard

-!- PUNCTION: Disease resistance protein. Resistance proteins guard

the plant against pathogens that contain an appropriate avirulence protein via an indirect interaction with this avirulence protein.

That triggers a defense system including the hypersensitive response, which restricts the pathogen growth. In contrast to RPB9, it does not specifically recognize the EmcoS avirulence protein from Peronospora parasitica.

-!- MISCELANBOUS: In or. Columbia and cv. Di-17, this protein is not present due to an unequal crossing over between the RPPB and RPBHA censes that creates a unique RPPB gene.

-!- SIMILARITY: Belongs to the disease resistance NB-LRR family.

RPPB/HRT SUbfanily.

-!- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.

-!- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.

-!- SIMILARITY: Contains 1 NB-ARC domain.

-!- SIMILARITY: Contains 2 NB-ARC domain.

-!- DATABASE: NAME-NIB-LRRS;

-!- DATABASE: NAME-NIB-LRRS;
 ö
 ö
 SECURNCE FROM N.A., AND FUNCTION.
STRAIN=cv. Landsberg erects;
MEDLINES9030193; PubMed=9811794;
MCDOWell J.M., Dhandsydham M., Long T.A., Aarts M.G.M., Goff S.,
Holub E.B., Dangl J.L.;
"Intragenic recombination and diversifying selection contribute to the evolution of downy mildew resistance at the RPP8 locus of Arabidopsis.";
 Gaps
 Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 Gaps
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 .
0
 Score 34; DB 1; Length 908;
Pred. No. 54;
2; Mismatches 2; Indels
 63.0%; Score 34; DB 1; Length 910; 60.0%; Pred. No. 55; 2; Indels :ive 2; Mismatches 2; Indels
 Interpro; servour. 2.
Pfam; PF00560; LT.
Pfam; PF0051; NB-ARC; 1.
PRINTS; PR00364; DISEASERSIST.
Plant defense; ATP-binding; Repeat; Leucine-rich repeat.
DOMAIN 10 45 LEUCINE-ZIPPER.
 602 625 LRR 1.
844 869 LRR 2.
192 199 ATP (POTENTIAL).
910 AA; 105263 MW; 5BIE9F65A19A12EE CRC64;
 10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Disease resistance protein RPH8A (RPP8 homolog A).
 Arabidopsis thaliana (Mouse-ear cress)
 WWW="http://niblrrs.ucdavis.edu".
InterPro; IPR007057, Disease_resist.
InterPro; IPR001611; IRR.
InterPro; IPR0021182, NB-ARC.
 63.0%;
 ilarity 60.0%;
Conservative
Query Match
Best Local Similarity 60.0.
Best Local 6; Conservative
 STANDARD;
 894
 883 EKLVPGGEDY 892
 459
625
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 1 EEVVPXGMDY 10
 EEVVPXGMDY 10
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EKLVPGGEDY
 Query Match
Best Local Similarity
Matches 6; Conserv
 homologs;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its way must by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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SEQUENCE FROM N.A.
MEDLINE=96337999; PubMed=8688087;
MEDLINE=96337999; PubMed=8688087;
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Sutton G.G., Blake J.A., FlizSerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherry B.A., Tomb J.-F., Adams M.D., Raich C.I.,
Overbeek R., Kirkness E.F., Weinston K.G., Merriack J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.
Ulterback R.K., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Raberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klank H.-P., Fraser C.M., Smith H.O., Wosse C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
 Score 33; DB 1; Length 276;
Pred. No. 26;
4; Mismatches 2; Indels
 TIGR; MJ0939; -.
InterPro; IPR001163; SDRNP Sm.
InterPro; IPR005358; UPP0153.
BYDAPCHELSOS PROSESS; UPP0153; 1.
BYDAPCHELSOS PROCESIN; Complete proteome.
SEQUENCE 276 AA; 33454 MW; 97BD69D392BC8FDF CRC64;
 Methanococcus jannaschii.
Archaea, Buryarchaeota; Methanococci; Methanococales;
Methanocaldococcaceae; Methanocaldococcus.
NCBI_TaxID=2190;
 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
11-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ0939.
PRT;
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45.5%;
 EMBL; U67537; AAB98946.1; -.
PIR; C64417; C64417.
 Science 273:1058-1073(1996)
 Query Match
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Matches 5; Conservative
 STANDARD;
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Search completed: June 3, 2004, 11:49:53 Job time: 4.86667 secs

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1 EEVVPXGMDYS 11

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Q94382 caulobacter Q9483 caulobacter Q9463 aeropyrum p Q81192 shigella fl Q852680 escherichia s Q94637 ardrographi Q956673 carcinus ma Q94643 callinectes O1704 caenorhabdi O52673 escherichia O52666 escherichia O52666 escherichia O27466 methanobact Q9829 rhizobium l Q8tbj7 homo sapien Q8ebj7 homo sapien Q8ebj8 streptococc Q8ebs streptococc Q8c29 streptococc Q8c29 streptococc Q8c29 streptococc Q8c29 streptococc Q8c29 streptococc Q8c29 streptococc Q8c29 streptococc Q8c29 streptococc Q8c29 streptococc Q8c29 streptococc Q8c29 streptococc Q8c29 streptococc Q8c29 streptococc Q8c29 streptococc Q8c29 streptococc Q8c29 streptococc Q8c29 streptococc Q8c29 streptococc Q8c29 streptococc Q8c29 streptococc Q8c29 streptococc Q8c20 acchaecellus Q7uf95 rhodopirell Q7uf95 rhodopirell Q7uf95 rhodopirell Q7uf95 rhodopirell Q7uf95 rhodopirell Q7uf95 rhodopirell Q7uf95 rhodopirell Q7uf95 rhodopirell

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Q7V6Q4 Q855K6

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SEQUENCE FROM N.A.
STRAIN=FY1679;
MEDLINE=94019318; PubMed=8413243;
Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlendy G.,
 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 Sherman F.; "CYC2 accodes a factor involved in mitochondrial import of yeast cytochrome C."; Mol. Cell. Biol. 13:6442-6451(1993).
 (1] _
SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
 to the EMBL/GenBank/DDBJ databases
 De haan M., Maarse A.C., Grivell L.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
 STRAIN=FY1679;
MEDLINE=94169519; PubMed=7764548;
 01,
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01-UUN-2003 (TrEMBLrel. 24
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PRELIMINARY;
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 SEQUENCE FROM N.A
 STRAIN=FY1679;
 012479
 RESULT 1
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 OBGENT oceanobacil
OSGEO archaeoglob
OSGESA enterococcu
0822A enterococcu
022081 citrus unsh
02096 citrus unsh
02095T arabidopsis
0905T arabidopsis
0906T ericotoris sativ
0806T oryza sativ
0806T oryza sativ
0806T ericotoris sativ
 012479 saccharomyc
 June 3, 2004, 11:35:06; Search time 29.8667 Seconds (without alignments) 116.206 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 1017041
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
 otal number of hits satisfying chosen parameters:
 1017041 segs, 315518202 residues
 SUMMARIES
 Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 M protein - protein search, using sw model
 Q8ESV7
Q30260
Q30260
Q82ZBH
Q22081
Q22081
Q9C9T7
P93T82
Q9SN30
Q4SN30
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Q8SO64
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sp_rvirus:*
sp_bacteriap:*
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sp_bacteria.*
sp_tungi.*
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sp_human.*
sp_invertebrate.*
sp_mammal.*
 sp_organelle:*
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sp_plant:*
sp_rodent:*
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Last sequence update)
Last annotation update)

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PRT;

ALIGNMENTS

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 [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM 14371 / JCM 11309; MEDLINE-22220767; PubMed=12235376; Takami H., Takaki Y., Uchiyama I.; Takami H., Takaki Y., Uchiyama I.; Takami H., Takaki Y., Uchiyama I.; Ridenome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme
 Gaps
Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
"Molecular cloning of a gene, DHS1, which complements a drug-hypersensitive mutation of the yeast Saccharomyces cerevisiae.";
Biosci. Biotechnol. Biochem. 58:391-395(1994).
EMBL; X74920; CAA99201.1; -.
EMBL; X87331; CAA60762.1; -.
EMBL; S54619; S54619.
SGD; S000539; YORO13W.
SGDUENCE 156 AA; 17881 MW; 380442B74C272B41 CRC64;
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 Bacteria; Firmicutes, Bacillales, Bacillaceae; Oceanobacillus.
NCBI_TaxID=182710;
 SEQUENCE FROM N.A.
STRAINS-VC-16 / DSM 4304 / ATCC 49558;
MEDLINE-98049343; PubMed-9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 70.4%; Score 38; DB 16; Length 319; 60.0%; Pred. No. 18; ive 3; Mismatches 1; Indels
 74.1%; Score 40; DB 3; Length 156; 77.8%; Pred. No. 3; 17.8%; Pred. No. 3; 1. Indels tive 1; Mismatches 1; Indels
 environments.";

Nucleic Acids Res. 30:3927-3935 (2002).

Nucleic Acids Res. 30:3927-3935 (2002).

InterPro; IPR001279; Blactmase-like.

Pfam, PR00753; lactamase B; 1.

Hyporhetical protein; Complete proteome.

SEQUENCE 319 AA; 35617 WW; 3BDAE4BF13E79E37 CRC64;
 Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical conserved protein.
 Last sequence update)
Last annotation update)
 319 AA
 01-07N-1998 (TrEMBLrel. 05, Created)
01-07N-1998 (TrEMBLrel. 05, Last seq.
01-UNY-2003 (TrEMBLrel. 24, Last anno
Hypothetical protein AF2411.
 Local Similarity 77.8
 Oceanobacillus iheyensis.
 6; Conservative
 PRELIMINARY;
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 189 EQLVPHGIDY 198
 Archaeoglobus fulgidus.
 1 EEVVPXGMDY 10
 58
 2 EVVPXGMDY 10
 50 EVMPLGMDY
 Best Local Similarity
Matches 6; Conserv
 NCBI_TaxID=2234;
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 030260
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Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Pleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougheity B.A., McKenney K., Adams M.D., Lofius B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocsyne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mann T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 Gaps
 A Makamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., A Makamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Matanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokwa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S., Sugimoto M., Takeunoto M., Matsumo A., Nakazaki N., Romplete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";

Thermosynechococcus elongatus BP-1.";

EMBL; AP005374; BAC09170.1; -.

R GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0006215; F:transporter activity; IEA.

GO; GO:0006810; P:transport; IEA.

R GO; GO:0006810; P:transport; IEA.

R GO; GO:0006810; Acrflvin_res.

R InterPro; IPR00464; HAB1.

R PRINTS; PR00973; ACR tran; 1.
 "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
EMBL: AR001109; AAB91255.1; -.
PIR; D69551; D69551.
 ö
 Score 38; DB 16; Length 1044;
Pred, No. 67;
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 2; Indels
 1044 AA; 113205 MW; 00E9C13F0F636D2F CRC64;
 elongatus)
 JUGN, FLETTO, 1780 103; Bac_luciferase.
Pfam; PF00296; Dac_luciferase; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 363 AA; 41736 MW; 0E976EAE788F4803 CRC64;
 Synechococcus elongatus (Thermosynechococcus elongatu:
Bacteria; Cyanobacteria; Chroococcales; Synechococcus
 01-MAR-2003 (TrENELrel. 23, Created)
01-MAR-2003 (TrENELrel. 23, Last sequence update)
01-JUN-2003 (TrEMELrel. 24, Last annotation update)
 2; Mismatches
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 TIGREAMS; TIGRO0915; 2A0602; 1.
 Multidrug efflux transporter.
 70.4%;
 Query Match
Best Local Similarity 63.00,
Best Local 7; Conservative
 | :|| |:|:|
ENIVPYGIDFS 130
 PRELIMINARY;
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843 EEVLPNGIGYS 853
 1 EEVVPXGMDYS 11
 1 EEVVPXGMDYS 11
 Local Similarity
 SEQUENCE FROM N.A.
 Complete proteome
SEQUENCE 1044 A
 NCBI TaxID=32046;
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Gaps

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STRAIN=cv. Miyagawa-Wase; TISSUE=Juice sacs and segment epidermis; Komatsu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.; "Differential expression of three sucrose-phosphate synthase isoforms during sucrose accumulation in citrus fruits (Citrus unshiu Marc.)."; EMBL; AB006319; BAA23215.1; -. BMBL; AB0649; S72649; P. P. S. S72649; S72649; P. S. S72649; S726
 SEQUENCE FROM N.A.
TISSUE-Juice sacs and segment epidermis;
Komatsu. A., Takanokura Y., Moriguchi T., Omura M., Akihama T.;
Komatsu. A., Takanokura Y., Moriguchi T., Omura M., Akihama T.;
"Differential expression of three sucrose-phosphate synthase isoforms during sucrose accumulation in citrus fruits (Citrus unshiu Marc.).";
Plant Sci. 140:169-178(1999).
PEMBL, AB006660; BAA22071.1; -.
PIR; S72650; S72650.
 Citrus unshiu (Satsuma orange).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Sapindales, Rutaceae, Citrus.
 ;
 TISSUE-Juice sacs and segment epidermis;
MEDLINE-96439842; PubMed-8842155;
Komatsu A., Takanokura Y., Omura M., Akihama T.;
"Cloning and molecular analysis of cDNA encoding three sucrose phosphate synthase isoforms from a citrus fruit (Citrus unshiu
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341 AA; 38136 MW; 61417A69C4560777 CRC64;
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 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Sucrose-phosphate synthase (Fragment).
 Created)
Last sequence update)
Last annotation update)
 348 AA
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 PRT;
 PRT;
 Mol. Gen. Genet. 252:346-351(1996)
 Q8W568;
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-0CT-2003 (TrEMBLrel. 25,
Atlg73750/F25P22_17.
 Best Local Similarity 66.77,
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 PRELIMINARY;
 348
 228 VIPPGMDFS 236
 234 VIPPGMDFS 242
 3 VVPXGMDYS 11
 3 VVPXGMDYS 11
 Query Match
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 SEQUENCE FROM N.A.
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 STRAIN=V583 / ATCC 700802;
MEDLINE=2255087; PubMed=12653927;
Paulsen I.T., Baneriei L., Myers G.S.A., Nelson K.E., Seshadri R.,
Read T.D., Foute D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
"Role of mobile DNA in the evolution of vancomycin-resistant
 Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus
NCBL_TaxID=1351;
 Gaps
 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Popermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Sapindales; Rutaceae; Citrus.
NCBI_TaxID=55188;
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Large conductance mechanosensitive channel protein.
MSCL OR EF3152.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Sucrose-phosphate synthase (Fragment)
 GO; GO:0016020; C:membrane; IEA.
GO; GO:0005216; F:ion channel activity; IEA.
GO; GO:0005810; F:ion channel activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR001185; MS_channel.
PEAM; PF0144; MSCL; I...
PRINTS; PR01264; MSCH-HANEL.
ProDom; PD007253; MS_channel; I.
TIGRRPMS; TIGR00220; MSCL; I.
COMplete proteome.
SEQUENCE 149 AA; 16127 WW; 555799BF1E47D341
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 PRT; 341 AA
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 darc.).";
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 Enterococcus faecalis.";
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Arabidopsis thaliana (Mouse-ear cress)

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Kim C.J., Chen H., Cheuk R., Shinn P., Banh J., Bowser L.,

Kim C.J., Chen H., Cheuk R., Shinn P., Banh J., Bowser L.,

A Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,

B shido J., Jones T., Karlina A., Karlin. Heumann G., Kawal J., Lam B.,

Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Southwick A.,

B Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,

B Anng C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,

Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Arabidopsis ORF clones";

"Arabidopsis ORF clones";

"Arabidopsis ORF clones";

"Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AF419606; AAL31938 1; ---

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EMBL; AR419606; Piprolyl oligopeptidase activity; IEA.

GO; GO:0004287; Fiprolyl oligopeptidase activity; IEA.

B TherPro; IRR00379; Sar Febrs.

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B ROUENCE 4S2 AA; 45682 MW; Al59955B21742C4A CRC64;
 Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale V.M., Goldsmith A.D., Hayashizaki Y.,
Bowser L., Carninci P., Dale J.M., Kamiya A., Karlin. Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Crin C.W., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y., Gill J.E., Goldamith A.D., Haans B., Hannen W.F., Hughes B., Huizar L., Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
 Gaps
 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots; rosids;
eurosids II, Brassicales; Brassicaceae, Arabidopsis.
 Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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 Score 36; DB 10; Length 452;
Pred. No. 69;
0; Mismatches 3; Indels
 Ecker J.R.;
"Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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Last sequence update)
Last annotation update)
 460 AA
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STRAIN=cv. Columbia;
MEDLINE=21016719; PubMed=11130712;
 .
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 66.78;
 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-OCT-2003 (TrEMBLrel. 25, Hypothetical protein.
 Query Match
Best Local Similarity 70.0.
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 210 EEDVPSAMDY 219
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 NCBI_TaxID=3702;
 Q9C9T7
 RESULT 9
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Lissual Lear;
Sugiharto B., Sakakibara H., Sugiyama T.;
Sugiharto B., Sakakibara H., Sugiyama T.;
Differential Expression of Two Genes for Sucrose-Phosphate Synthase
in Sugarcane: Molecular Cloning of the cDNAs and Comparative Analysis
of Gene Expression.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB001337; BAA19241.1;
GO; GO:0046524; F:sucrose-phosphate synthase activity; IEA.
GO; GO:001658; P:biosyntheis; IEA.
InterPro; IPRO01296; Glyco_transf.
InterPro; IPRO01296; Glyco_transf.
Pfam; PPR00534; Glycos transf. 1;
Glycosyltransferase; Transferase.
 Gaps
 Gaps
 Saccharum officinarum (Sugarcane).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Lillopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Saccharum.
Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P., Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A., Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I., Bai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M., Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M. Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.; Arabidopsis Lhaliana.",
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 ö
 Length 1047;
 66.7%; Score 36; DB 10; Length 460; 70.0%; Pred. No. 70; cive 0; Mismatches 3; Indels
 Score 36, DB 10; Length 10
Pred. No. 1.8e+02;
2; Mismatches 1; Indels
 1047 AA; 116379 MW; DOEDB34961E1D83D CRC64;
 Mature 408 816-820(2000).

BMBL, AC012679, AAG52073.1; -
PIR, G96764, G96764.

CO, G0:0003824; F:catalytic activity; IEA.

GO; G0:0004287; F:prolyl oligopeptidase activity; IEA.

GO; G0:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR002471; Pept S9 AS.

PROSIER; PS00708; PRO ENDOREP_SER; 1.
 01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14) (Fragment)
 PRT; 1047 AA
 2; Mismatches
 66.7%;
 Best_Local Similarity 70.0
Matches 7; Conservative
 Conservative
 PRELIMINARY;
 218 EEDVPSAMDY 227
 1 EEVVPXGMDY 10
 Local Similarity
es 6; Conserv
 SEQUENCE FROM N.A.
 NCBI_TaxID=4547;
 Hypothetical
SEQUENCE 46
 TISSUE=Leaf;
 Query Match
 SEQUENCE
 Query Match
 P93782
ID P93782
 RESULT 10
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PRELIMINARY;
 6; Conservative
 453 VIPPGMDFS 461
 469 VIPPGMDFS 477
 3 VVPXGMDYS 11
 3 VVPXGMDYS 11
 Query Match
Best Local Similarity
Matches 6; Conserv
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A. TISSUE=Gill;
 NCBI_TaxID=95602;
 088064
 RESULT 13
Q8S064
 RESULT 14
 Q9G004
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 PIR; T04062; T04062.

GO; GO: 0046524; F: Sucrose-phosphate synthase activity; IEA.

GO; GO: 0001675; P: Encaraferase activity, transferring glycosyl. . ; IEA.

GO; GO: 0001675; P: Losynthesis; IEA.

InterPro; IPR001296; Glyco_trans 1.

Ffam; PF00534; Glyco_trans 1.

Glycosyltransferase; Transferase.

SEQUENCE 1083 AA; 122688 MW; EPC126FCA2137BB1 CRC64;
 01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Sucrose-phosphate synthase-like protein (EC 2.4.1.14).
F23M11.40 OR AT4G10120.
Arabidopsis thaliana (Mouse-ear oress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II, Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
 Gaps
 SEQUENCE FROM N.A.
Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
Mayer K.F.X., Lemcke K., Schueller C.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
 Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae,
Enrhartoideae, Oryzeae, Oryza.
 ö
 66.7%; Score 36; DB 10; Length 1083; 66.7%; Pred. No. 1.8e+02; tive 2; Mismatches 1; Indels (
 [2]
SEQUENCE FROM N.A.
EU Arabidopsis sequencing project;
Submitted (SEP-1999) to the BMBL/GenBank/DDBJ databases
 EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL04948F3; CAB39764.1;
EMBL; AL04516; CAB78135.1;
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 24, Last annotation update)
Sucrose phosphate synthase.
 PRT; 1083 AA
 PRT; 1084 AA
 Query Match
Best Local Similarity 60...
6; Conservative
 PRELIMINARY;
 PRELIMINARY;
 483 VIPPGMDFS 491
 3 VVPXGMDYS 11
 SEQUENCE FROM N.A.
 NCBI_TaxID=4530;
 08N30
 043010
 RESULT 12
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Weihrauch D., Towle D.W.;

"Na+/H+-exchanger and Na+/K+/2Cl--cotransporter are expressed in gills of the euryhaline Chinese crab Eriocheir sinensis.";

Comp. Biochem. Physiol. 126:S158-S158(2000).

EMBL; AF301160; AAG39938.1; -.

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219 AA; 24159 MW; 599442DA26F0D3F1 CRC64;
 Clostridium perfringens.
Bactridium, Pirmicutes; Clostridia, Clostridiales; Clostridiaceae;
Clostridium, NCBI_TaxID=1502;
 ;
0
 64.8%; Score 35; DB 16; Length 253;
50.0%; Pred. No. 58;
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219 Aa; 24159 MW; 599442DA26F0D3F1 CRC64;
 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein CPE0057.
 253 AA.
 PRT;
 Query Match
Best Local Similarity 50.0
Matches 5; Conservative
 PRELIMINARY;
 107 VPQGLDYS 114
 4 VPXGMDYS 11
 SEQUENCE FROM N.A.
 QBXPA8
 RESULT 15
Q8XPA8
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0; Gaps

Search completed: June 3, 2004, 11:57:33 Job time: 29.8667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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protein search, using sw model OM protein 3, 2004, 11:31:01 ; Search time 45.9333 Seconds (without alignments) 67.664 Million cell updates/sec June

Run on:

US-09-909-164-42 52 1 EEVVPXGXHYS 11 Perfect score: Sequence: Title:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A Geneseq 29Jan04:\*

1: geneseqp1980s:\*

2: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2001s:\*

6: geneseqp2003s:\*

7: geneseqp2003s:\*

geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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|-----------|---------------------|------------|----------|---------------|--------------------|----------|-----------|-----------|----------|----------|-----------|----------|-----------|------------|----------|------------|----------|----------|-----------|----------|----------|------------|----------|----------|-----------|--------------------|
| SUMMARIES | Д                   | ABB80546   | ABB80554 | ABB80550      | ABB80555           | ABB80523 | ABB80558  | ABB80537  | ABB80560 | ABB80527 | ABB80541  | ABB80532 | ABB80531  | ABB80548   | ABB80549 | ABB80547   | ABB80544 | ABB80556 | ABB80557  | ABB80551 | ABB80553 | ABB80552   | ABB80545 | ABB80525 | ABB80534  | ABB80561           |
|           | DB                  | <u>်</u> ဟ | ß        | Ŋ             | Ŋ                  | Ŋ        | Ŋ         | 'n        | w        | ഗ        | Ŋ         | Ŋ        | Ŋ         | 'n         | Ŋ        | Ŋ          | Ŋ        | Ŋ        | ហ         | 'n       | ហ        | ß          | 'n       | ß        | Ŋ         | Ŋ                  |
|           | ength               | 11         | 11       | 11            | 11                 | 11       | 11        | 11        | 11       | 11       | 11        | 11       | 11        | 11         | 11       | 11         | 11       | 11       | 11        | 11       | 11       | 11         | 11       | 11       |           |                    |
|           | %<br>Query<br>Match | 94.2       | 94.2     | 94.2          | 94.2               | 92.3     | 92.3      | 92.3      | 92.3     | 92.3     | 92.3      | 92.3     | 92.3      | 76.9       | 76.9     | 76.9       | 76.9     | 76.9     | 76.9      | 76.9     |          | 76.9       | 76.9     |          | 75.0      | 'n                 |
|           | Score               | 4.04       | 49       | 49            | 49                 | 48       | 48        | 48        | 48       | 4 8      | 48        | 48       | 48        | 40         | 40       | 40         | 40       | 40       | 40        | 40       | 40       | 40         | 40       | 39       | 39        | 39                 |
|           | Result<br>No.       |            | 5        | e             | S<br>4             | r.       | ø         |           | 8        | 6        | 10        | 11       | 12        | 13         | 14       | 15         | 16       | 17       | 18        | 19       | 20       | 21         | 22       | 23       | 24        | 25                 |

| Hepatitis<br>Hepatitis<br>Hepatitis<br>Hepatitis |                              |                              | 444444                                                               |
|--------------------------------------------------|------------------------------|------------------------------|----------------------------------------------------------------------|
| Abb80521<br>Abb80522<br>Abb80536<br>Abb80566     | 50000                        | 22323                        | Abb80538 Abb80540 Abb80562 Abb80559 Abb80559 Abb80526 Abb80526       |
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| ABB80521<br>ABB80522<br>ABB80536<br>ABB80566     | 3056<br>3056<br>3056<br>3056 | 3053<br>3053<br>3053<br>3056 | ABB80538<br>ABB80540<br>ABB80562<br>ABB80559<br>ABB80526<br>ABB80526 |
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|                                                  |                              |                              | 4 4 4 4 4 4<br>0 4 4 6 4 7                                           |

## ALIGNMENTS

Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide. Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #26. ABB80546 standard; peptide; 11 AA. (first entry) 08-OCT-2002 Synthetic. ABB80546; ABB80546 

'note= "N-terminal acetyl" Location/Qualifiers Key Modified-site Modified-site

/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7" 11 /note= "C-terminal amide" Modified-site

WO200208251-A2.

31-JAN-2002.

19-JUL-2001; 2001WO-US023169.

21-JUL-2000; 2000US-0220101P.

(CORV-) CORVAS INT INC.

Brunck TK; Lim-Wilby M, Levy OE,

WPI; 2002-361643/39.

virus Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis Cprotease.

Claim 17; Page 65; 69pp; English.

The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of

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Gaps

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Indels

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Mismatches

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Conservative

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Matches

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have invention activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV procease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 ô
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #34.
 ö
 Score 49; DB 5; Length 11; Pred. No. 0.0045;
 Score 49; DB 5; Length 11; Pred. No. 0.0045; 0; Mismatches 1; Indels
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 'note= "D-form residue"
 Location/Qualifiers
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 Claim 17; Page 65; 69pp; English.
 Brunck
 ABB80554 standard; peptide; 11
 21-JUL-2000; 2000US-0220101P.
 94.2%;
 94.2%;
 19-JUL-2001; 2001WO-US023169
 (first entry)
 Query Match
Best Local Similarity 90.9
Matches 10, Conservative
 1 EEVVPXGXHYS 11
 1 EEVVPXGTHYS 11
 (CORV-) CORVAS INT INC
 Levy OE,
 WPI; 2002-361643/39.
 Misc-difference
 Sequence 11 AA;
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 Synthetic
 Query Match
 ABB80554;
 protease
 RESULT 2
 ABB80554
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 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 note= "Norvalyl carbonyl forming keto-amide linkage with
 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #30
 .
0
 ; DB 5; hears.
 Score 49; DB 5
Pred. No. 0.004
0; Mismatches
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 'note= "D-form residue"
 Location/Qualifiers
 Brunck TK;
 ABB80550 standard; peptide; 11 AA.
 Claim 17; Page 65; 69pp; English.
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169.
 residue 7'
 (first entry
 Local Similarity 90.9
Les 10; Conservative
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1 EEVVPXGXHYS 11
 Levy OE,
 (CORV-) CORVAS INT INC
 1 EEVVPXGXHYS
 1 EEVVPXGSHYS
 BEVVPXGSHYS
 WPI; 2002-361643/39.
 Similarity
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Novel peptide
activity usefu
 Modified-site
 Modified-site
 Lim-Wilby M,
 Modified-site
 08-OCT-2002
 31-JAN-2002.
 Synthetic
 protease.
 Query Match
 ABB80550;
 virucide.
 Best Loca
Matches
 ABB6550

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 RESULT 3
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RESULT

Best Local Similarity

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Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #3.
 Location/Qualifiers
 Brunck TK;
 ABB80558 standard; peptide; 11 AA.
 Claim 17; Page 64; 69pp; English.
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 92.3%;
 (first entry)
 Query Match
Best Local Similarity 90.9
Matches 10, Conservative
 1 EEVVPXGXHYS 11
 1
 (CORV-) CORVAS INT INC
 Levy OE,
 EEVVPXGMHYS
 WPI; 2002-361643/39.
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Novel peptide
activity usefu
 Modified-site
 Key
Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 Synthetic
 protease.
 ABB80558;
 virucide
 RESULT 6
 요
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 The sequence represents a peptide compound of the invention having the peptides of the invention are alpha **Retoantde peptide analogues. The peptides have virucide activity. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 virus
 Gaps
 Hepatitis C virus, HCV, serine protease, inhibitor, alpha-ketoamide;
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #35
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 Score 49; DB 5; Length 11;
Pred. No. 0.0045;
0; Mismatches 1; Indels
 note= "N-terminal acetyl"
 /note= "C-terminal amide"
 'note= "D-form residue"
 note= "D-form residue"
 Location/Qualifiers
 Brunck TK;
 ABB80523 standard; peptide; 11 AA.
 Ź
 Claim 17; Page 65; 69pp; English.
ABB80555
ID ABB80555 standard; peptide; 11
 94.2%;
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 entry)
 Query Match
Best Local Similarity 90.9
 11
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 Levy OE,
 (CORV-) CORVAS INT INC
 1 EEVVPXGXHYS
 EEVVPXGSHYS
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 WPI; 2002-361643/39
 Misc-difference
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 31-JAN-2002
 08-OCT-2002
 Synthetic
 ABB80523;
 protease
 ABB80555
 virucide
 Ŋ
```

(first entry)

08-OCT-2002

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ö
 The sequence represents a peptide compound of the invention having hepetities C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 virus
 Gaps
Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis \mathsf{C}^-
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #38
 ..
 Score 48; DB 5; Length 11;
Pred. No. 0.0072;
0; Mismatches 1; Indels
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 'note= "D-form residue"
 Synthetic
 ABBBOSSB

LID ABBB

XX ABBB

XX ABBB

XX ABBB

XX Hepa

KW Virt

XX YATT
```

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Sequence 11 AA;
 WO200208251-A2
Modified-site
 31-JAN-2002
 protease
ò
 셤
 ö
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "Norvaly1 carbony1 forming keto-amide linkage with
 note= "Norvalyl carbonyl forming keto-amide linkage with
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #17.
 ö
 Score 48; DB 5; Length 11;
Pred. No. 0.0072;
0; Mismatches 1; Indels
 note= "N-terminal acetyl"
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 /note= "D-form residue"
 note= "Oxymethionine"
 Location/Qualifiers
Location/Qualifiers
 Brunck TK;
 ABB80537 standard; peptide; 11 AA.
 Claim 17; Page 65; 69pp; English
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 92.3%;
 residue 7"
 residue 7"
 (first entry)
 10; Conservative
 Ħ
 1 EEVVPXGXHYS 11
 Levy OE,
 (CORV-) CORVAS INT INC
 EEVVPXCMHYS
 WPI; 2002-361643/39
 Local Similarity
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Key
Modified-site
 Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 Synthetic
 ABB80537;
 virucide.
 protease
 Query Match
 Matches
 ABB8053
 RESULT
 THEFFER
```

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Gaps
 Hepatitis C virus, HCV, serine protease, inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #40
 ö
 Score 48; DB 5; Length 11;
Pred. No. 0.0072;
 1; Indels
 0; Mismatches
 'note= "N-terminal acetyl"
11
/note= "C-terminal amide"
 /note= "C-terminal amide"
 'note= "D-form residue"
 note= "D-form residue"
 'note= "Oxymethionine"
 RESULT 8
ABB80560 standard; peptide; 11 AA.
XX
AC ABB80560;
XX
DT 08-OCT-2002 (first entry)
XX
DY Hepatitis C virus NS3/NS4a serine procestive virucide.
XX
XX
DY Synthetic.
XX
Synthetic.
XX
Synthetic.
XX
FT Key
FT Modified-site | 10ccation/Qualifiers
FT Modified-site | 10ccation/Qualifiers
FT Modified-site | 10ccation/Qualifiers
FT Modified-site | 10ccation/Qualifiers
FT Misc-difference | 10ccation/Gualifiers
FT Misc-difference | 10ccation/FT Misc-difference | 10ccation/FT Modified-site | 10ccation/FT Modified-site | 10ccation/FT Modified-site | 10ccation/FT Modified-site | 11
XX
WO200208251-A2.
 Location/Qualifiers
 Brunck TK;
 Claim 17; Page 64; 69pp; English.
 92.3%;
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169
 Query Match
Best Local Similarity 90.9
Matches 10; Conservative
 1 EEVVPXGXHYS 11
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 EEVVPXGQHYS
 WPI; 2002-361643/39
```

ö

X4X4X4X4X1X4X4144X8X222222228

```
note= "N-terminal acetyl"
 /note= "C-terminal amide"
 /note= "D-form residue"
 Location/Qualifiers
 Brunck TK;
 ABB80541 standard; peptide; 11 AA.
 Brunck TK;
 Claim 17; Page 64; 69pp; English.
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P.
 Query Match 92.3%;
Best Local Similarity 90.9%;
Matches 10; Conservative
 (first entry)
 11
 11
 Lim-Wilby M, Levy OE,
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 1 REVVPXGXHYS
 1 EEVVPXGMHYS
 WPI; 2002-361643/39.
 WPI; 2002-361643/39
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Novel peptide
activity usefu
 Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002
 Synthetic.
 ABB80541;
 virucide.
 protease
 RESULT 10
 ABB80541
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 ઠ
 ;
0
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 'note= "Norvalyl carbonyl forming keto-amide linkage with
 virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #7.
 ö
 92.3%; Score 48; DB 5; Length 11; 90.9%; Pred. No. 0.0072; ive 0; Mismatches 1; Indels
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 'note= "D-form residue"
 Location/Qualifiers
 Brunck TK;
 ABB80527 standard; peptide; 11 AA.
 Claim 17; Page 65; 69pp; English.
 19-JUL-2001; 2001WO-US023169.
 21-JUL-2000; 2000US-0220101P.
 21-JUL-2000; 2000US-0220101P
 19-JUL-2001; 2001WO-US023169
 residue 7"
 (first entry)
 92.3
Best Local Similarity 90.9
Matches 10; Conservative
 11
 1 EEVVPXGXHYS 11
 Levy OE,
 (CORV-) CORVAS INT INC.
 (CORV-) CORVAS INT INC
 EEVVPXGMHYS
 WPI; 2002-361643/39.
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Novel peptide
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 31-JAN-2002
 Synthetic
 activity protease.
 ABB80527;
 virucide.
```

**ABB8052** RESULT

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```
The sequence represents a peptide compound of the invention having the peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #21.
 ö
 Length 11;
 Score 48; DB 5; Length 11; Pred. No. 0.0072; 0; Mismatches 1; Indels
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pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Synthetic
 ABB80531;
 protease.
 Query Match
 Matches
 Matches
 RESULT 12
 ABB8053
 SXXX
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 The sequence represents a peptide compound of the invention having the peptides of the invention are alpha **etcoande** peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat alsorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcomide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #12.
 ö
 Score 48; DB 5; Length 11;
Pred. No. 0.0072;
0; Mismatches 1; Indels
 note= "N-terminal acetyl"
 /note= "C-terminal amide"
 note= "D-form residue"
 Location/Qualifiers
 ABB80532 standard; peptide; 11 AA.
 Brunck TK;
 Claim 17; Page 64; 69pp; English.
 Claim 17; Page 65; 69pp; English
 92.3%;
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 (first entry)
 10; Conservative
 1 EEVVPXGXHYS 11
 디
 Levy OE,
 CORVAS INT INC
 EEVVPXGQHYS
 WPI; 2002-361643/39.
 Query Match
Best Local Similarity
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 Synthetic
 virucide.
 ABB80532;
 protease
 Matches
 RESULT 11
 ABB8053
 XXXXXXXXXXXXXXXXXXXXXXXXXX
 8
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ö
 ö
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue ?"
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Gaps
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #11.
 ö
 ö
 92.3%; Score 48; DB 5; Length 11; 90.9%; Pred. No. 0.0072; tive 0; Mismatches 1; Indels
 Score 48; DB 5; Length 11;
Pred. No. 0.0072;
0; Mismatches 1; Indels
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 Location/Qualifiers
 ŦŸ,
 ABB80531 standard; peptide; 11 AA.
 Claim 17; Page 64; 69pp; English.
 ö
 Brunck
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169.
 92.3%;
 (first entry)
 Conservative
 Conservative
 1 EEVVPXGXHYS 11
 1 EEVVPXGGHYS 11
 1 EEVVPXGXHYS 11
 OE,
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39.
 Levy
 Query Match
Best Local Similarity
 Local Similarity
 Sequence 11 AA;
Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 10;
 31-JAN-2002
 10;
 à
```

/note= "Norvalyl carbonyl forming keto-amide linkage with

residue 7"

Misc-difference

Modified-site

/note= "C-terminal amide" 'note= "D-form residue"

WO200208251-A2

31-JAN-2002

Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.

Location/Qualifiers 'note= "N-terminal

Key Modified-site Modified-site

Synthetic

Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #29

08-OCT-2002

ABB80549;

11

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```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide annalogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
 note= "Norvalyl carbonyl forming keto-amide linkage with
 pharmaceutical composition comprising the peptide as an active ingredient
is useful for treating disorders associated with hepatitis C virus
 Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide;
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #28
 DB 5; Length 11
 Score 40; DB Pred. No. 0.29, 0; Mismatches
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 note= "D-form residue"
 Location/Qualifiers
 standard; peptide; 11 AA
 Brunck TK;
 Claim 17; Page 65; 69pp; English.
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169
 76.9%;
 residue 7"
 (first entry)
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39
 Ouery Match
Best Local Similarity
Matches 9; Conserv
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002
 ABB80548
ID ABB80548
 Synthetic
 virucide.
 ABB80548
 protease
RESULT 13
```

ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus

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Brunck

WPI; 2002-361643/39

Lim-Wilby M,

Novel peptide

protease.

virus

activity

(CORV-) CORVAS INT INC

19-JUL-2001; 2001WO-US023169. 21-JUL-2000; 2000US-0220101P.

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hepatifis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
 The sequence represents a peptide compound of the invention having
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #27
 ö
 Length 11;
 2; Indels
 Score 40; DB 5;
Pred. No. 0.29;
0; Mismatches
 ABB80547 standard; peptide; 11 AA.
 Claim 17; Page 65; 69pp; English.
 76.9%;
81.8%;
 (first entry)
 Query Match 76.9
Best Local Similarity 81.8
Matches 9; Conservative
 11
 Π
 EEVVPXGXHYS
 EEVVPXGSSYS
 Sequence 11 AA;
 08-OCT-2002
 Н
 ABB80547;
 RESULT 15
ABB80547
유
 ZZXEXEXEX
ZXXEXEX
 8
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Gaps

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2; Indels

0.29;

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Conservative

1 EEVVPXGXHYS 11

à g

11

EEVVPXGTDYS

RESULT 14 ABB80549 ID ABB80549 standard; peptide; 11 AA. XX

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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 note= "N-terminal acetyl"
 note= "C-terminal amide"
 Location/Qualifiers
 Brunck TK;
 Claim 17; Page 65; 69pp; English.
 19-JUL-2001; 2001WO-US023169.
 21-JUL-2000; 2000US-0220101P.
 (CORV-) CORVAS INT INC.
 Lim-Wilby M, Levy OE,
 WPI; 2002-361643/39.
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 31-JAN-2002.
 Synthetic.
 protease.
```

The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus 0; Gaps Query Match 76.9%; Score 40; DB 5; Length 11; Best Local Similarity 81.8%; Pred. No. 0.29; Matches 9; Conservative 0; Mismatches 2; Indels Sequence 11 AA;

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Search completed: June 3, 2004, 11:48:24 Job time: 45.9333 secs 1 EEVVPXGTDYS 11 q

1 EEVVPXGXHYS 11

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ALIGNMENTS
 TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
 Query Match 73.1
Best Local Similarity 70.0
Matches 7; Conservative
1 EEVVPXGXHY 10
 EAVVPGGEHY 73
US-09-252-991A-21444
 RESULT 2
US-09-134-001C-4794
860H86666666444444
860H86666666444444
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 Sequence 21444, A Sequence 4794, Ap Sequence 3, Appli Sequence 3, Appli Sequence 182, Appli Sequence 182, Appli Sequence 6, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli
 6440, Ap
7304, Ap
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 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-875-096-3
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US-08-530-010-9
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 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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 Gapop 10.0 , Gapext 0.5
 finimum DB seq length: 0 faximum DB seq length: 2000000000
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52
1 EEVVPXGXHYS 11
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Match Length DB
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 Perfect score:
 scoring table:
 Score
 M protein
 Database :
 seguence:
 searched:
 suo uns
 lesult
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Sequence 4794, Application US/09134001C
; Fatent No. 6380370
; GENERAL INVERMATION:
 Title OF INVERMITON: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 TITLE OF INVERMITON: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 TITLE OF INVERMITON: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 TITLE OF INVERMITON: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 CURRENT APPLICATION NUMBER: US/09/134,001C
 CURRENT PILING DATE: 1994-08-13
 PRIOR FILING DATE: 1997-11-08
 PRIOR FILING DATE: 1997-10-08
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NOS: 5674
 TYPE: PRI
 TY
 VS-09-222-991A-21444

i Sequence 21444 Application US/09252991A

j Sequence 21444 Application US/09252991A

j Sequence 21444 Application US/09252991A

j Setent No. 6551795

j GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 APPLICANT: Marc J. RUCLEIC AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

j TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

j TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

rILE REFERENCE: 107166.136

current application NUMBER: US/09/252,991A

current application NUMBER: US 60/074,788

pRIOR FILING DATE: 1999-02-18

pRIOR FILING DATE: 1999-07-27

j SEQ ID NOS: 33142

LENGTH: 856

LENGTH: 856
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Sequence 11, Appl
Sequence 5, Appli
Sequence 7, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 12960, Ap
Sequence 7284, Ap
Sequence 7284, Ap
Sequence 15, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
 Gaps
 ö
 73.1%; Score 38; DB 4; Length 856; 70.0%; Pred. No. 18; tive 0; Mismatches 3; Indels
US-08-484-101B-7

US-08-484-101B-9

US-08-484-101B-1

US-08-714-524D-3

US-08-714-524D-5

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US-08-714-524D-1

US-08-714-524D-1

US-08-714-524D-1

US-09-134-001C-3950

US-09-134-001C-4185

US-09-134-001C-4185

US-09-348-053A-8065

US-09-342-647-4

US-08-459-065-2

US-08-459-065-2

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US-08-459-065-2

US-08-459-065-2

US-08-459-065-2
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 Gaps
 ö
 65.4%; Score 34; DB 2; Length 126; 66.7%; Pred. No. 14; ive 1; Mismatches 2; Indels
 Jos-09-215-096-3

Sequence 3, Application US/09215096

Patent No. 6008194

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Lal, Preeti

APPLICANT: Kaser, Matthew R.

TILLE OF INVENTION: HUMAN PREPROTACHYKININ B

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 314 Porter Drive

CITY: Palo Alto

COUNTRY: USA

ZIP: CA
 COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FEBLEBG FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,096
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,995
NAME: Billings, Lucy J.
REGISTRATION UNDER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0326 US
RELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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 PF-0326 US
 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
 INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
 Query Match
Best Local Similarity 66.7.
Series 6; Conservative
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 1 EEVVPXGXH 9
 TYPE: amino acid
STRANDEDNESS: sir
 GenBank
 TOPOLOGY: line
IMMEDIATE SOURCE:
 LIBRARY: GenBe
; CLONE: 163590
US-08-879-995A-3
 CLONE: 163590
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 RESULT 3
US-09-252-991A-26615
Sequence 26615, Application US/09252991A
Sequence 26615, Application US/09252991A
Sequence 26615, Application US/09252991A
Sequence 26615, Application US/09252991A
Setent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ACRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT PILING DATE: 1999-02-18
PRIOR PELICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-07-17
PRIOR FILING DATE: 1999-07-27
NUMBER FOR FOR FOR DIAGNOS: 33142
SEQ ID NO 26615
LENGTH: 277
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 Score 36; DB 4; Length 1037;
Pred. No. 56;
1; Mismatches 3; Indels
 Score 35; DB 4; Length 277;
Pred. No. 21;
0; Mismatches 4; Indels
 Sequence 3, Application US/08879995A
Sequence 3, Application US/08879995A
Patent No. 5985606
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
CITY: Palo Alto
CONTEXT: CA
COUNTRY: USA
COUNTRY: USA
 COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/879,995A
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
 ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4794
 ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26615
 69.2%;
 Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
 Query Match
Best Local Similarity 63.6
Matches 7; Conservative
 199 KEVVSNGLHYS 209
 1 EEVVPXGXHYS 11
 1 EEVVPXGXHYS 11
 48 EETVPGGGHTS 58
 RESULT 4
US-08-879-995A-3
 TYPE: PRT
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Sequence 182, Application US/09536784

Patent No. 6573082
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
Sequence 182, Application US/08961083
Parent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
 Score 33; DB 3; Length 447;
Pred. No. 89;
1; Mismatches 2; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
 3.50 inch, 1.4Mb storage
 STREET: 9410 Key West Avenue CTTY: Rockville STATE: Maryland COUNTRY: USA
 COUNTER: USA

ZIP: 20850
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION UNMBER: BP340P2
PRIOR APPLICATION NUMBER: PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BLOSKed, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION PROPERS!
TELECOMMUNICATION SYSTEM
TELECOMMUNICATION SYSTEM
SEQUENCE CHARACTERICSICS:
SEQUENCE CHARACTERICSICS:
 63.5%;
62.5%;
 LENGTH: 447 amino acids
TYPE: amino acid
STRANDEDNESS: single
 Query Match
Best Local Similarity 62.5
Matches 5; Conservative
 linear
 :|| | ||
178 IVPHGGHY 185
 3 VVPXGXHY 10
 RESULT 8
US-09-536-784-182
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 Sequence 6771, Application US/09107532A
Sequence 6731, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette Stamm and David Bush
TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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 Score 34; DB 3; Length 126;
Pred. No. 14;
1; Mismatches 2; Indels
 63.5%; Score 33; DB 4; Length 63;
45.5%; Pred. No. 10;
tive 3; Mismatches 3; Indels
 CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1996
PRICR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
 , NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...63
; SEQUENCE DESCRIPTION: SEQ ID NO: 6771:
US-09-107-532A-6771
 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
 ZIP: 02354
COMPUTER READABLE FORM:
MEDLUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
 TELECOMMUNICATION INFORMATION.
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6771:
SEQUENCE CHARACTERISTICS:
TENGTH: 63 amino acide
TYPE: amino acide
 NUMBER OF SEQUENCES: 7310
 CITY: Waltham
STATE: Massachusetts
 Query Match
Best Local Similarity 45.5
Matches 5, Conservative
 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
 1 EEVVPXGXHYS 11
 28 EQVVPGGGH 36
 1 EEVVPXGXH 9
 RESULT 6
US-09-107-532A-6771
 RESULT 7
US-08-961-083-182
 PEATURE
 JS-09-215-096-3
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SSEE: No. 58211040 No. 5821104disk of No. 5821104th America, Inc.
I: 405 Lexington Avenue
New York
 Score 33; DB 2; 1
Pred. No. 1.2e+02;
0; Mismatches 2,
 COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskerte
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,118
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
 COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCTHWARE: FESTESC for Windows Version 2.0
SOCHWARE: FESTESC for Windows Version 2.0
CURRENT AFPLICATION DATA:
APPLICATION NUMBER: US/08/821,119
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambling, Blias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4107.204-US
TELECHOMONICATION INFORMATION:
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TELECHOMONICATION INFORMATION:
TELECHOMONICATION INFORMATION:
 STREET: 405 Lexington Avenue CIIY: New York
 ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
 INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
IENGTH: 600 amino acids
TYPE: amino acid
 Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
 MOLECULE TYPE: protein FRAGMENT TYPE: internal
 single
 ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
CORRESPONDENCE ADDRESS:
 4 VPXGXHYS 11
 31 VPKGWHYS 38
 linear
 STRANDEDNESS:
 USA
 USA
 STATE: N
COUNTRY:
 COUNTRY:
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 Sequence 6, Application US/09468656A

Sequence 6, Application US/09468656A

Patent No. 6582706

GENERAL INFORMATION:
APPLICANT: Johnson, Leslie S.
APPLICANT: Johnson, John B.
TITLE OF INVENTION: Wacifie Group A and B Having Selected Structural
TITLE OF INVENTION: Motifie
TITLE OF INVENTION: Motifie
FILE REFERENCE: 469201-444

CURRENT APPLICATION NUMBER: US/09/468,656A

CURRENT APPLICATION NUMBER: 60/113,048

PRIOR PILING DATE: 1998-12-21

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 6

LENGTH: 484

TYPE: PRT

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 Score 33; DB 4; Length 484; Pred. No. 97; 2; Indels
 Query Match 63.5%; Score 33; DB 4; Length 447; Best Local Similarity 62.5%; Pred. No. 89; Matches 5; Conservative 1; Mismatches 2; Indels
 Sequence 19, Application US/08821119
Patent No. 5821104
GENERAL INFORMATION:
APPLICANT: Holm, Kaj Andre
APPLICANT: Halkier, Grethe
APPLICANT: Lehmbeck, Jan
TITLE OF INVENTION: Tripeptidyl Aminopeptidase
NUMBER OF SEQUENCES: 23
 PRIOR APPLICATION COLLIGATION
PRIOR APPLICATION NUMBER: 08/961,083
FILING DATE: 0CT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 182:
SEQUENCE CHARACTERISTICS:
 TOPOLOGY: linear
MOLECULE TYPE: procein
SEQUENCE DESCRIPTION: SEQ ID NO: 182:
US-09-536-784-182
 CLASSIFICATION: <Unknown>
 LENGTH: 447 amino acids
TYPE: amino acid
STRANDEDNESS: single
 63.5%;
 Query Match
Best Local Similarity 62.5'
 178 IVPHGGHY 185
 3 VVPXGXHY 10
 3 VVPXGXHY 10
 US-09-468-656A-6
 RESULT 9
US-09-468-656A-6
 US-08-821-119-19
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 No. 59898890 No. 5989889disk of No. 5989889th America, Inc.
 Gaps
Length 600;
 Sequence 2, Application US/08821118
Patent No. 598989
GENERAL INFORMATION:
APPLICANT: Rey, Michael
APPLICANT: GOLIGHLY, Elizabeth
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES
TITLE OF INVENTION: ACTIVITY
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: NO. 5989889Gisk of No. 5989889
 Indels
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184 IVPHGDHY 191

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US-09-153-784-66
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US-09-153-784-66
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 Sequence 56, Application US/08961083

Sequence 56, Application US/08961083

Patent No. 6159469

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STRIEE: Maryland
COUNTRY: USA
 Length 763;
 2; Indels
 ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 Query Match 63.5%; Score 33; DB 4; ; Best Local Similarity 62.5%; Pred. No. 1.6e+02; Matches 5; Conservative 1; Mismatches 2.
 STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-09-536-784-66
 :|| | ||
184 IVPHGDHY 191
 3 VVPXGXHY 10
 RESULT 14
US-08-961-083-56
 ;
0
 RESULT 12

Sequence 66, Application US/08961083

Sequence 66, Application US/08961083

Patent No. 6159469

GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION:
TITLE OF INVENTION:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STREET: 9410 Key West Avenue
CITY: Rockville
STREET: 9410 Key West Avenue
CITY: Rockville
STREET: 940 Key West Avenue
CITY: Rockville
STREET: 9410 Key West Avenue
CITY: Rockville
STREET: 9410 Key West Avenue
CITY: Rockville
STREET: 9880

COUNTRY: USA
ZIF: 20850
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCIT Feat
COMPUTER: HP Vectra 486/33
OPERATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION NUMBER: ELING BATE:
FILING DATE:
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 ö
 DB 3; Length 763;
 Score 33; DB 2; Length 600;
Pred. No. 1.2e+02;
 Query Match 63.5%; Score 33; DB 3; Length 763
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels
 0; Mismatches
REFERENCE/DOCKET NUMBER: 4107
TELEPHONE: 212-867-0123
TELEPAX: 212-878-9655
TELEX: 122-878-9655
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 600 amino acids TYPE: amino acid STRANDEDNESS: 81ngle TOPOLOGY: linear MOLECULE TYPE: procein FRAGMENT TYPE: internal 15-08-821-118-2
 Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative (
 TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
 , MOLECULE TYPE: protein US-08-961-083-66
 4 VPXGXHYS 11
 3 VVPXGXHY 10
 31 VPKGWHYS 38
 linear
 STRANDEDNESS
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Gaps

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COMPUTER HP Vectra 446/33

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STRANDEDNESS: single

'' FOPOLOGY: linear

'' MOLECULE TYPE: protein

'' SEQUENCE DESCRIPTION: SEQ ID NO: 56:

US-09-536-784-56

Query Match

Best Local Similarity 62.5%; Pred. No. 1.7e+02;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0,

Qy 3 VVPXGXHY 10

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Db 185 IVPHGDHY 192

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Job time: 11.8 secs
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Sequence

ALIGNMENTS

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 June 3, 2004, 11:57:42; Search time 33.7333 Seconds (without alignments) 91.741 Million cell updates/sec
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Sequence 1
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 Description
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 Published Applications AA:*

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3: \(\cgn3_6 \) \\ ptodata/1 \) \\ pubpaa/USO6 \\ NEW \\ PUB.pep:*

4: \(\cgn2_6 \) \\ ptodata/1 \) \\ pubpaa/USO6 \\ NEW \\ PUB.pep:*

5: \(\cgn2_6 \) \\ ptodata/1 \) \\ pubpaa/USO6 \\ PUBCOMB.pep:*

6: \(\cgn2_6 \) \\ ptodata/1 \) \\ pubpaa/USO8 \\ PUBCOMB.pep:*

7: \(\cgn2_6 \) \\ ptodata/1 \) \\ pubpaa/USO8 \\ PUBCOMB.pep:*

8: \(\cgn2_6 \) \\ ptodata/1 \) \\ pubpaa/USO8 \\ PUBCOMB.pep:*

9: \(\cgn2_6 \) \\ ptodata/1 \) \\ pubpaa/USO8 \\ PUBCOMB.pep:*

10: \(\cgn2_6 \) \\ ptodata/1 \) \\ pubpaa/USO8 \\ PUBCOMB.pep:*

11: \(\cgn2_6 \) \\ ptodata/1 \) \\ pubpaa/USO9 \\ PUBCOMB.pep:*

13: \(\cgn2_6 \) \\ ptodata/1 \) \\ pubpaa/USO9 \\ PUBCOMB.pep:*

14: \(\cgn2_6 \) \\ ptodata/1 \) \\ pubpaa/USO8 \\ PUBCOMB.pep:*

15: \(\cgn2_6 \) \\ ptodata/1 \) \\ pubpaa/USO8 \\ PUBCOMB.pep:*

16: \(\cgn2_6 \) \\ ptodata/1 \) \\ pubpaa/USO8 \\ PUBCOMB.pep:*

17: \(\cgn2_6 \) \\ ptodata/1 \) \\ pubpaa/USO8 \\ PUBCOMB.pep:*

16: \(\cgn2_6 \) \\ ptodata/1 \) \\ pubpaa/USO8 \\ PUBCOMB.pep:*

17: \(\cgn2_6 \) \\ ptodata/1 \) \\ pubpaa/USO8 \\ PUBCOMB.pep:*

18: \(\cgn2_6 \) \\ ptodata/1 \) \\ pubpaa/USO8 \\ PUBCOMB.pep:*

18: \(\cgn2_6 \) \\ ptodata/1 \) \\ pubpaa/USO8 \\ PUBCOMB.pep:*

18: \(\cgn2_6 \) \\ ptodata/1 \) \\ pubpaa/USO8 \\ PUBCOMB.pep:*

18: \(\cgn2_6 \) \\ ptodata/1 \) \\ pubpa/USO8 \\ PUBCOMB.pep:*

18: \(\cgn2_6 \) \\ ptodata/1 \) \\ pubpa/USO8 \\ PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 US-09-909-164-30
US-09-909-164-38
US-09-909-164-38
US-09-909-164-7
US-09-909-164-11
US-09-909-164-15
US-09-909-164-15
US-09-909-164-15
US-09-909-164-15
US-09-909-164-21
US-09-909-164-25
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US-09-909-164-28
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US-09-909-164-28
US-09-909-164-28
US-09-909-164-28
 Total number of hits satisfying chosen parameters:
 1155919 seqs, 281338677 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 finimum DB seq length: 0 (aximum DB seq length: 2000000000
 US-09-909-164-42
52
1 BEVVPXGXHYS 11
 Query
Match Length
 Fitle:
Perfect score:
Sequence:
 Scoring table:
 Score
 M protein
 Searched:
 Jatabase
 tun on:
 4664666
 Result
 No.
```

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APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
URRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 30
LENGTH: 11
 TYPE: PRT
PREADMES: artificial sequence
PRATURE:
OTHER INFORMATION: 11-mer synthesized according to example
 Length 11;
 12;
 DB
 49;
 Score
 Sequence 30, Application US/09909164; Publication No. US20020068702A1; GENERAL INFORMATION:
 FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
US-09-909-164-30
 FEATURE:
NAME/KEY: NOD_RES
LOCATION: (1) ...(1)
OTHER INFORMATION: ACETYLATION
REATURE:
NAME/KEY: NOD_RES
LOCATION: (11) ...(11)
OTHER INFORMATION: AMIDATION
 94.2%;
RESULT 1
US-09-909-164-30
 Query Match
```

24

Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

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APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
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APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVERTION NUMBER: US/09/909,164
CURRENT APPLICANTON NUMBER: US/09/909,164
CURRENT APPLICANTON NUMBER: 00/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTY NOS: 62
INVERTICANTY NOS: 92
LENGTH: 11
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0
 Gaps
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 OTHER INFORMATION: 11-mer synthesized according to example 1 PEATURE:
 OTHER INFORMATION: 11-mer synthesized according to example 1
 94.2%; Score 49; DB 12; Length 11; 90.9%; Pred. No. 0.0038; tive 0; Mismatches 1; Indels
 Sequence 39, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
 NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
 LOCATION: (6). (6)

CTHER INFORMATION: norvaline-(CO)

US-09-909-164-38
 NAME/KEY: MOD_RES
LOCATION: (1)...(1)
CTHER INFORMATION: ACETYLATION
FRATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
 NAME/KEY: MISC FEATURE
LOCATION: (8). (8)
OTHER INFORMATION: D-amino acid
 SOFTWARE: Patentin version 3.1 SEQ ID NO 38 LEWGTH: 11 TYPE: PRT ORGANISM: artificial sequence PEATURE:
 NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FRATURE:
 TYPE: PRT ORGANISM: artificial sequence
 NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
FEATURE:
 Query Match
Best Local Similarity 90.9'
 1 EEVVPXGXHYS 11
 1 EEVVPXGSHYS 11
NUMBER OF SEQ ID NOS: 62
 NAME/KEY: MISC FEATURE LOCATION: (6)...(6)
 FEATURE: NAME/KEY: MISC_FEATURE LOCATION: (8)..(9)
 ઠ
 셤
 Sequence 34, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Lin-Wilby, Marguerita

APPLICANT: Lin-Wilby, Marguerita

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Houncy, Odile E

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

TITLE OF INVENTION NUMBER: US/09/909,164

CURRENT APPLICATION NUMBER: 60/220,101

PRIOR PELICATION DATE: 2003-03-25

PRIOR PELICATION NUMBER: 60/220,101

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFWARE: Patentin version 3.1

SEQ ID NO 34

LENGTH: 11
 Se-09-09-164-38
Se-09-09-164-38
Sequence 38, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Lim-Wallby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
FRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
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 TYPE: PRT
ORGANISM: artificial sequence
ORGANISM:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
 Query Match

94.2%; Score 49; DB 12; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.0038;

Matches 10; Conservative 0; Mismatches 1; Indel8
Pred. No. 0.0038;
0; Mismatches 1; Indels
 NAME/KEY: MISC FEATURE
LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
 NAME/KEY: MISC_FEATURE

LOCATION: (9)...(9)

COTHER INFORMATION: D-amino acid

MS-09-909-164-34
 NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
Best Local Similarity 90.9%;
Matches 10; Conservative
 FEATURE:
NAME/KEY:
NOD RES
LOCATION: (11)...(11)
FEATURE:
INFORMATION: AMIDATION
 1 EEVVPXGXHYS 11
 1 EEVVPXGSHYS 11
 1 EEVVPXGXHYS 11
 RESULT 2
US-09-909-164-34
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Sequence 15. Application US/09909164

| Sequence 15. Application No. US20020068702A1
| Publication No. US20020068702A1
| Publication No. US20020068702A1
| APPLICANT: Corvas International, Inc.
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| FILE REFERENCE: NOUNBER: 60/220,101
| PRIOR FILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SEQ ID NO 15
| Lim-Wilby, Marguerita Version 3.1
| Lim-Wilby, Marguerita
| Lim-Wilby, Marguerita
| Lim-Wilby, Marguerita
| Lim-Wilby, Marguerita
| Lim-Wilby, Marguerita
| Lim-Wilby, Marguerita
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| Lim-Wilby, Marguerita
| Lim-Wilby, Marguerita

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 FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
 OTHER INFORMATION: 11-mer synthesized according to example 1 FEATURE:
 Length 11;
 1; Indels
 DB 12;
 Score 48; DB 12;
Pred. No. 0.006;
0; Mismatches
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENT VERSION 3.1
SEQ ID NO 11
LENGTH: 11
 NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
PEATURE:
 , LOCATION: (8). (8) , OTHER INFORMATION: D-amino acid US-09-909-164-11
 NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
 LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
 92.3%;
 TYPE: PRT
ORGANISM: artificial sequence
PEATURE:
 TYPE: PRT ORGANISM: artificial sequence
 NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 Query Match
Best Local Similarity 90.9
Matches 10; Conservative
 1 EEVVPXGXHYS 11
 1 EEVVPXGMHYS 11
 NAME/KEY: MISC_FEATURE LOCATION: (8)...(8)
 FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6).7(6)
 NAME/KEY: MOD RES
LOCATION: (11)...(
 NAME/KEY: MOD_RES
 ઠ
 셤
 APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lery, Odile E
APPLICANT: Extuncy, Odile E
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
 Sequence 11, Application US/0990164
Publication No. US20020068702A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Corves International, Inc.
APPLICANT: Lim.Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Perunck
APPLICANT: Perunck
APPLICANT: Perunck
APPLICANT: Perunck
APPLICANT: Perunck
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
 ö
 Gaps
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 FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1 FEATURE:
 Score 49; DB 12; Length 11;
Pred. No. 0.0038;
0; Mismatches 1; Indels
 92.3%; Score 48; DB 12; Length 11; 90.9%; Pred. No. 0.006; 1; Indels tive 0; Mismatches 1; Indels
 NAME/KEY: MOD_RES
LOCATION: (1)...(1)
CTHER INFORMATION: ACETYLATION
FEATURE:
NAMES/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
 Sequence 7, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
; OTHER INFORMATION: D-amino acids US-09-909-164-39
 LOCATION: (9). (9)
OTHER INFORMATION: D-amino acid
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
 TYPE: PRT
ORGANISM: artificial sequence
 LOCATION: (11); (11); OTHER INFORMATION: AMIDATION US-09-909-164-7
 Query Match
Best Local Similarity 90.9
Matches 10; Conservative
 1 EEVVPXGXHYS 11
 1 EEVVPXGXHYS 11
 1 EEVVPXGSHYS 11
 1 EBVVPXGMHYS 11
 NAME/KEY: MISC FEATURE
 NAME/KEY: MOD RES
 US-09-909-164-11
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Sequence 25, Application US/09909164

Publication No. US20020068702A1

GENERAL INCOMMATION

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPRENCE: INJUNI32-US

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT PILING DATE: 2003-03-25

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3:1

LENGTH: 11
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 OTHER INFORMATION: 11-mer synthesized according to example 1
 OTHER INFORMATION: 11-mer synthesized according to example 1
 Query Match 92.3%; Score 48; DB 12; Length 11; Best Local Similarity 90.9%; Pred. No. 0.006; Matches 10; Conservative 0; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/09/909,1
CURRENT FILLING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILLING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEQ ID NO 21
LENGTH: 11
 LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
 NAME/KEY: MISC_FEATURE
| LOCATION: (9)...(9)
| CTHER INFORMATION: D-amino acid
| US-09-909-164-21
 FEATURE:
NAME/KRY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 TYPE: PRT ORGANISM: artificial sequence
 TYPE: PRT ORGANISM: artificial sequence
 FRATURE:
NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 1 REVVPXGXHYS 11
 1 EEVVPXGQHYS 11
 FRATURE:
NAME/KEY: MISC_FEATURE
 NAME/KEY: MISC_FRATURE LOCATION: (6)...(6)
 FEATURE:
NAME/KEY: MOD_RES
 g
 Sequence 21, Application US/09909164
Sequence 21, Application No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
 APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEFATITIS C
FILE REFRENCE: INOI192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR PELING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
LENGTH: 11
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 FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
 Score 48; DB 12; Length 11;
Pred. No. 0.006;
0; Mismatches 1; Indels
 92.3%; Score 48; DB 12; Length 11; 90.9%; Pred. No. 0.006;
 0; Mismatches
 Sequence 16, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
 FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
 ; OTHER INFORMATION: norvaline-(CO)
US-09-909-164-15
 FEATURE:
NAME/KEY: NOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NOAME/KEY: NOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
 LOCATION: (9)...(9)
CTHER INFORMATION: D-amino acid
US-09-909-164-16
 TYPE: PRT
ORGANISM: artificial sequence
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
 10; Conservative
 1 EEVVPXGGHYS 11
 1 EEVVPXGXHYS 11
 1 EEVVPXGGHYS 11
 1 EEVVPXGXHYS 11
 NAME/KEY: MISC_FEATURE
 Query Match
Best Local Similarity
Matches 10; Conserva
 RESULT 9
US-09-909-164-21
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...cricant: brunck, Terence K; TITLE OF INVELTIONS AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C; FILE REFERENCE: INVOIGE PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C; FILE REFERENCE: INVOIGE VOIG-03-25; CURRENT APPLICATION NUMBER: US/09/909,164; PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
SPRIOR FILING DATE: 2000-07-21
SUMPARE: PARENTIN VARIABING SCAPARE: PARENTIN VARIABING SCAPARE: PARENTIN VARIABING SEQ ID NOS: 62
SOFTWARE: PARENTIN VARIABING 3.1
IENGTH: 11
TYPE: ...
 ö
 FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
 OTHER INFORMATION: 11-mer synthesized according to example 1
 Length 11;
 0; Indels
 92.3%; Score 48; DB 12;
100.0%; Pred. No. 0.006;
tive 0; Mismatches 0
 LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
 NAME/KEY: MISC FEATURE
LOCATION: (8). (9)
OTHER INFORMATION: D-amino acids
 NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
 ORGANISM: artificial sequence
 FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 Query Match 92.3
Best Local Similarity 100.
Matches 11; Conservative
 LOCATION: (8). . (8)
OTHER INFORMATION: Met(0)
 1 EEVVPXGXHYS 11
 1 EEVVPXGXHYS 11
 FEATURE:
NAME/KEY: MISC_FEATURE
 NAME/KEY: MISC_FEATURE
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 Sequence 42

Sequence 42

Sequence 42

Sequence 42

Sequence 42

Sequence 42

Sequence 42

Sequence 42

Sequence 42

Sequence 42

Sequence 42

Sequence 42

APPLICANT: Corvas International, Inc.

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Sequence K

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REPERENCE: INTO 122-105

FILE REPERENCE: LOGI-02-25

PRIOR FILING DATE: 2003-03-25

PRIOR PILIANG DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

LENGTH: 11

LENGTH: 11
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 FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
 Score 48; DB 12; Length 11;
Pred. No. 0.006;
0; Mismatches 1; Indels
 Score 48; DB 12; Length 11;
Pred. No. 0.006;
 0; Indels
 0; Mismatches
 US-00-909-164-44
Sequence 44, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
 OTHER INFORMATION: norvaline-(CO) FEATURE:
 LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
 NAME/KEY: MISC_FEATURE
1.0CATION: (8)...(8)
7.0CHER INFORMATION: D-amino acid
32.09-909-164-25
 92.3%;
 NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OCHER INFORMATION: ACETYLATION
FEATURE:
 Query Match 92.3%;
Best Local Similarity 90.9%;
Matches 10; Conservative
 TYPE: PRT
ORGANISM: artificial sequence
 LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 Query Match
Best Local Similarity 100.
Matches 11; Conservative
 COTHER INFORMATION: Met(O) US-09-909-164-42
 1 EEVVPXGXHYS 11
 1 EEVVPXGXHYS 11
 1 EEVVPXGQHYS 11
 1 EEVVPXGXHYS 11
 FEATURE:
NAME/KEY: MISC_FEATURE
 NAME/KEY: MISC FEATURE
 NAME/KEY: MOD RES
LOCATION: (11)..(
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Search completed: June 3, 2004, 12:57:16
Job time : 33.7333 secs
 1 EEVVPXGXHYS 11
 1 EEVVPXGTDYS 11
 Query Match
Best Local Similarity
Matches 9; Conserval
 RESULT 14
US-09-09-164-29
US-09-09-164-29
Sequence 29, Application US/09909164
Publication No. US20020068002A1
GENERAL INPORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lernce K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERENCE: 1001192-105
FURRENT PELICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
FRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Version 3.1
SEQ ID NO 29
LENGTH: 11
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 OTHER INFORMATION: 11-mer synthesized according to example 1 FERTURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
 Score 40; DB 12; Length 11;
Pred. No. 0.24;
0; Mismatches 2; Indels
 Query Match 76.9%; Score 40; DB 12; Length 11; Best Local Similarity 81.8%; Pred. No. 0.24; Matches 9; Conservative 0; Mismatches 2; Indels
 .24;
es 2; Indels
 FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
CTHER INFORMATION: norvaline-(CO)
US-09-909-164-28
 NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
 NAME/KEY: MISC_FEATURE

LOCATION: (9)...(9)

COTHER INFORMATION: D-amino acid
US-09-909-164-29
OTHER INFORMATION: ACETYLATION FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
 TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
 Query Match 76.9%;
Best Local Similarity 81.8%;
Matches 9; Conservative
 FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 1 ERVVPXGXHYS 11
 1 EEVVPXGTSYS 11
 1 EEVVPXGXHYS 11
 EEVVPXGTSYS 11
```

RESULT 15 US-09-909-164-31 ; Sequence 31, Application US/09909164

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June 3, 2004, 11:35:47 ; Search time 9 Seconds (without alignments) 117.567 Million cell updates/sec Run on:

US-09-909-164-42 52 1 EEVVPXGXHYS 11 ritle:
Perfect score:
Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues searched:

283366 Total number of hits satisfying chosen parameters:

Ainimum DB seq length: 0
Aaximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_78:\*
1: Pir1:\*
2: Pir2:\*
3: Pir3:\*
4: Pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|      | Description  | DNA binding protei | protein | cell division prot | dependent | shaped tail |     | tachykinin B precu |      | _   | coenzyme F420-quin | hypothetical 92.4K | carbamoy1-phosphat | hypothetical prote | trans-regulatory s | conserved hypothet | hypothetical prote | 2-methyl-branched- | hypothetical prote | TSI8.1 protein - A | U      |      | g    | hypothetical prote | ъ    | hypothetical prote | ø   | d hyp | .2  | probable monoxygen |
|------|--------------|--------------------|---------|--------------------|-----------|-------------|-----|--------------------|------|-----|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|------|------|--------------------|------|--------------------|-----|-------|-----|--------------------|
|      |              | 25                 | 722     | 8                  | F32       | 368         | 24  | σ                  | 55   | 287 | 692                | T46758             | F89892             | an.                | VKLJSI             | D82618             | AE2001             | A48702             | S69046             | 864                | S38143 | 9513 | 9513 | 9800               | 9511 | 9798               | 8   | 9511  | 798 | 093                |
|      | DB           |                    |         |                    |           |             |     |                    |      |     |                    |                    |                    |                    |                    |                    |                    |                    | N                  |                    |        |      |      |                    |      |                    |     |       |     |                    |
|      | Watch Length | 233                | 308     | 360                | 1028      | m           | 102 | 126                | 279  | 495 | 534                | 822                | 1057               | 46                 | 124                | 156                | 252                | 412                | 460                | 510                | 743    | 802  | 819  | 828                | 839  | 853                | 855 | 1039  | 0   | 162                |
| de ( | Match        | 67.3               | -       | -                  | 67.3      | ~           | S   | S                  | 65.4 | ď.  | ഗ                  | 'n.                | 65.4               | ω.                 | ς.                 | ω.                 | φ.                 | ω,                 | 63.5               | ω,                 | ω,     | ω,   | ن    | ω.                 | ω.   | <u>ښ</u>           | ۳.  | ω.    | ς.  | ÷.                 |
|      | Score        | 35                 | 35      | 35                 | 35        | 35          | 34  | 34                 | 34   | 34  | 34                 | 34                 | 34                 | 33                 | 33                 | 33                 | 33                 | 33                 | 33                 | 33                 | 33     | 33   | 33   | 33                 | 33   | 33                 | 33  | 33    | 33  | 32                 |
| 1    | ž            | <br> <br> <br>     | 7       | ٣                  | 4         | 2           | 9   | 7                  | 80   | σ   |                    | 11                 |                    | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19                 | 20     | 21   | 22   | 23                 | 24   | 25                 | 56  | 27    | 28  | 29                 |

| hypothetical prote | promibitin z limpo<br>GMP synthetase, su | hypothetical prote | hypothetical prote | probable aspartate | hypothetical prote | probable non-photo | probable bZIP tran | aldehyde dehydroge | DNA mismatch repai | phage transposase | hypothetical prote | macrophage-stimula | ethylene-response |
|--------------------|------------------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|-------------------|
| 857810             | C86169<br>H69194                         | AF3211             | T17267             | G69119             | T24111             | G96568             | G84598             | AI3544             | A69663             | A91247            | 861239             | JC5061             | A48246            |
|                    | N (N                                     |                    |                    | -                  |                    | ۲۱                 |                    | 7                  |                    |                   |                    |                    |                   |
| 225                | 311                                      | 322                | 3 0 0              | 374                | 425                | 454                | 513                | 536                | 627                | 969               | 701                | 716                | 738               |
| 61.5               | 61.5                                     | 61.5               | 61.5               | 61.5               | 61.5               | 61.5               | 61.5               | 61.5               | 61.5               | 61.5              | 61.5               | 61.5               | 61.5              |
| 88                 | 7 C1                                     | 9.5                | 3 C                | 32                 | 32                 | 35                 | 32                 | 32                 | 32                 | 32                | 32                 | 32                 | 32                |
| 30                 | 33T                                      | 93                 | უ ო<br>ტ სე        | 36                 | 37                 | 38                 | 39                 | 04                 | 41                 | 42                | 43                 | 44                 | 4.5               |

## ALIGNMENTS

DNA binding protein EREBP-2 - common tobacco () Species Nicciana tabacum (common tobacco) () Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 21-Jul-2000 () Accession: T02590 #sequence\_revision 05-Mar-1999 #text\_change 21-Jul-2000 () Accession: T02590 #soquence\_revision 05-Mar-1999 #text\_change 21-Jul-2000 () Accession: T02590 A: 17111e: Ethylene-inducible DNA binding proteins that interact with an ethylene responsion A: Reference number: 214671; MUID:95276459; PMID:7756828 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590 A: Accession: T02590

ö Gaps ö Score 35; DB 2; Length 233; Pred. No. 9.8; 1; Mismatches 3; Indels 67.3%; Query Match 67.3 Best Local Similarity 60.0 Matches 6; Conservative

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RESULT 2 A72207

first proteinase activity modulator HflK - Thermotoga maritima (strain MSB8)
C; Species: Thermotoga maritima
C; Species: Thermotoga maritima
C; Species: Thermotoga maritima
C; Species: Thermotoga maritima
C; Species: Thermotoga maritima
C; Spacession: A72207
R; Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

Auture 399, 323-329, 1999
AyItle: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
AyReference number: A72200; MUID:99287316; PMID:10360571
AyAccession: A72207
AyAccession: A72207
AyActage: preliminary
AyNolecule type: DNA
AyResidues: 1-308 ARNA
AyResidues: 1-308 ARNA
AyCrosar-references: GB:AE001819; GB:AE000512; NID:g4982396; PIDN:AAD36885.1; PID:g498240
AyExperimental source: strain MSB8

A;Gene: TM1822 C;Superfamily: erythrocyte band 7 integral membrane protein

Gaps ö Score 35; DB 2; Length 308; Pred. No. 13; 0; Mismatches 2; Indels Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative

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41 WPSGIHY 48

WPXGXHY

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FIRST Lett. 70.00, Automotive, A42452
V1 protein - tobacco yellow dwarf virus (strain Australia)
C;Species: tobacco yellow dwarf virus
C;Species: tobacco yellow dwarf virus
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Accession: A45452
R;Accession: A4452
R;Accession: A42452
A;Title: The nuclectide sequence of the infectious cloned DNA component of tobacco yell
A;Title: The nuclectide sequence of the infectious cloned DNA component of tobacco yell
A;Reference number: A42452
A;Accession: A42452
A;Accession: A42452
A;Accession: C;Accession: A42452
A;Accession: A42452
A;Accession: C;Accession: A42452
A;Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
R;Kaliman, A.V.; Kulshin, V.E.; Shlyapnikov, M.G.; Ksenzenko, V.N.; Kryukov, V.M.
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 tachykinin B precursor - bovine
N;Alternate names: neuromedin K
S;Species Bos primigenius taurus (cattle)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
C;Accession: A25905
 Accession: A2505

A705Cession: H.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.

Proc. Natl. Acad. Sci. U.S.A. 83, 7074-7078, 1986

A711tle: Structure and gene organization of bovine neuromedin K precursor.

A; Reference number: A25905; MUD:86313713; PMID:3462746

A; Accession: A25905

A; Accession: A25905

A; Accession: A25905

A; Cross-references: GB:M14351; NID:9163587; PIDN:AAA30723.1; PID:9163590

C; Superfamily: neurokinin B precursor

F;1-26/Domain: signal sequence #status predicted <SIG>

F;27-126/Product: protachykinin B #status predicted <MAT>
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 2; Length 1396;
 Query Match 65.4%; Score 34; DB 2; Length 102; Best Local Similarity 60.0%; Pred. No. 6.5; Matches 6; Conservative 2; Mismatches 2; Indels
 3; Indels
 / Match 67.3%; Score 35; DB Local Similarity 50.0%; Pred. No. 68; les 5; Conservative 2; Mismatches
 C; Keywords: late protein; tail fiber
 : | | | | |
1360 KTIPAGDHYS 1369
 2 EVVPXGXHYS 11
 2 EVVPXGXHYS 11
 Query Match
 C, Genetics:
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Matches
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 Gil division protein - Methanobacterium thermoautotrophicum (strain Delta H)
Cispecies: Methanobacterium thermoautotrophicum
Cispecies: Os-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
Ciscossion: E69086
Rismith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Ciu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
J. Macteriol. 179, 7135-7155, 1997
J. Maccession: E69086
A; Accession: E69086
 Ciprogendent DNA helicase BMEI0275 [imported] - Brucella melitensis (strain 16M)
CiSpecies: Brucella melitensis
Ciprocies: Brucella melitensis
Cipate: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
CiAccession: AF3286
Cipate: 01-Feb-2004 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
CiAccession: AF3286
Cipate: N.; Goltsman, E.; Selkov, E.; Blara, P.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, E.; Selkov, E.; Blara, P.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A; Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
 A;Molecule type: DNA
A;Reafdudes: 1-560 «MTH»
A;Crosa-references: GB:AE000923; GB:AE000666; NID:g2622766; PIDN:AAE86115.1; PID:g262277
A;Experimental source: strain Delta H
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 A,Status: preliminary
A,Moleoule type: DNA
A,Residues: 1-1028 «KUR»
A,Cross-references: GB:AE008917; PIDN:AAL51457.1; PID:g17982167; GSPDB:GN00190
 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
 L-shaped tail fiber protein - phage TS
N;Alternate names: ltf protein
C;Species: phage TS
C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 17-Nov-2000
C;Accession: 865934; 801984; 336851
 Gaps
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 Score 35, DB 2, Length 1028;
Pred. No. 49;
2; Mismatches 3, Indels
 67.3%; Score 35; DB 2; Length 360; 45.5%; Pred. No. 16;
 2; Indels
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4; Mismatches

5; Conservative

Local Similarity

Best Loc Matches

Query Match

|::|| | |:: 98 EDLVPMGSHHT 108 1 EEVVPXGXHYS 11

A, Experimental source: strain 16M

Accession: AF3286

67.3%; 54.5%;

Query Match
Best Local Similarity 54.5
Matches 6; Conservative

|::|| | | | EKIVPPGARYS 86 REVVPXGXHYS 11

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C;Superfamily: cell division protein MJ0174

C, Genetics: A, Gene: MTH1642

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coenzyme F420-quinone oxidoreductase (EC 1.6.5.-) 56K chain - Archaeoglobus fulgidus N;Alternate names: sarcosine oxidase alpha chain soxA homolog C;Species: Archaeoglobus fulgidus C;Date: 05-Dec-1997 #text_change 19-May-2000 C;Accession: A69284; 845665
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodsol; Fleischmann, ED; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Natures 390, 364-370, 1997
A.A.Muthors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S Smith, H.O.; Wosse, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaes A;Reference number: A69280; MUID:98049343; PMID:9389475
A;Accession: A69284
A;Genter and Gequence not shown; translation not shown
A;Residues: 1-534 «KLES
A;Cossion: A69284
A;Residues: 1-534 «KLES
A;Cossion: A0401086; GB:AE001086; GB:AE000782; NID:g2689409; PIDN:AAB90959.1; PID:g26503: R;Knnow, J.; Linder, D.; Stetter, K.O.; Thauer, R.K.
Bur. J. Biochem. 223, S03-511, 1994
A;Title: F(420)H(2): quinone oxidoreductase from Archaeoglobus fulgidus. Characterizatic A;Reference number: S45665; MUID:94333340; PMID:8055920
 carbamoyl-phosphate synthase large chain [imported] - Staphylococcus aureus (strain N315 C; Species: Staphylococcus aureus (c; Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C; Accession: F89892 C; Accession: F89892 T; Uchiyama, I; Baba, T; Yuzawa, H; Kobayashi, I; Cui, L; Oguc ma, A; Mizutani-Ui, Y; Kobayashi, N; Sawano, T; Inoue, R; Kalto, C; Sekimizu, K;
 Rispellerberg, B.; Rozdzinski, B.; Martin, S.; Weber-Heynemann, J.; Schnitzler, N.; Luet Infect. Immun. 67, 871-878, 1999
Affiller Lmb, a protein with similarities to the LraI adhesin family, mediates attachmer A;Reference number: 224091; MUID:99115568; PMID:9916102
A;Accession: 146758
 'n
 A; Modecule type: protein
A; Residues: 2, X', 4, X', 6-7, X', 9-10,'XX',13-14 <KUN>
A; Note: the authors could not distinguish between glutamate and cysteine for residues
C; Superfamily: glutamate synthase small chain
C; Keywords: oxidoreductase
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 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-822 <SPEL-
A;Cross-references: SPBL-AF062533; NID:g4249622; PIDN:AAD13797.1; PID:g4249624
A;Cross-remeital source: strain R268
C;Superfamily: Streptococcus agalactiae hypothetical 92.4K protein
 C;Species: Streptococcus agalactiae
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000
C;Accession: T46758
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 65.4%; Score 34; DB 2; Length 534;
45.5%; Pred. No. 39;
 3; Indels
 lypothetical 92.4K protein - Streptococcus agalactiae
 3; Mismatches
 Query Match
Best Local Similarity 45.5
Matches 5; Conservative
 :: | | | |:
119 DKVFPHGSHYT 129
 1 EEVVPXGXHYS 11
 350 WPHGDHY 357
 3 VVPXGXHY 10
 RESULT 12
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 hypothetical protein - Deinococcus radiodurans (strain R1)
Cispecies: Deinococcus radiodurans
Cispecies: Deinococcus radiodurans
Cispecies: 03-105-11999 #sequence_revision 03-105-11999 #text_change 28-Jul-2000
CiAccession: C75518 #sequence_revision 03-105-11999 #text_change 28-Jul-2000
CiAccession: C75518 #sequence_revision 03-105-11999 #text_change 28-Jul-2000
CiAccession: C75518 #sequence_revision of the radioresis #sequence in the radioresis #sequence radiodurans R1.
A. Shen, M.; Venter, J.C.; Fraser, C.M.
Solience 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresis and bacterium Deinococcus radiodurans R1.
A;Reference number: A75550; MUID:20036896; PMID:10567266
 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-279 <WHI>
A;Cross-references: GB:AE001889; GB:AE000513; NID:g6457944; PIDN:AAF09867.1; PID:g645795
A;Experimental source: strain R1
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Rosidues: 1-95 <GRAA
A;Rosidues: 1-95 <GRAA
A;Cross-references; EMBL.AF022972; PIDN:AAC48234.1; GSPDB:GN00023; CESP:FlOD2.3
A;Experimental source: strain Bristol N2; clone FlOD2
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 hypothetical protein F10D2.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999 C;Accession, T; Wohldmann, P.; Gillam, B. submitted to the EMBL Data Library, September 1997 A;Description: The sequence of C. elegans cosmid F10D2. A;Reference number: Z2O515 A;Accession: T28117
 Gaps
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 A,Map position: 1
C,Superfamily: Deinococcus radiodurans hypothetical protein DR0271
 Query Match 65.4%; Score 34; DB 2; Length 279; Best Local Similarity 75.0%; Pred. No. 19; Matches 6; Conservative 0; Mismatches 2; Indels
 65.4%; Score 34; DB 2; Length 495; ilarity 50.0%; Pred. No. 36; Conservative 2; Mismatches 3; Indels
 DB 2; Length 126;
 2; Indels
 A;Gene: CESP:F10D2.3
A;Map position: 5
A;Introns: 37/2; 90/1; 113/1; 183/3; 356/3; 380/3; 428/2
 Score 34; DB 2
Pred. No. 8.2;
1; Mismatches
 Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
 218 ENIVPTGKHH 227
 1 EEVVPXGXHY 10
 28 EQVVPGGGH 36
 100 VPLGRHYS 107
 Query Match
Best Local Similarity
'-hea 5; Conserval
 σ
 4 VPXGXHYS 11
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RESULT 10 A69284

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C;Superfamily: AIDS trans-regulatory splicing protein
C;Keywords: AIDS; immunodeficiency; splicing protein; transcription regulation
 Search completed: June 3, 2004, 12:00:01
Job time : 9 secs
 63.5%;
 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
 Best Local Similarity 55.6
Matches 5; Conservative
 107 ETVPAGGNYS 116
 2 EVVPXGXHYS 11
 ||::| | |
EEILPQGVH 127
 1 EEVVPXGXH 9
 A; Status: preliminary A; Molecule type: DNA
 A, Accession: D82618
 A; Gene: XF1950
 Query Match
 Genetics
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 trans-regulatory splicing protein - simian immunodeficiency virus SIVCpz

NyAlternate names: anti-repression trans-activator; art protein; rev protein; trs protein
C;Species: simian immunodeficiency virus SIVCpz
A;Note: host Pan troglodytes (chimpanzee)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: S09988
R;Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
A;Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A;Reference number: S09983; MUID:90259077; PMID:2188136
 A;Gene: pyrAB
C;Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain; biotin
 C;Accession: E97985
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E, R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; N. Y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: E97985
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C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1255-1240, 2001
Tritle: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUD:21311952; PMID:11418146
A;Accession: R9892
A;Actus: preliminary
A;Molecule type: DNA
A;Residues: 1-1657
A;Cross-references: GB:BA000018; PID:g13701002; PIDN:BAB42298.1; GSPDB:GN00149
A;Experimental source: strain N315
 A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-46 «KUR»
A,Cross-references: GB:AE007317; PIDN:AAK99713.1; PID:g15458516; GSPDB:GN00174
 hypothetical protein spr0909 [imported] - Streptococcus pneumoniae (strain R6) C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
 Gaps
 Gaps
 A; Cross-references: EMBL; X52154; NID: 958866; PIDN: CAA36405.1; PID: 9763085
 ö
 ö
 Score 34; DB 2; Length 1057;
Pred. No. 82;
 A, Status: nucleic acid sequence not shown; translation not shown
 Score 33; DB 2; Length 46;
Pred. No. 4.5;
 3; Indels
 2; Indels
 1; Mismatches
 1; Mismatches
 63.5%;
 Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
 Conservative
 |:| | |||
190 EIVSNGLHYS 199
 2 EVVPXGXHYS 11
 3 WPXGXHY 10
 21 IVPHGGHY 28
 Query Match
Best Local Similarity
Matches 5, Conserv
 A; Molecule type: DNA
A; Residues: 1-124 <HUE>
 A; Gene: rev; trs; art
A:Introns: 27/1
 A; Gene: spr0909
 C, Genetics:
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Alexportmental source: strain gac

Risimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;

Briones, M.R.S.; Beano, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer,

as-Neco, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A.A. Authors: Ferralara, V.C.A.; Ferro, J.A.; Franca, S.C.; Franco, M.C.; Froh

J.D.; Jungueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins,

A.A. Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.N.; Mircha, A.Y.; Marchins,

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmaci, D.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawass

A.;Authors: da Silva, A.C.R.; da Silva, R.M.; Silva Jr., W.A.; da Silva,

M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;

A.;Contents: annotation
 Conserved hypothetical protein XF1950 [imported] - Xylella fastidiosa (strain 9a5c) CiSpecies: Xylella fastidiosa (cipate: 18-Aug-2000 #text_change 20-Aug-2000 (cipate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 (cipate: 18-Aug-2000 #text_change 20-Aug-2000 (cipate: 18-Aug-2000 #text_change 20-Aug-2000 Ryanonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seque Nature 406, 151-157, 2000 Airite The genome sequence of the plant pathogen Xylella fastidiosa. Airite ference number: A82515, MID:20365717, PMID:10910347 Airite for a complete list of authors see reference number A59328 below
 A;Residues: 1-156 <SIM>
A;Cross-references: GB:AE004014; GB:AE003849; NID:g9107044; PIDN:AAF84752.1; GSPDB:GNOC
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 Gaps
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 Score 33; DB 2; Length 156;
Pred. No. 17;
2; Mismatches 2; Indels
1; Length 124;
Score 33; DB
Pred. No. 13;
 1; Mismatches
 55.64;
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METAL
SEQUENCE
 Query Match
 RESULT 3
 Matches
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 Zhang Y.-C., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
A zhang Y.-C., Ren S.-X., Li H.-L., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
A yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
Yan m. Z.-H., Zhao G.-P., Qu D., Danchin A.-W.;
Tenome-based analysis of virulence genes in a non-biofilm-forming
T. Tenome-based analysis of virulence genes in a non-biofilm-forming
T. Tenophylococcus epidermidis strain (ARCC 12228).";
Mol. Microbiol. 49:1577-1593(2003).
T. CATALIVITY Z ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +
Diosphate + L-glutamine + CO(2) + H(2)O = 2 ADP +
Diosphate + L-glutamine to acrbamoyl phosphate.
T. COPACTOR: Binds 3 manganese ions per subunit (By similarity).
T. PATHWAY: Pyrimidine biosynthesis; first step.
T. SUBUNIT: Composed of two chains; the small (or glutamine) chain
T. STBUNIT: Composed of two chains; the small (or glutamine) which is used by
The large (or ammonia) chain conthesize carbamoyl phosphate (By
T. SIMILATICY).
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 EMEL; AEO16746; AAO04476.1; ---

R HAMAP; MF_01210; -; 1.

R InterPro; IPR006549; Cara_L_D1.

R InterPro; IPR006549; CPase_L_D2.

R InterPro; IPR006549; CPase_L_D2.

R InterPro; IPR00649; CPase_L_D2.

R InterPro; IPR004362; MGS_like.

R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R InterPro; IPR00436; MGS=RESE_L_D2; 2.

R InterPro; IPR00436; MGS=RESE_L_D2; MGS=RESE_L_D2; MGS=RESE_L_D2; MGS=RESE_L_D2; MGS=RESE_L_D2; MGS=RESE_L_D2; MGS=RESE_L_D2; MGS=
 OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN
ALLOSTERIC DOMAIN.
 15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
16-MAR-2004 (Rel. 43, Last annotation update)
17-MAR-2004 (Rel. 43, Last annotation update)
17-MAR-2004 (Rel. 43, Last annotation update)
18-MAR-2004 (Rel. 43, Last annotation u
 Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
 SIMILARITY: Belongs to the carB family.
 STANDARD;
 SEQUENCE FROM N.A.
STRAIN=ATCC 12228;
PubMed=12950922;
 CARB STAEP
Q8CPJ4;
RESULT 2
CARB STAEP
```

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 Gaps
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB OR FN0422.
 .
 Score 36; DB 1; Length 1057;
Pred. No. 14;
1; Mismatches 3; Indels
00 MANGANESE 2 (BY SIMILARITY).
20 MANGANESE 3 (BY SIMILARITY).
32 MANGANESE 3 (BY SIMILARITY).
117391 MW; 8944D7D8DBICAE59 CRC64;
 Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
Fusobacterium.
 HAMAR; MP_01210; ; 1.

THRENDER; IPRO06275; GARA_L.glu.

INTERPRO; IPRO05479; CPASE_L.D2.

INTERPRO; IPRO05409; CPASE_L.D2.

INTERPRO; IPRO05409; CPASE_L.D3.

INTERPRO; IPRO05401; CPASE_L.D3.

INTERPRO; IPRO04362; MGS_ITke.

Pfam; PPO02789; CPASSE_L.Chain; 2.

Pfam; PPO2787; CPASSE_L.D3; 1.

Pfam; PPO21787; MGS; II.

PRINTS; PRO0198; CPSASE.

TIGRFAMS; TIGR01369; CPSASEI._Irg; 1.
 EMBL; AE010554; AAL94625.1; ALT_INIT.
 69.2%;
63.6%;
 7; Conservative
 STANDARD;
 189 KEVVSNGLHYS 199
 1 EEVVPXGXHYS 11
 300
820
832
 300 30
820 82
832 83
1057 AA;
 Local Similarity
 [1]
SEQUENCE FROM N.A.
 NCBI_TaxID=76856;
 CARB FUSNN
QBRG86;
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Gaps

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 SECUENCE FROM N.A.
MEDLINE=92188518; PubMed=1546458;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.B.;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.B.;
The nucleotide sequence of the infectious cloned DNA component of
tobacco yellow dwarf virus reveals features of geminiviruses
infecting monocotyledonous plants.";
Virology 187:633-642(1992).
 Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Ammanlai, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
NCBI_TaxID=9913;
 Score 35; DB 1; Length 1396;
Pred. No. 31;
2; Mismatches 3; Indels
 Score 34; DB 1; Length 102;
Pred. No. 3.4;
2; Mismatches 2; Indels
 -> A (IN REF. 2).
18CD2192F65FFFC1 CRC64;
 l protein. —
102 Aa; 11178 MW; A40ECF1E0AF55B67 CRC64;
 Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
 01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurokinin B precursor (NKB) (Neuromedin K).
 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-CT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
 126 AA.
 102 AA
 PRT;
 PRT;
 986 V ->
; 147989 MW;
 PIR; A42452; A42452.
InterPro; IPROD622; Gemini mov.
Pfam; PF01708; Gemini mov; I.
Hypothetical protein.
 EMBL; M81103; AAA47947.1; -.
 65.4%;
 67.3%;
 5; Conservative
 : : | | | | | 1369 | 1369
 STANDARD;
 6; Conservative
 STANDARD;
 2 EVVPXGXHYS 11
 2 EVVPXGXHYS 11
 PIR; S65934; S36851.
Late protein.
CONFLICT 986 96
SEQUENCE 1396 AA;
 986 9
1396 AA;
 Query Match
Best Local Similarity
 Query Match
Best Local Similarity
 NCBI_TaxID=31599;
 RESULT 6
TKNK BOVIN
ID TKNK BOVIN
AC PO8858;
 Y11K TYDVA
P31619;
 SEQUENCE
 Matches
 Matches
 STXR
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 Gapa
PROSITE; PS00867; CPSASE_1; 2.
PROSITE; PS00867; CPSASE_2; 2.
ATGININE biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat; ATF-binding; Manganese; Complete proteome.
DOMAIN 402 546 OLIGOMERIZATION DOMAIN.
DOMAIN 547 929 CARRAMOYL PROSPHATE SYNTHETIC DOMAIN.
 ATP (POTENTIAL).

ATP (POTENTIAL).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).
 Bacteriophage T5.
Viruses; deDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
T5-like viruses.
VCBI_TaxID=10726;
 PRELIMINARY PARTIAL SEQUENCE FROM N.A. MEDILINE-88289370; PubMed=3267228; MEDILINE-88289370; PubMed=3267228; Kaliman A.V., Kryukov V.M., Bayvev A.A.; Bayvev A.A.; "The nucleotide sequence of bacteriophage TS DNA at the region "The nucleotide sequence of sequence of bacteriophage TS DNA at the region between early and late genes.", Nucleic Acids Res. 16:6230-6230(1988).
 ö
 SEQUENCE FROM N.A.
MEDLINE=95309401; PubMed=7789514;
MRIMAN A.V., Kulshin V.E., Shlyapnikov M.G., Ksenzenko V.N.
Kaliman e.V., W.,
"The mucleotide sequence of the bacteriophage T5 ltf gene.";
FEBS Lett. 366:46-48(1995).
 mucleotide sequence of the bacteriophage T5 ltf gene."; Lett. 366:46-48(1995).
 Score 35; DB 1; Length 1058; Pred. No. 23; 2; Mismatches 2; Indels
 Kaliman A.V.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
 ALLOSTERIC DOMAIN
 VLTF_BPT5
VLTF_BPT5
STANDARD; PRT; 1396 AA.
AC 913390; O48502;
OT 01-JAN-1990 (Rel. 13, Created)
OT 01-FEB-1996 (Rel. 33, Last sequence update)
OT 30-MAX-2000 (Rel. 39, Last annotation update)
DE 1-shaped tail fiber protein (LTF protein).
 EMBL; X69460; CAA49220.1; -.
EMBL; AJ001191; CAA04591.1; -.
PIR; S01982; S01982.
 67.3%;
 117451
 polymannose O antigen.
 Conservative
 190 EIVPNGLNYS 199
 1058
546
1058
210
352
 2 EVVPXGXHYS 11
 832 83
1058 AA;
 Query Match
Best Local Similarity
 [2]
SEQUENCE FROM N.A.
 9
 SEQUENCE
 DOMAIN
REPEAT
REPEAT
NP_BIND
NP_BIND
METAL
 METAL
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Matches

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RESULT 4

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Gaps

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PHERONOLOGICA PRESENTA ```
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                                                                                                                                               Lancet 357:1225-1240(2001).

-!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + phosphate + L-glutamate + carbamoyl phosphate.

-!- COFACTOR: Binds a manganese ions per subunit (By similarity).
-!- PATHWAY: Arginine biosynthesis.
-!- PATHWAY: Pyrimidine biosynthesis, first step.
-!- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).
-!- SIMILARITY: Belongs to the carB family.
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
aureus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN
ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 ATP (POTENTIAL).
52 ATP (POTENTIAL).
64 MANGANESE 1 (BY SIMILARITY).
68 MANGANESE 1 AND 2 (BY SIMILARITY).
60 MANGANESE 2 (BY SIMILARITY).
50 MANGANESE 3 (BY SIMILARITY).
61 MANGANESE 3 (BY SIMILARITY).
62 MANGANESE 3 (BY SIMILARITY).
63 MANGANESE 3 (BY SIMILARITY).
64 MANGANESE 3 (BY SIMILARITY).
65 MANGANESE 3 (BY SIMILARITY).
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Pred. No. 38;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1057 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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1057 AA;
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CARB STAAW
ID CARB STAAW
AC P58940;
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NP BIND
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       SEQUENCE FROM N.A. DubMed=3462746; Makanishi S.; MEDLINE=86313713; PubMed=3462746; Medline=86313713; PubMed=3462746; Medline=86313713; PubMed=3462746; Medline=86313713; PubMed=3462746; Medline=86313713;  Medline=863137; Medline=86313
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SEQUENCE FROM N.A.
STRAIN-MALSO / ATCC 700699, and N315;
MEDLINE=21311952 .

Ruroda M., Ohta T., Pubhed=11418146;
Ruroda M., Oguchi A., Aoki K.-T., Nagai Y., Lian J.-C., Ito T.,
Cui L., Oguchi A., Aoki K.-T., Nagai Y., Lian J.-C., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q99UE5;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last annotation update)
phosphate synthetase ammonia chain.
CARB OR PYRAB OR SATU03 OR SA1046.
Staphylococcus aureus (strain MuSO / Arcc 700699), and
Staphylococcus aureus (strain N315).
Bacteria, Firmicutes, Bacillales; Staphylococcus.
NCBI_TAXID=158878, 158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMIDATION (G-96 PROVIDE AMIDE GROUP) 446EF433498EC059 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R EMBL; M14351; AAA30723.1; --
R EMBL; M14348; AAA30723.1; --
R EMBL; M14348; AAA30723.1; JOINED.
R EMBL; M14349; AAA30723.1; JOINED.
R EMBL; M14349; AAA30723.1; JOINED.
R EMBL; M14350; AAA30723.1; JOINED.
R INCEPTO; JR8002040; TACHYLIND.
R INCEPTO; JR8002040; TACHYLIND.
R PFODOM; PD020370; Neurokinin.
R ProDOM; PD020370; Neurokinin.
R PRODOM; PD020370; Neurokinin.
R PRODOM; PN020570; TACHYKININ; 1.
R PROSITE; PS00267; TACHYKININ; 1.
R Amidation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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21 83 NEC
86 95 126
99 126 95
126 AA, 13871 MW, 4
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Best Local Similarity
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Matches
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                                                                                                                                                                                                                                                              phosphate + L-glutamate + carbamoyl phosphate.
-- CORACTOR: Binds 3 manganese ions per subunit (By similarity).
--- CORACTOR: Binds 3 manganese ions per subunit (By similarity).
--- PATHWAY: Arginine biosynthesis,
--- PATHWAY: Arginine biosynthesis, first step.
--- PATHWAY: Pyrimidine biosynthesis, first step.
--- PATHWAY: Pyrimidine biosynthesis, the small (or glutamine) chain promoces the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).
--- SIMILARITY: Belongs to the carB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS, TIGRO1369; CESASE_1; 2.
PROSITE; PS00866; CPSASE_1; 2.
PROSITE; PS00867; CPSASE_2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat; Arginine biosynthesis; Pyrimidine broteome.
ATP-binding; Manganese; Pyrimidine broteome.
CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
1 402 546 CLIGOMERIZATION DOMAIN.
CARBOXAIN 547 929 CARBOXOL PHOSPHATE SYNTHETIC DOMAIN.
CARBOXOL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
                                                                                                                                             SEQUENCE FROM N.A.
MEDIJNB=22040717; PubMed=12044378;
MEDIJNB=22040717; PubMed=12044378;
MEDI T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
                                              6.3.5.5) (Carbamoyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 ATP (POTENTIAL).

52 ATP (POTENTIAL).

84 MANGANESE 1 (BY SIMILARITY).

98 MANGANESE 1 AND 2 (BY SIMILARITY).

100 MANGANESE 2 (BY SIMILARITY).

101 MANGANESE 3 (BY SIMILARITY).

117185 MW, D8E3B09F9BC6F152 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 1; Length 1057;
Pred. No. 38;
1; Mismatches 3; Indels
                                                                                       Staphylococcus aureus (strain MW2).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, inst sequence update)
28-FEB-2003 (Rel. 41, inst annotation update)
Carbamoyl-phosphate synthase large chain (EC opposphate syntheteae ammonia chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0098; CPSASE.
TIGREAMS; TIGR01369; CPSASEI_lrg; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF 01210; -; 1.
InterPro; IPR006275; CarA L glu.
InterPro; IPR005481; CPase L D2.
InterPro; IPR005481; CPase L D3.
InterPro; IPR005481; CPase L Chain; 2.
Pfam; PF00289; CPSase L Chain; 2.
Pfam; PF02786; CPSase L D3; 1.
Pfam; PF02787; CPSase L D3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP004825; BAB94951.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.4%;
                                                                                                                                                                                                                                                      359:1819-1827(2002)
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302 35
284 28
298 29
300 30
820 820
832 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                   NCBI_TaxID=196620;
                                                                                                                                                                                                                                         acquired MRSA.";
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SEQUENCE
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Gaps

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Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-90259077, PubMed=2188136;
Huet T., Cheynier R., Meyerhans A., Roelants G., Wain-Hobson S.;
"Genetic organization of a chimpanzee lentivirus related to HIV-1.";
Mature 346:356-359(1990).
-I- FUNCTION: REV APPEARS TO ACT POST-TRANSCRIPTIONALLY TO RELIEVE
NEGATIVE REPRESSION OF GAG AND ENV PRODUCTION.
-I- SUBCELLULAR LOCATION: Nuclear; accumulates in the nucleoli.
-I- PTM: Phosphoprotein whose state of phosphorylation is mediated by a specific serine kinase activity present in the nucleus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription regulation, AIDS, Phosphorylation, Nuclear protein.
SEQUENCE 124 AA, 13701 MW, FSB77DIBDF65A7B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID=4932;
                                                                                                                                                                                                                            01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 4L. Last annotation update)
REV protein (Anti-repression transactivator protein) (ART/TRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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Pred. No. 6.8;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mallory M.J., Strich R.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                    Viruses, Retroid viruses, Retroviridae, Lentivirus
NCBI_TaxID=11723,
                                                                                                                                                                                                                                                                                                                                                                 Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UME1 YEAST STANDARD; PRT; 460 AA. 003010; P87330; Created) 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Neiosis negative regulator UME1. WHIN3 OR PRIJ39C OR LETT. Saccharomyces cerevisiae (Baker's peat).
                                                                                                                                                                               124 AA
                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, X52154; CAA36405.1; -.
PIR; S0998; VKLJSI.
HIV, X52154; REVSCPZ.
InterPro; IPR000625; REV_protein.
Pfam; PP00424; REV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.5%;
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                                                                                                                                                                               STANDARD;
                                             190 EIVSNGLHYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 ETVPAGGNYS 116
2 EVVPXGXHYS 11
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                                                                                                                                                                            REV SIVCZ
P17280;
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                                                                                                                           MEDLINE-22456901; PubMed=1252265;
WEDLINE-22456901; PubMed=1252265;
WEDLINE-22456901; PubMed=1252265;
WEDLINE-22456901; PubMed=1252265;
WEDLINE-22456901; C.H.J., Kamerbeek J., Postigo M., Silva P.J.,
Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva P.J.,
Tamames J., Viguera E., Latorre A., Valencia A., Moran P., Moya A.;
Reductive genome evolution in Buchnera aphidicola.";
Proc. Natl. Acad. Sci. U.S. 100:581-586(2003).
--- SUNCELLULAR LOCATION: Integral membrane protein (Potential).
--- SIMILARITY: Belongs to the ABC transporter family. MDR subfamily.
                              Buchnera aphidicola (subsp. Baizongia pistaciae).
Bacteria: Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
MCBI_TaxID=135842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          van Vlief-Reedijk J.C., Planta R.J.;
Submitted (MRR-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELJULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: STRONG, TO YEAST YBLOIIW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NUV-1997 (Rel. 35, Last amoutation update)
Hypothetical 83.6 kDa protein in CCP1-MET1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE014017; AA027114.1; -.
InterPro; IPR001140; ABC_TM_transpt.
InterPro; IPR003439, ABC_transporter.
Pfam; PF00664; ABC membrane; 1.
Pfam; PF00665; ABC_tran; 1.
PROSITE; PS50229; ABC_TYAIF; 1.
PROSITE; PS00221; ABC_TRANSPORTER_1; FALSE_NEG.
PROSITE; PS50833; ABC_TRANSPORTER_2; 1.
ATP-binding; Transport; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3B84848CE196ADF7 CRC64;
         Multidrug resistance-like ATP-binding protein mdlB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.5%; Score 33; DB 1; 50.0%; Pred. No. 34;
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POTENTIAL.
POTENTIAL.
ABC TRANSPORTER.
ATP (POTENTIAL).
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Best Local Similarity 50.0.
Best Local Si Conservative
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SEQUENCE FROM N.A.
STRAIN=S288C;
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             CCEPRENCOCCEPTE
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GGO; GO:0005634; C:nucleus; IDA.
GGO; GO:0005144; F:transcription co-repressor activity; IDA.
GGO; GO:0040020; P:regulation of meiosis; IGI.
InterPro; IPR001680; WD40.
SMART; SM00320; WD40; 3.
PROSITE; PS000678; WD REPEATS 1; FALSE NEG.
PROSITE; PS500678; WD REPEATS 1; FALSE NEG.
PROSITE; PS50082; WD REPEATS RECION; FALSE NEG.
PROSITE; PS50084; WD REPEATS RECION; FALSE NEG.
Transcription regulation; Melosis; Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.5%; Score 33; DB 1; Length 460; 62.5%; Pred. No. 26; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA6F60448B7BCBA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 42, Created)
(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U10280; AAB40937.1; -. EMBL; U43703; AAB68221.1; -.
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GermOnline; 144121; -.
TRANSFAC; T04309; -.
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85 IVPLGLHY 92
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5; Conserve
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10-OCT-2003
10-OCT-2003
10-OCT-2003
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Best Local S
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SOLUTION SOLUTION SERVICE SERV

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RESULT 11
MDLB BUCBP

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or send an email to license@isb-sib.ch)
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Matches
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       STARRANGS
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=RIMD 2210633 / Serotype 03:K6;

MEDIINE—2250454; PubMed=12620739;

A maxino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

A rayunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae.";

RL Lancet 361:743-749(2003).

CC -!- FUNCTION: Has an important function as a repair enzyme for proteins that have been inactivated by oxidation. Catalyzes the creversible oxidation-reduction of methionine sulfoxide in proteins competible oxidation-reduction of methionine sulfoxide in proteins competible oxidation-reduction Lenthionine 4 oxidized thioredoxin = protein L-methionine S-oxide + reduced thioredoxin = protein L-methionine S-oxide + reduced thioredoxin.
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                                                                                                                                                                                                                                                                                                                           PIR; 938143; 538143.

GermOnline; 140046; -

SGD; GO:0001775; GPT2.

GO; GO:0005783; C:endoplasmic reticulum; IDA.

GO; GO:0004366; F:glycerol-3-phosphate O-acyltransferase acti. . .; IDA.

GO; GO:0008654; P:phospholigid biosynthesis; IDA.

InterPro; IPR002123; Acyltransferase.

Ffam; PR01553; Acyltransferase; 1.

SMART; SM00563; Pl8C; 1.

TRANSMEM 69 POTENTIAL.

TRANSMEM 69 POTENTIAL.
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10-0cT-2003 (Rel. 42, Last sequence update)
10-0cT-2003 (Rel. 42, Last annotation update)
10-0cT-2003 (Rel. 42, Last annotation update)
methionine sulfoxide reductase msrA (RC 1.8.4.6) (Proteinmethionine-S-oxide reductase) (Peptide Met (O) reductase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Vibrionaceae, Vibrio.
NCBI_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 63.5%; Score 33; DB 1; Length 743; Best Local Similarity 75.0%; Pred. No. 43; ... Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84B9946E56B82F15 CRC64;
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MSRA_VIBPA
SOUND STATE THE SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SO
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                                                                                                                                                                                                                                                                                                                                                         Gaps
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-!- CATALYTIC ACTIVITY: ATP + xanthosine 5'-phosphate + L-glutamine H(2)0 = AMP + diphosphate + GMP + L-glutamate.

-!- PATHWAY: GMP biosynthesis.

-!- SUBUNIT: Heterodimer composed of a glutamine amidotransferase subunit (A) and a GMP synthase subunit (B) (Pocential).

-!- SIMILARITY: Belongs to the GMP synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-PBB-2003 (Rel. 41, Last annotation update)
GMP synthase [glutamine-hydrolyzing] subunit B (BC 6.3.5.2) (GMP synthetase).
                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF_00345; -; 1.
InterPro; IPR001674; GMP_synth_C.
Pfam; PF00958; GMP_synt_C; TICRFAMS; TICRF0884; guaA_Crerm; 1.
Ligase; GMP_biosynthesis; Purine_biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                               61.5%; Score 32; DB 1; Length 212; llarity 55.6%; Pred. No. 19; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 184 GMP-BINDING (BY SIMILARITY).
29 35 ATP (BY SIMILARITY).
308 AA; 34403 MW; F2DCF6ED202CAEC1 CRC64;
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HSSP; P04079; 1GPM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 5; Conserv
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and characterization of a full-length cDNA coding for ovine aldolase B from fetal mesonephros.";
Biochim. Biophys. Acta 1213:223-22714944).
-!- Biochim. Biophys. Acta 1213:223-22714944).
-!- CATALYTIC ACTIVITY:
--- Diyceraldehyde 3-phosphate.
-!- PATHWAY: Glycolysis; sixth step.
-!- PATHWAY: Glycolysis; sixth step.
-!- SUBUNIT: Homoretramer (By similarity).
-!- SUBUNIT: Homoretramer (By similarity).
-!- MISCELLANBOUS: In vertebrates, three forms of this ubiquitous glycolytic enzyme are found, aldolase A in muscle, aldolase B in liver and aldolase C in brain.
-!- SIMILARITY: Belongs to class I fructose-bisphosphate aldolase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           base; Glycolysis; Miltigene family.

C1-PHOSPHATE GROUP OF THE SUBSTRATE.

SCHIPP-BASE WITH DIHYDROXYACETONE-P.

SSERVIAL FOR ENHANCED ACTIVITY OF THE ENZYME TOWARD PRUCTOSE 1,6-BISPHOSPHATE.

AS COMPARED WITH FRUCTOSE 1-PHOSPHATE.

AA, 39500 MW; FC8B45666821E2BD CRC64;
                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Fructose-bisphosphate aldolase B (BC 4.1.2.13) (Liver-type aldolase).
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Mesonephros;
MEDLINE=94368863; PubMed=8086469;
Gianquinio L., Pailhoux E.A., Bezard J., Servel N., Kirszenbaum M.,
                                                                                                                                                                                                                                                                                                                                                                Ovis aries (Sheep).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                             ô
Score 32; DB 1; Length 308;
Pred. No. 29;
0; Mismatches 4; Indels
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Pred. No. 34;
1; Mismatches 2; Indel8
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PIR; 547540; 547540.
INTERPRO, 1ADO.
INTERPRO, 1PRO00741; Aldolase_I.
Promm, PP002124; 91ycolytic_ensy; 1.
PROSITE; PS00128; Aldolase_I; 1.
PROSITE; PS00158; Aldolase_I; 1.
INTERPROSITE; PS00158; ALDOLASE_CLASE_INSTERMINET
INIT MET
ENDING SS SS C-1-PHOS
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  Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                      216 EEVVESGLHES 226
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                                                                                 1 EEVVPXGXHYS 11
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189 EVIPDGSH 196
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Search completed: June 3, 2004, 11:49:54 Job time: 5.86667 secs

2 EVVPXGXH 9

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Gaps

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Scoring table:

Searched:

Database

Title: Perfect score:

Sequence:

protein

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Run on:

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Q911AB thermoplasm
O16612 caenorhabdi
O29966 archaeoglob
Q877y2 streptococc
Q821AG streptococc
Q844B1 streptococc
Q845G1 streptococc
Q845G1 streptococc
Q845G1 streptococc
Q85G1 streptococc
Q95G1 streptococc
Q95G1 streptococc
Q97G1 streptococc
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Q81G1 bos streptococc
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Q867a5 tragulus ja
Q8hxy9 bos taurus
Q7vp43 haemophilus
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Osign5 drosophila
Q08523 ascaris suu
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BG032195; A4132195.1; -.
MGD; MG1:191574; Tada31.
GO; GO:0030374; F:ligand-dependent nuclear receptor transcrip. ..; IDA.GO; GO:0005515; F:protein binding; IPI.
GO; GO:0005515; F:protein binding; IPI.
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to expressed sequence A1987856.
TADA3L OR 1110004B19RIK.
Mam musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. MSLI TaxiD=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 11; Length 413;
Pred. No. 2.7;
1; Mismatches 3; Indels
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Last sequence update)
Last annotation update)
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Q57489
Q9PC35
Q87D36
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Q8YWP1
Q867A5
                                                                                                     Q8E4U1
Q8DZ81
Q8NZ82
Q8K5Q1
Q99XV4
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Q8CYU7
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(TrEMBLrel. 01, I
(TrEMBLrel. 25, I
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Matches 7; Conservative
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SEQUENCE FROM N.A.
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01-NOV-1996
01-NOV-1996
01-OCT-2003
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Q91450 nicotiana t
Q91450 nicotiana s
Q9810 rhizobium 1
Q9222 thermotoga
Q9252 pertanobaci
Q27679 methanobaci
Q7xtg3 oryza sativ
Q925x cercopithec
Q8110 brucella me
Q8yj11 brucella me
Q8yj11 brucella me
Q8yj11 brucella me
Q8yj11 brucella me
Q7wb7 bordetella
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Q46486 corynebacte
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                   1017041 segs, 315518202 residues
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                                                                                      protein search, using sw model
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1: SP_archea:*
2: Sp_bacteria:*
3: Sp_fungi:*
4: Sp_nwan:*
5: Sp_nwan:*
6: Sp_mammal:*
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6: Sp_phage:*
6: Sp_phage:*
6: Sp_voran:*
6: Sp_voran:*
6: Sp_vorus:*
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Q46486
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Q9X2E2
Q38317
Q27679
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Q281KG
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Q8DIH0
Q7WNB7
Q7W0Z3
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
Listing first 45 su
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Maximum DB seq length: 200000000
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52
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Match 1
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Score

Result No.

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Local Similarity 63.6%;
nes 7; Conservative
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SEQUENCE FROM N.A.

SEQUENCE C. Striatum; STRAIN=M82B;

MEDLINE=20194806; PubMed=10732668;

Tauch A., Krieft S., Kalinowski J., Puhler A.;

Initially identified in scribtum M82B is composed of DNA segments

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CARAIN=ATCC 12228;
CARAIN=ATCC 12228;
CANAGE CONTRAIN=ATCC 12228;
CANAGE CONTRAIN=ATCC 12228;
CANAGE CONTRAIN=ATCC 12228;
CANAGE CONTRAIN=ATCC 12228;
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SPECIES=C.xerosis; STRAIN=W82B;
MEDLINE=6117603; PubMed=8559800;
MEDLINE=6117603; PubMed=8559800;
Tauch A.; Kassing F., Kalinowski J., Puhler A.;
"The Corynebacterium xerosis composite transposon Tn5432 consists of two identical insertion sequences, designated I81249; flanking the errythromycin resistance gene ermCX.";
plasmid 34:119-131(1995).
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                                                                         Corynebacterium xerosis, and Corynebacterium striatum.
Corynebacterium striatum.
Bacteria; Actinobacteria; Actinobacteridae; Corynebacterineae; Co
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01-WAR-2003 (TrEWBLrel. 23, Last sequence update)
01-OCT-2003 (TrEWBLrel. 25, Last annotation update)
Carbamoyl-phosphate synthase large chain.
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
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Hypothetical protein (GcrA).
GCRA,
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids, lamiids, Solanales, Solanaceae, Nicotiana.
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SEQUENCE FROM N.A.

STEALN=EB44 TISSUE=Leaf;

STEALN=EB44 TISSUE=Leaf;

STEALN=EB44 TISSUE=Leaf;

MEDLINE=95276459; Pubmed=7756828;

Change-Takadi M., Shinshi H.;

"Ethylene-inducible DNA binding proteins that interact with an ethylene-inducible DNA binding proteins that interact with an EMB1; D38126; BAA07324.1; -.

REMB1; D38126; BAA07324.1; -.

REMB2; D80337; 2020.

REMB2; C000056337; C10259.

REMB2; PRO01700; Firanscription of transcription, DNA-dependent; LEA.

G0; G0:0005700; Firanscription of transcription, DNA-dependent; LEA.

REMINIS; PRO01471; TF ERF.

PRINTS; PRO01471; TF ERF.

PRINTS; PRO01423; TF ERF.

PRINTS; PRO01423; TF ERF.

SMART; SMO0380; AP2; 1.

SMART; SMO0380; AP2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                             1057 AA; 117391 MW; 8944D7D8DB1CAES9 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUM-2003 (TrEMBLrel. 24, Last annotation update)
EREBP-2.
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UK INTERPRO) IPRO04861, KGBSE L.N.

INTERPRO) IPRO0169; SHDTOT acsite.

DR Pfam; PF00289; CPSASE L.Chain; 2.

DR Pfam; PF002786; CPSASE L.Chain; 2.

DR Pfam; PF002786; CPSASE L.D3; 1.

DR PRINTS; PR00088; CPSASE.

DR TIGRPAMS; TIGR01369; CPSASE.

R PROSITE; PS00866; CPSASE 1; 2.

R PROSITE; PS00866; CPSASE 1; 2.

R RROSITE; PS008639; THIOL_PROTEASE_HIS; 1.

K Complete proteome.
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67.3%;
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01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
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PRINTS; PR00721; STOMATIN.
SMART; SM00244; PHB; 1.
                                                                   Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                     3 VVPXGXHYS 11
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SEQUENCE FROM N.A.
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                                           Query Match
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                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
lamiids, Solanales, Solanaceae, Nicotiana.
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-20199450; Pubmed=10945353;
Kitajima S., Koyama T., Ohme-Takagi M., Shinshi H., Sato F.;
Kitajima S., Koyama T., Ohme-Takagi M., Shinshi H., Sato F.;
"Characterization of gene expression of NBERFS, transcription factors
of basic PR genes from Nicotiana sylvestris.";
Plant Cell Physiol. 41:817-824(2000).
HSSP; O80337; 2GCC.
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MEDINTRE=2108290; PubMed=11214968;
MEDINTRE=21082930; PubMed=11214968;
MEDINTRE=21082930; PubMed=11214968;
Matanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbictic bacterium
Mesochizobium loti.";
DNA Res. 7:331-338(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001471; TF ERF.
Pfam; PF00847; AP2-domain; 1.
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EMBL; AP003000; BAB49770.1; -.

GO; GO:0005746; C:mitcochondrial electron transport chain; IEA.

GO; GO:0005895; F:electron transporter activity; IEA.

GO; GO:0006118; P:electron transport; IEA.

InterPro; IPR003245; CytC, heme_BS.

InterPro; IPR002326; Cyt_Cl.

Pfam; PF02167; Cytcchrome C1; 1.

PRINTS; PR00603; CYTCCHROMEC1.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Ethylene-responsive element binding factor.
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                   Nicotiana sylvestris (Wood tobacco)
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Complete proteome.
SEQUENCE 285 AA; 30961 MW; 31D
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ProDom; PD001423; IF ERF; 1.
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Best Local Similarity
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                                                                                                                                                                                                                                                         NCBI TaxID=4096;
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RA MEDLINE-99287316; Pubmed=10360571;

RA Helson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

RA Haft D.H., Hickey B.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

RA Heidelberg J., Sutton G., Pratt M.S., Phillips C.A., Richardson D.,

Raberg L., Sutton G.G., Fleischmann R.D., Elsen J.A., White O.,

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"The sequence of Thermotoga maritima.";

Rature 399:323-329(1999).

REMBL; AR001819; AAD36885.1; -.

REMBL; AZ207; AZ207;
                                                  Gaps
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=12417;
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Pred. No. 39;
0; Mismatches 2; Indels
Score 35; DB 16; Length 285;
Pred. No. 35;
                                                  Indels
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Altermann E.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 308 AA; 34778 MW; ADE03603E5101A9D CRC64;
                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
FTSH protease activity modulator HFLK.
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(TrEMBLrel. 16, I
(TrEMBLrel. 25, I
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Best Local Similarity 45.59,
Best Local Similarity 45.59,
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98 EDLVPMGSHHT 108
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Q9E1X6;
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01-MAR-2001 (
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Q9E1X6
ID Q9E1X
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MEDLINE-93231538; Pubmed-8472961;
Fremaux C., De Antoni G., Raya R., Klaenhammer T.;
Genetic organization and sequence of the region encoding integrative functions from Lactobacillus gasseri temperate bacteriophage phi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDGUENCE FROM N.A.
Engel G., Altermann E., Klein J., Henrich B.;
"Structure of a genome region of the Lactobacillus gasseri temperate phia edh covering a repressor gene and cognate promoters.";
Gene 210:67-70 (1998).
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                                                   MEDLINE=99384014; PubMed=10452953; Altermann E., Klein J., Henrich B.; Primary Etructure and features of the genome of the Lactobacillus gasseri temperate bacterlophage phi-adh."; Gene 236:333-346(1999).
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MICHAES 98037514, PubMed=9371463;

MICHAES 1, Doucette-Stam L.A., DeLoughery C., Lee H.-M., Dubois C.

Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

Harrison D., Hoang L., Kesgle P., Lumm W., Pothier B., Qiu D.,

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McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
                                                                                                                                                                                                                                                       MEDIINE=99138034; PubMed=7836307;
Henrich B., Binishofer B., Blaesi U.;
"Primary structure and functional analysis of the lysis genes of
Lactobacillus gasseri bacteriophage phi-adh.";
J. Bacteriol. 177:723-732(1995).
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Methanobacteriaceae; Methanothermobacter.
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Last sequence update)
Last annotation update)
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Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.O., Zhu G.F., Tu Y.F., Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao Y., Hu H.F., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H., Gu J.L., Chen S.T., Zhang W., Wang L.J., Ding C.W., Hu R. J., Liu Y.L., Mu J., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.C., Yu S.L., Liu X.H., Lu T., Zhang Y.J., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang Y., Hu H., Jia P.X., Zhang R.Q., Guan J.P., Hong G.F.; Shang H., Jia P.X., Shang R.Q., Guan J.P., Hong G.F.; Shang R.Q., Zhang L., Wu M., Shang R.Q., Shang S.Q., Shang R.Q., Shang R.Q., Shang R.Q., Shang S.Q., Shang R.Q., Shang R
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J. Bacteriol. 179:7155(1997).

EMBL; AB000923; AB185-7155(1997).

PIR; E69086; E65086.

R G0; G0:0005910; P:cytckinesis; IEA.

R G0; G0:000910; P:cytckinesis; IEA.

R G0; G0:000910; P:cytckinesis; IEA.

R G0; G0:0009112; P:protein biosynthesis; IEA.

R InterPro; IPR00141; eRF1_2.

InterPro; IPR00141; eRF1_3.

InterPro; IPR00465; PelA.

P Fam; PF03464; eRF1_2; 1.

P Fam; PF03464; eRF1_2; 1.

P Fam; PF03464; eRF1_2; 1.

R TIGRFAMS; TIGR00111; Pelota; 1.

R TIGRFAMS; TIGR00111; Pelota; 1.

R TIGRFAMS; TIGR00111; Pelota; 1.

Cell division; Complete protecome.

Cell division; Complete protecome.
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Sukaryora, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Enrhartoideae, Oryzeae, Oryza.
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45.5%; Pred. No. 46;
.ive 4; Mismatches 2; Indels
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
0J991214_12.4 protein.
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RN SEQUENCE FROM N.A.

RN SEQUENCE FROM N.A.

RAGEN M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RAGEN M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandrews J., Rahmorner M., Henderson S.N.,

RA Abril J.F., Agbayani A., Davler E.G., Helt G., Nelson C.R., Gabor G.L.,

RA Abril J.F., Agbayani A., Barachale J., Bayraktaroglu L., Beasley E.M.,

RA Abril J.F., Bernan B.P., Brokstein P., Brottier P.,

RA Beeson K.Y., Bernan B.P., Buller H., Cadleu E., Center A., Chandra I.,

RA Glerry J.M., Cawley S., Dahlke C., Davenport L.B., Davise P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davise P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davise P.,

RA Cherry J.M., Cawley S., Dahlke C., Perrara C., Perriera S., Pluscheman W.,

RA Chory M. S., Gong F., Gorrell J.H., Guller W.M., Glasser K.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Mathei B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Liu X., Mattei B., McIntosh T.C., Moreod M.P., Morherson D.,

Andran B. M., Moy M., Murphy B., Marryy D.M., Nelson D.L.,

RA Merkulov G., Malishina N.V., Moyarry C., Morris J., Puri V., Reese M.G.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Shue B.C., Siden-Klamos I., Simpson M., Schoeler F., Shen H.
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                                                                                                                                     Gray W.L., Stranes H.B., White M.W., Ashburn C.V., Mahalingam R., "Complete Sequence of the Simian Varicella Virus Genome."; Submitted (MAR-2001) to the EMBL/GenBank/DDBU databases.

EMBL, AF275348; AAG27217.1; -...
GO, GO:0005323; P:DNA packaging; IEA.

InterPro., IPRO/Af40; Herpes UL17.

Pfam; PF04559; Herpes UL17; 1.

Hypothetical protein.

SEQUENCE 678 AA; 75850 MW; A17B09E30512FE3C CRC64;
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CG30437.PC.
CG30437.PC.
CG30437 OR CG10398 OR CG10408.
CG30437 OR CG10398 OR CG10408.
Exceptional melanogaster (Fruit fly).
Exceptional melanogaster (Fruit fly).
Exceptional melanogaster (Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                           67.3%; Score 35; DB 12; Length 678; 50.0%; Pred. No. 90;
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                 Cercopithecine herpesvirus 7.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Best Local Similarity
Matches 5; Conserv
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                                                                              NCBI_TaxID=35245;
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Celuiker S.B., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.A.
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Adoson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibeyam C., Jalai M., Kruse D., Lip., Mattei B., Moshrefi A.,
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
Razleton M., Strong R., Svirskas R., Tector C., Tyler D.,
Williams S.M., Zavari J.S., Suith H.O., Venter J.C., Rubin G.M.;
Supmitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergann C., Berman B., Carlson J.W., Cellniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith B., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        855 AA; 94532 MW; 39BD5A516D6312DB CRC64;
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Last sequence update)
Last annotation update)
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TIGRFAMS; TIGR00915; 2A0602; 1.
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Q7WNB7
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X MEDLINE=2225144; PubMed=12240834;

MEDLINE=2225144; PubMed=12240834;

MEDLINE=2225144; PubMed=12240834;

Matanabe A., Iriguchi M., Racko T., Kimura T., Kishida Y.,

Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,

Kiyokawa C., Kohara M., Takeuchi C., Yamada M., Tabata S.;

A Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

Tomplete genome structure of the thermophilic cyanobacterium

Thermosynechococcus elongatus BP-1.";

DNA Res 9:122-130(2002).

I DNA Res 9:122-130(2002).

R GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0006211; C:integral to membrane; IEA.

GO; GO:0006211; C:integral to membrane; IEA.

R GO; GO:0006310; P:integral to membrane; IEA.

R GO; GO:0006310; P:integral T. IEA.

R InterPro; IPRO1036; Acrflvin_res.
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SEQUENCE FROM N.A.
STRAILISEA, ABTCC 23456 / Biotype 1;
MEDLINE=20020109; PubMed=11756688;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Selkov B., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
The genome sequence of the facultative intracellular pathogen
Brucella melitensis.";
Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
EMBL, AE009470; AR51286.
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Pred. No. 1.4e+02;
2; Mismatches 3; Indels 0
                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
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GO; GO:0005524; F.ATP dependent helicase activity; IEA.
GO; GO:0003676; F:ATP dependent helicase activity; IEA.
GO; GO:0003676; F:muclaic acid binding; IEA.
GO; GO:0016421; F:cxidoreductase activity; IEA.
CO; GO:0016421; F:cxidoreductase activity; IEA.
CO; GO:001642; F:metabolism; IEA.
InterPro; IPR001666; Aldehyde_dehydr.
InterPro; IPR001669; Helicase_C.
C.
C. Pfam; PF00271; helicase_C; 1.
C. SMART; SW00490; HELICS; 1.
C. PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
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Bacteria, Cyanobacteria, Chroococcales, Synechococcus.
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Multidrug efflux transporter.
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PRINTS; PR00702; ACRIFLAVINRP.
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ilarity 54.5%;
Conservative
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76 EKIVPPGARYS 86
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                                         Brucella melitensis.
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Best Local Similarity
Matches 6; Conserv
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SOOCCOOR REPARENCE OF SOOR SOOCCOOR SOOR SOOCCOOR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCOCCOS DET REPRESENTATION OF STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET
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SEQUENCE FROM N.A.

STRAIN-REBOO / ATCC BAA-588;

STRAIN-REBOO / ATCC BAA-588;

MEDLINE-2287954; PubMed=12910271;

MEDLINE-2287954; PubMed=12910271;

MEDLINE-2287954; PubMed=12910271;

METRIE D.B., Holden M., Preston A., Murphy L.D., Thomson N., Mungall J., Sebainia M., Temple L., James K., Harris D.B., Uaull M.A., Cerdeno-Tarraga A.M., Temple L., James K., Harris D.B., Ouall M.A., Achtman M., Aktin R., Baker S., Basham D., Bason N., Cherevach I., Achtman M., Aktin R., Mannin N., Hauser H., Holroyd S., Jagels K., Feltwell T., Goble A., Hamlin N., Meuser H., Holroyd S., Jagels K., A. Leather S., Morberczak H., O'Neil S., Ormond D., Price C., Rabbinowitsch B., Rutter S., Sanders M., Saunders D., Seeger K., Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Onwin L., Whitchead S., Barrell B.G., Maskell D.J.,

Comparative analysis of the genome sequences of Bordetella pertussis, Bordetella parapertussis and Bordetella bronchiseptica.";

BABL, BX649440; CAE31621.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
NCBI_TaxID=518;
                                                                          Length 1044;
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                                                                             67.3%; Score 35; DB 16; Length 10
63.6%; Pred. No. 1.4e+02;
ive 1; Mismatches 3; Indels
Complete proteome. SEQUENCE 1044 AA; 113205 MW; 00E9C13F0F636D2F CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                 262 AA.
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Job time: 29.8667 secs
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                                                                                                               63.6%;
                                                 Query Match
Best Local Similarity 65.0.
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nes 6, Conservative
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SEQUENCE 262 AA
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
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Modified-site
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ALIGNMENTS

/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7" Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide. Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C $^{\circ}$ Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #29. 'note= "N-terminal acetyl" /note= "C-terminal amide" 'note= "D-form residue" Location/Qualifiers ABB80549 standard; peptide; 11 AA. Brunck TK; 19-JUL-2001; 2001WO-US023169. 21-JUL-2000; 2000US-0220101P.

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Gaps

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Indels

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Mismatches

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invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protesse. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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Pred. No. 0.014;
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Best Local Similarity
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DB 5; 0.014;

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93.8%;

Query Match Best Local Similarity

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ABB80552

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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #25
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                                                                                                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #32.
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                                                                                                                08-OCT-2002
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                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB80545;
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                                                                                ABB80552;
                                                                                                                                                                                               virucide
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Gaps

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1; Indels

RESULT 5
ABB80545
ID ABB8
XX
AC ABB8
XX
DT 08-0

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21-JUL-2000; 2000US-0220101P.
                                                                                                                 WPI; 2002-361643/39.
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                                                                                                                                                                                                                                                                 Sequence 11 AA;
        WO200208251-A2
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                                                                                                                                  Novel peptide
activity usefu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Modified-site
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                          31-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                       ABB80522
                                                                                                                                                      protease
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                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Norvalyl carbonyl forming keto-amide linkage with
                         /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                            Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                          Score 44; DB 5; Length 11;
Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "N-terminal acetyl"
                note= "N-terminal acetyl"
                                                                              /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11
/note= "C-terminal amide"
                                                             note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
Location/Qualifiers
                                                                                                                                                                                          Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB80521 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                 Claim 17; Page 64; 69pp; English
                                                                                                                                    19-JUL-2001; 2001WO-US023169.
                                                                                                                                                                                                                                                                                                                                                                           91.7%;
90.9%;
                                                                                                                                                       21-JUL-2000; 2000US-0220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 1 EEVVPXGXSYS 11
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                                                                                                                                                                                          Lim-Wilby M, Levy OE,
                                                                                                                                                                        (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                 EEVVPXGMSYS
                                                                                                                                                                                                            WPI; 2002-361643/39.
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Best Local Similarity
Matches 10; Conserv
                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                            Sequence 11 AA;
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Key
Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus, HCV, serine protease, inhibitor, alpha-ketoamide, virucide.
                                                                                                                                                                                                                                                          ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 5;
Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                       Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB80522 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                       Claim 17; Page 64; 69pp; English.
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19-JUL-2001; 2001WO-US023169
                                                21-JUL-2000; 2000US-0220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.5%,
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                                                                                                                                                       Lim-Wilby M, Levy OE,
                                                                                                      (CORV-) CORVAS INT INC
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Gaps

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1; Indels

Mismatches

DB 5;

Score 44; Pred. No.

91.7%; 90.9%;

Brunck TK;

Levy OE,

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
                                                                                                                                    Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel peptide compound having hepatitis C virus protease inhibitory
                                                                                                                                                                                                                                                                                                                                             pharmaceutical composition comprising the peptide as an active ingits useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB80536 standard; peptide; 11 AA.
                                                                                                                                                                                                           Claim 17; Page 64; 69pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EEVVPXGXSYS 11
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                    (CORV-) CORVAS INT INC
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                                                                                             WPI; 2002-361643/39
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11 AA;
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Modified-site
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                                                      Lim-Wilby M,
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                                                                                                                                                                          protease.
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Matches
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ABB80536
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(first entry)

carbonyl forming keto-amide linkage with

note= "N-terminal acetyl"

/note= "Norvalyl

residue 7"

Location/Qualifiers

/note= "C-terminal amide"

Brunck TK;

'note= "D-form residue"

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                                                                      The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoemide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "2-aminoisobutyryl carbonyl residue forming a keto
activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          serine protease inhibitor peptide #46
                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                            Score 44; DB 5; Length 11;
Pred. No. 0.023;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "C-terminal amide"
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                                            Claim 17; Page 64; 69pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                  ABB80566 standard; peptide; 11
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                                                                                                                                                                                                                             91.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus NS3/NS4a
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                       91.7
Best Local Similarity 90.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                        1 EEVVPXGXSYS 11
                                                                                                                                                                                                                                                                                                                    EEVVPXGQSYS 11
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                                                                                                                                                                                                  Sequence 11 AA;
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                 protease
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EEVVPXGMSYS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                         Novel peptide
                                                                                                                                                                                          Key
Modified-site
                                                                                                                                                                                                                      Modified-site
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                                                                                                   08-OCT-2002
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                                                                                                                                                                       Synthetic.
                                                                                ABB80565;
                                                                                                                                                   virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                    activity
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pharmaceutical composition comprising the peptide as an active ingredient
is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                     /note= "Valyl carbonyl forming keto-amide linkage with residue 7"
                                                                     Gaps
                                                                                                                                                                                                                                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #43
                                                                     ö
                                                Score 44; DB 5; Length 11;
Pred. No. 0.023;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 11;
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Pred. No. 0.023;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                              note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                              /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                          Location/Qualiflers
                                                                                                                                                           ABB80563 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUL-2001; 2001WO-US023169.
                                                 91.7%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-2000; 2000US-0220101P
                                                                                                                                                                                                  (first entry)
                                           Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                       1 EEVVPXGXSYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORV-) CORVAS INT INC
                                                                                                           EEVVPXGMSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 10; Conserv
                              Sequence 11 AA;
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                                                                                                                                                                                                                                                                                                                                                                                  WO200208251-A2
                                                                                                                                                                                                                                                                                          Key
Modified-site
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activity usefu
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                                                                                                                                                                                                                                                                                                                      Modified-site
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                                                                                                                                                                                                                                                                       Synthetic.
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The sequence represents a peptide compound of the invention having the peptides of the invention are alpha **Retoant e peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carbonyl forming keto-amide linkage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                   Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #45.
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ABB80565 standard; peptide; 11 AA.
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virucide.
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Pred. No. 0.023;
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virucide.
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virucide.
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GenCore version 5.1.6
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US-09-201-945-236
US-09-201-945-236
US-09-134-006-4848
US-09-114-006-4848
US-09-144-97B-34
PCT-US91-02714-26
US-08-459-16-2
US-08-459-16-2
US-08-459-06-2
US-08-459-06-2
US-08-26-18BB-28
US-08-26-18BB-28
US-08-26-18BB-28
US-08-26-18BB-28
US-09-325-78BS-2
US-09-325-78BS-2
US-09-325-66-8
US-09-325-66-8
US-09-135-06-6
US-09-135-06-6
US-09-135-06-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389414 seqs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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48
1 EEVVPXGXSYS 11
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Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
No.
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Gaps

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Score 36; DB 4; Length 3472; Pred. No. 1.8e+02; 3; Mismatches 2; Indels

75.0%;

6; Conservative 1 BEVVPXGXSYS 11

Query Match Best Local Similarity Matches 6; Conserv |:|:| | |:| 2294 EDVIPRGISFS 2304

8 8

US-00-637-759B-236
Sequence 236, Application US/08637759B
Sequence 236, Application US/08637759B
Patent No. 5876931
JEDENT NO. 5876931
JITLE OF INVENTION: Identification of Gen
TITLE OF INVENTION: Identification of Gen
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER: FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible

28 30 62.5 626 3 US-08-961-083-220 Sequence 220, App 29 30 62.5 626 4 US-09-156-084-220 Sequence 220, App 30 62.5 3009 4 US-09-13-14-90 Sequence 220, App 31 32 20 62.5 3079 3 US-09-413-114-90 Sequence 93, App 132 29 60.4 10.2 US-09-13-14-90 Sequence 19, App 132 29 60.4 10.5 PC-US93-07964-19 Sequence 19, App 135 29 60.4 10.5 PC-US93-07964-19 Sequence 19, App 136 29 60.4 10.5 PC-US93-1552-7964-19 Sequence 27, App 136 29 60.4 10.0 1 US-09-413-144-4 Sequence 27, App 137 29 60.4 10.0 2 US-09-17-196-8 Sequence 27, App 138 29 60.4 10.0 2 US-09-17-196-8 Sequence 27, App 140 29 60.4 145 3 US-08-413-884-4 Sequence 27, App 140 29 60.4 145 3 US-08-413-84-414-4 Sequence 27, App 140 29 60.4 145 3 US-08-413-884-4 Sequence 4, App 11 29 60.4 145 3 US-08-413-84-4 Sequence 4, App 11 29 60.4 145 3 US-08-413-84-4 Sequence 4, App 11 29 60.4 145 3 US-08-413-84-4 Sequence 4, App 11 29 60.4 145 3 US-08-413-84-4 Sequence 4, App 11 29 60.4 145 3 US-08-413-84-4 Sequence 4, App 11 29 60.4 145 3 US-08-413-84-4 Sequence 4, App 11 29 60.4 165 3 US-08-413-284-4 Sequence 4, App 11 29 60.4 165 3 US-08-413-84-4 Sequence 4, App 11 29 60.4 165 3 US-08-413-284-4 Sequence 4, App 11 29 60.4 165 3 US-08-413-284-4 Sequence 4, App 11 29 60.4 165 3 US-08-413-284-4 Sequence 4, App 11 29 60.4 165 3 US-08-413-284-4 Sequence 4, App 11 29 60.4 165 3 US-08-413-284-4 Sequence 4, App 11 29 60.4 165 3 US-08-413-284-4 Sequence 4, App 11 29 60.4 165 3 US-08-413-284-4 Sequence 4, App 11 20 US-08-413-284-4 Sequence 4, App 11 20 US-08-413-284-4 Sequence 4, App 11 20 US-08-413-284-4 Sequence 4, App 11 20 US-08-413-284-4 Sequence 4, App 11 20 US-08-413-284-4 Sequence 4, App 11 20 US-08-413-284-4 Sequence 4, App 11 20 US-08-413-284-4 Sequence 4, App 11 20 US-08-413-284-4 Sequence 4, App 11 20 US-08-413-284-4 Sequence 4, App 11 20 US-08-413-284-4 Sequence 4, App 11 20 US-08-413-284-4 Sequence 4, App 11 20 US-08-413-284-4 Sequence 4, App 11 20 US-08-413-284-4 Sequence 4, App 11 20 US-08-413-284-4 Sequence 4, App 11 20 US-08-413-284-4 Sequence 4, App 11 20 US-08-413-284-4 Se

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66.7%; Score 32; DB 3; Length 45; 60.0%; Pred. No. 9.9;
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TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 45 amino acids
                                                  45 amino acida
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Best Local Similarity 60.0
Matches 6; Conservative
                            SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
                                                                                                                                                                                                                                                       6; Conservative
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                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-871-355A-236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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Best Local Similarity
Matches 6; Conserva'
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Pred. No. 9.9;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1201 West Peachtree Street
CITY: Alanta
STREET: 1201 West Peachtree Street
CITY: Alanta
STREET: Georgia
COUNTRY: Georgia
COMPUTER: Georgia
COMPUTER READABLE FORM:
MEDIUM TYPE: FORDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BEAPLE FORM:
MAPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/871,355A
FILING DATE: 09-UNM-1997
CLASSIFICATION: 435
PRIOR APPLICATION HASE: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION WOMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION NUMBER: 31,284
REGISTRATION NUMBER: 31,284
REGISTRATION NUMBER: 31,284
TELEPHONE: (404) 873-8794
TELEPHONE: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTAARB: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Paber, Patena L.
REGISTRATION NUMBER: 31,284
REFERNCE/DOCKET NUMBER: 31,284
REFERNCE/DOCKET NUMBER: 31,284
REFERNCE/DOCKET NUMBER: 31,284
REFERNCE/DOCKET NUMBER: 31,284
TELEFAX: (404) 873-8795
INFORMATION: (404) 873-8795
INFORMATION SEQ ID NO: 236:
SEQUENCE CRARACTERISTICS:
LENGTH: 45 amino acids
LENGTH: 45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 236, Application US/08871355A
Patent No. 6015669
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patera L. Peabet
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EEVVPXGXSY 10
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RESULT 4
US-09-201-945-236
US-09-201-945-236
Sequence 236, Application US/09201945
Patent No. 642215
Patent No. 642215
GENERAL INFORMATION:
APPLICANT: David William Holden
TILLE OF INVENTION:
CORRESSENDENCE ADDRESS:
ADDRESSEN Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COMPUTR: USA
ZIP: 30309-3450
COMPUTR: INP PC Compatible
COMPUTR: INP PC Compatible
COMPUTR: INP PC Compatible
COMPUTR: INP PC Compatible
COMPUTR: INP PC Compatible
COMPUTR: INP PC Compatible
COMPUTR: INP PC COMPAT:
FILING DATE:
CLASSIFICATION NUMBER: US/09/201,945
FILING DATE:
CLASSIFICATION NUMBER: 08/637,759
FILING DATE:
CLASSIFICATION NUMBER: 31,284
REGISTRATION NUMBER: 31,284
REGISTRATION NUMBER: 31,284
REGISTRATION TELECATION:
TELECOMMUNICATION NUMBER: RPMS: 101
TELECOMMUNICATION NUMBER: RPMS: 101
TELECOMMUNICATION:
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Sequence 4948, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FABCALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.6%; Score 31; DB 3; Length 159; 66.7%; Pred. No. 63;
64.6%; Score 31; DB 2; Length 159; 66.7%; Pred. No. 63;
                                                                                                                                                                                                                              US-09-018-211-4

J Sequence 4, Application US/09018211

Patent No. 604816

GENERAL INFORMATION:

APPLICANT: Lawlor, Elizabeth

TITLE OF INVENTION:

NOMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

COTY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Comparithle
COMPUTER: IBM Comparithle
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/018,211
FILING DATE:
                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING JABES:
FLIANG APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/844,086
FLING DATE: 18-APR-1997
APPLICATION NUMBER: 960793.4
FILING DATE: 18-APR-1996
ATTORNEY/AGRAT INCRNAFION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRORE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 159 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7
Matches 6, Conservative
                                                6; Conservative
                                                                                                                                        123 EEVLPDGTS 131
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  Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: King
STATE: PA
                                                                      GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 73
LENGTH: 947
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTE: FA
COMPUTER: FA
COMPUTER: READBALE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASISED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,086
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: 9607993.4
FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi. Edward R
REGISTRATION NUMBER: 38,891
REGISTRATION NUMBER: 38,891
REGISTRATION NUMBER: 38,891
RELEPONEN: 610-270-4418
TELLEPONE: 610-270-4418
TELLEPONE: 610-270-4418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32; DB 4;
Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                              Sequence 73, Application US/09228986 Patent No. 6359198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08844086
Patent No. 5866390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 159 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66./
6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein JS-08-844-086-4
                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Pinus radiata
IS-09-228-986-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    686 VMPSGISYS 694
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  ESULT 5
S-09-228-986-73
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PCT-US91-02714-26
Sequence 26, Application PC/TUS9102714
Sequence 26, Application PC/TUS9102714
GENERAL INFORMATION:
MAPPLICANT:
MIGHER, COLICELII, John J.
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
MUSHERS OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: MAREHAIL, O'Toole, Geretein, Murray &
MUSHESSEE: MAREHAIL,
STREET: TWO First National Plaza, 20 South Clark
                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US SEQUENCE 34, Application US/09424978B

Patent No. 666444B

GENERAL INNORMATION:
APPLICANT: Falco, Saverio Carl
APPLICANT: Rafalski, J. Antoni
APPLICANT: Hitz, William D.
APPLICANT: Hitz, William D.
APPLICANT: Hitz, William D.
APPLICANT: Hitz, William D.
APPLICANT: Hitz, William D.
APPLICANT: Hitz, William D.
APPLICANT: Hitz, William D.
APPLICANT: Hitz, William D.
APPLICANT: Hitz, William D.
APPLICANT: Horpe, Catherine J.
TILE OF INVENITOR: 1991-12-02
FILE REFERENCE: BB-1087
CURRENT APPLICATION NUMBER: US/09/424,978B
CURRENT FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-03
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 43
SEQ ID NOS: 43
LENGTH: 507
TYPE: PRI
                                                                                                                                                                                                                                                                        Score 31; DB 4; Length 181;
Pred. No. 73;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31; DB 4;
Pred. No. 2.3e+02;
1; Mismatches 3
CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR FILING DATE: 1997-08-15 NUMBER OF SEQ ID NOS: 6812 SOFTWARE: Patentin version 3.1 SEQ ID NO 4448 LENGTH: 181
                                                                                                                                                                                   TYPE: PRT
ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Burkholderia capacia
US-09-424-978B-34
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative (
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Best Local Similarity 60.0.
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                                                                                                                                                                                                                                US-09-134-000C-4848
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TELEMONY STREET FORM:

MEDIAM FYEER: FLORAGE FORM:

MEDIAM FYEER: FLORAGE FORM:

CONTURER: IMP COMPACTION:

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Pred. No. 2.8e+02; 0; Mismatches 1; Indels

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85.78;
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Best Local Similarity 75.0
Local 6; Conservative
                                       Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein US-07-688-352C-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 VVPAGGSY 208
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                                                                                                                                        1 EEVVPXG 7
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US-08-474-379C-28
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; Sequence 2, Application US/08459065
; Patent No. 5882642
; GENERAL INFORMATION:
APPLICANT: Choi, Gil Ho
TITLE OF INVENTION: Genetically Engineered Transmissible
TITLE OF INVENTION: Hypovirulence
NUMBER OF INVENTION: 3
CORRESPONDENCE 3
ADDRESSE:
ADDRESSE: ADORESSE:
CITY: Nutley Kingsland Street
STREET: New Jersey
STREET: New Jersey
COUNTRY: New Jersey
COUNTRY: New Jersey
COUNTRY: New Jersey
COUNTRY: New Jersey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: U/110
COMPUTER: ELADRY disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,065
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/832,117
APPLICATION NUMBER: US 07/832,117
APPLICATION NUMBER: 34,240
ATTORNEY AGENT INFORMATION:
NAME: ROSSEMEN CARACTINE R
REGISTRATION NUMBER: 34,240
TELECOMMUTATION INFORMATION:
TELECOMMUTATION INFORMATION:
TELECOMMUTATION INFORMATION:
TELECOMMUTATION INFORMATION:
TELECOMMUTER: (201) 235-3500
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: LENGTH: CASTERISTICS:
LENGTH: CASTERISTICS:
LENGTH: CASTERISTICS:
LENGTH: CASTERISTICS:
LENGTH: CASTERISTICS:
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LENGTH: CASTERISTICS:
LENGT
                                TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TOPLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

CRIGINAL SOUNCE:

ORGANISM: Endothia parasitica (Cryphonectria

STRAIN: EP713

US-08-459-146-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.6%; Score 31; DB 2; ]
85.7%; Pred. No. 2.8e+02;
tive 0; Mismatches 1.
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ORGANISM: parasitica)
STRAIN: EP713
INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS: LENGTH: 622 ami-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 622 amino acids
amino acid
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Best Local Similarity 85.7
Matches 6; Conservative
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 EEVVPAG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Goolicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell O'Toole, Gerstein, Michael Bord, O'Toole, Gerstein, Michael Bord, O'Toole, Gerstein, Michael Bord, O'Toole, Gerstein, Michael Bord, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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APPLICANT: Wigler, Michael H.
APPLICANT: Colicell, John J.
TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
TITLE OF INVENTION: PROCESSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 688;
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; Pred. No. 3.2e+
0; Mismatches
US-07-688-352C-28
; Sequence 28, Application US/07688352C
; Patent No. 5527896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 28, Application US/08474379C; Patent No. 5977305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
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VESOUR 12

Sequence 28, Application US/09146249A

Patent No. 6669240.

Patent No. 6669240.

PAPPLICANT: Wigher, Michael H.

APPLICANT: Colicelli, John J.

TITLE OF INVENTION: Cloning by Complementation and Related

TITLE OF INVENTION: Concesses

NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS: 85

CORRESPONDENCE ADDRESS: 85

CORRESPERSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: Giolo Sears Tower, 233 South Wacker Drive

CITY: Chicago

STREET: Illnois

CONTYRY: United States of America

CONTYRY: United States of America

COMPUTER: Ribabale FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 213 South Wacker Drive/6300 Sears Tower CITY: Chicago STATE: 111inois STATE: 111inois COUNTRY: United States of America ZIP: G606-640.

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: BACHON Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/474,379C FILING DATE: 07-JUN-1995 CLASSIFICATION NUMBER: US/08/474,379C FILING DATE: 07-JUN-1995 CLASSIFICATION NUMBER: US/08/11,715 FILING DATE: US-ARR-1990 FILING DATE: US-ARR-1990 FILING DATE: US-ARR-1990 FILING DATE: US-ARR-1991 APPLICATION NUMBER: US-ARR-1991 APPLICATION NUMBER: US-ARR-1991 APPLICATION NUMBER: US-ARR-1991 ATPLICATION UMBER: US-ARR-1991 UMBER: US-ARR-1991 UMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 688;
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Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Best Local Similarity 75.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-379C-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 WPAGGSY 208
NUMBER OF SEQUENCES:
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APPLICATION NUMBER: US/09/146,249A
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY AGENT INFORMATION:
NAME: Clough, David W.
FEGISTRATION NUMBER: 36,107
TELEPHONE: 312/44-6300
TELEPHONE: 312/44-6300
TELENGTH: SEGIST INFORMATION:
TELEPHONE: 312/44-6300
TELENGTH: SEGIST INFORMATION:
TELENGTH: SEGIST INFORMATION: US:
TELENGTH: GR amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: protein
US-09-146-249A-28
Query Match
Best Local Similarity 75.0%; Pred: No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels

Qy
3 VVPXGXXY 10
Db 201 VVPAGGSY 208
Search completed: June 3, 2004, 12:03:08
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Sequence 9, A
Sequence 10,
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Sequence 29,
Sequence 33,
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Sequence 36,
Sequence 37,
Sequence 5, 1
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Sequence 19,
Sequence 20,
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14: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.ppp:*
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1 EEVVPXGXSYS 11
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Sequence 28 Application US/09909164

| Sequence 28 Application US/09909164
| Publication No. US2020068702A1
| GENERAL INFORMATION:
| APPLICANT: Corves International, Inc.
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Devy, Odile E
| APPLICANT: Devy, Odile E
| APPLICANT: NOVEL PEFTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
| TITLE OF INVENTION NUMBER: US/09/909,164
| CURRENT FILING DATE: 2003-03-25
| CURRENT PILING DATE: 2000-07-21
| PRIOR FILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SOFTWARE: Patentin version 3.1
| Languerian Novel Devi US-09-909-164-28

ORGANISM: artificial sequence TYPE: PRT

PEATURE:
| PEATURE:
| PEATURE:
| NAME/KEY: NOD RES|
| LOCATION: (1) ... (1) |
| OTHER INFORMATION: ACETYLATION |
| PEATURE:
| NAME/KEY: MOD RES|
| LOCATION: (11) ... (11) |
| OTHER INFORMATION: AMIDATION |
| PEATURE:
| NAME/KEY: MOS RES|
| LOCATION: (11) ... (11) |
| OTHER INFORMATION: AMIDATION |
| PEATURE:
| NAME/KEY: MISC FEATURE |
| COCATION: (6) ... (6) ... (6) |
| OTHER INFORMATION: NOTVAline-(CO) |

Length 11; DB 12; 93.8%; Score 45; Query Match

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Sequence 36, Application US/09909164
; Sequence 36, Application US/09909164
; Publication No. US20020068702A1
; GENERAL INFORMATION:
    APPLICANT: Corvas International, Inc.
    APPLICANT: Lin-Wilby, Marguerita
    CURRENT FILING DATE: 2000-07-21
    NUMBER OF SEQ ID NOS: 62
    SOFTWARE: PatentIn version 3.1
    SEQ ID NO 36
    LENGTH: 11
    LENGTH: 11
    LENGTH: 11
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OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
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90.9%; Pred. No. 0.0077;
tive 0; Mismatches 1;
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STHER INFORMATION: norvaline-(CO)
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OTHER INFORMATION: norvaline-(CO)
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LOCATION: (1)..(1)
LOCATION: (1)..(1)
PEATURE:
NAME/KEY: MOD_RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                               NAME KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INPORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
PEATURE:
NAME/KEY: MSC_FEATURE
LOCATION: (6)...(6)
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LOCATION: (9)...(9)
CTHER INFORMATION: D-amino acid
US-09-909-164-33
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ORGANISM: artificial sequence
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 33
LENGTH: 11
                                                                                                                                      TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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| Sequence 29, Application US/0909164
| Publication No. US20020068702A1
| GENERAL INFORMATION:
| APPLICANT: Corvas International, Inc. APPLICANT: Lin-Wilby, Marguerita
| APPLICANT: Lin-Wilby, Marguerita
| APPLICANT: Lin-Wilby, Marguerita
| APPLICANT: Lin-Wilby, Marguerita
| APPLICANT: Lin-Wilby, Marguerita
| APPLICANT: Lin-Wilby, Marguerita
| APPLICANT: Lin-Wilby, Marguerita
| APPLICANT: Lin-Wilby, Marguerita
| APPLICANT: Lin-Wilby, Marguerita
| APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
| FILL REPRENCE: 10013-25
| CURRENT PILING DATE: 2003-03-25
| PRIOR FILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SEQ ID NO 29
| LENGTHAL: Lin-Wilby DATE: Lin-Wilb
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Publication No. US20020068702A1
Publication No. US20020068702A1
Publication No. US20020068702A1
APPLICANT: Lin-Willy, Marguerita
APPLICANT: Lin-Willy, Marguerita
APPLICANT: Levy, Oddie E
APPLICANT: Levy, Oddie E
APPLICANT: Levy, Oddie E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE REPERBNCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR FILING DATE: 2000-07-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.8%; Score 45; DB 12; Length 11; 90.9%; Pred. No. 0.0077;
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          Pred. No. 0.0077;
0; Mismatches 1; Indels
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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COCATION: (9)...(9)
COTHER INFORMATION: D-amino acid
08-09-909-164-29
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
          Best Local Similarity 90.9%;
Matches 10; Conservative (
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NAME/KEY: MOD RES
LOCATION: (11)...(11)
CTHER INFORMATION: AMIDATION
FEATURE:
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Best Local Similarity
Matches 10; Conserva
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Sequence 6, Application US/09909164
; Sequence 6, Application US/09909164
; Publication No. US20020068702A1
; GENERAL INFORMATION:
    APPLICANT: Corvas International, Inc.
    APPLICANT: Lin-Wilby, Marguerita
    APPLICANT: Levy, Odile B
    APPLICANT: Evy, Odile B
    APPLICANT: Brunck, Terence K
    TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
    TURRENT APPLICATION NUMBER: US/09/909,164
    CURRENT PILING DATE: 2000-07-21
    PRIOR PILING DATE: 2000-07-21
    NUMBER OF SEQ ID NOS: 62
    SEQ ID NOS: 62
    SEQ ID NO 6
    IEBOTH: 11
    IEBOTH: 11
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NAME/KRY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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Pred. No. 0.013;
0; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/09/909,164
               CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 5
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OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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LOCATION: (9). 7(9)
OTHER INFORMATION: D-amino acid
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LOCATION: (1)...(1)
COTHER INFORMATION: ACETYLATION
FEATURE:
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                                                                                                                                                                                    TYPE: PRT ORGANISM: artificial sequence
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Best Local Similarity 90.9%;
Matches 10; Conservative
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NAME/KEY: MOD RES:
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
US-09-909-164-5
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                                                                                                                                                                                                                                                                                                            Sequence 37, Application US/0990164
Sequence 37, Application US/0990164
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lavy. Odile E
APPLICANT: Lavy. Odile E
APPLICANT: Lavy. Odile E
APPLICANT: Lavy. Odile E
APPLICANT: Lavy. Odile E
APPLICANT: Lavy. Solie E
APPLICANT: NOVIL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOPTWARE: Patentin version 3.1
SEQ ID NO 37
SEQ ID NO 37
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Publication No. US20020068702A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: PERTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
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                                                                           Length 11;
                                                                        Score 45; DB 12; Length 11
Pred. No. 0.0077;
0; Mismatches 1; Indels
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OTHER INFORMATION: norvaline-(CO)
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COTHER INFORMATION: D-amino acids US-09-909-164-37
OTHER INFORMATION: D-amino acid
JS-09-909-164-36
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FRATURE:
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ORGANISM: artificial sequence
                                                                        Query Match 93.8%;
Best Local Similarity 90.9%;
Matches 10; Conservative
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OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.9.
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LOCATION: (11)...(
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Sequence 14, Application US/09909164

| Sequence 14, Application US/09909164
| Publication US20020068702A1
| Publication USZ0020068702A1
| Publication USZ0020068702A1
| Publication Infermational, Inc. | APPLICANT: Lim-Wilby, Marguerita | APPLICANT: Lim-Wilby, Marguerita | APPLICANT: Lim-Wilby, Marguerita | APPLICANT: Lim-Wilby, Marguerita | APPLICANT: Lawy, Odile B | APPLICANT: Lawy, Odile B | APPLICANT: Brunck, Terence K | TITLE OF INVENTION: NOWBER: US/09/909,164 | CURRENT FILING DATE: 2003-03-25 | CURRENT FILING DATE: 2003-03-25 | PRIOR FILING DATE: 2000-07-21 | NUMBER OF SEQ ID NOS: 62 | SOUTHARE: Patentin version 3.1 | SEQ ID NO 14 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 11 | LENGTH: 
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CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 10
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LOCATION: (11)...(11)
COTHER INFORMATION: AMIDATION
FRATURE: MANGE FRATURE
LOCATION: (6)...(6)
OTHER INFORMATION: NOLVALINE-(CO)
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CTHER INFORMATION: D-amino acids
US-09-909-164-10
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LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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NAMES/KEY: MOD RES
LOCATION: (1) ... (1)
PEATURE INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
FEATURE:
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ORGANISM: artificial sequence
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Best Local Similarity
Matches 10; Conserva
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Sequence 9, Application US/09909164

Bublication No. US20020068702A1

GENERAL INFORMATION:
APPLICANT: Corvae International, Inc.
APPLICANT: Law, doile E
APPLICANT: Law, odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT PILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/200,101
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Version 3.1
SEQ ID NO 9
LENGTH: 11
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APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile B
APPLICANT: Levy, Odile B
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERENCE: IN01192-US
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                                                                                                                                    Score 44; DB 12; Length 11;
Pred. No. 0.013;
0; Mismatches 1; Indels
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1 Similarity 90.9%; Pred. No. 0.013;
10; Conservative 0; Mismatches
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Publication No. US20020068702A1
GENERAL INFORMATION:
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OTHER INFORMATION: norvaline-(CO)
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| PRATURE:
| NAME/KEY: MISC_FEATURE
| LOCATION: (8)...(8)
| OTHER INFORMATION: D-amino acid
| US-09-909-164-9
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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Best Local Similarity 90.9%;
Matches 10; Conservative
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OTHER INFORMATION: AMIDATION
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ORGANISM: artificial sequence
FRATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
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THER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: MISC FEATURE LOCATION: (6)...(6) OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MISC_FRATURE
| LOCATION: (9)...(9)
| OTHER INFORMATION: D-amino acid
US-09-909-164-20
                                                                                                                                                                        FEATURE:
NAME/KEY: MOD RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
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LOCATION: (1) ...(1)
OTHER INFORMATION: ACETYLATION
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 11
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OTHER INFORMATION: AMIDATION
FEATURE:
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Matches 10; Conservative
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APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Lovy, Odile E
APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPRENCE: IN01192-US
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 19
TYPE: PRT
TYPE: RAT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEFATITIS C
FILE REFERENCE: INOING.
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
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                                                              Score 44; DB 12; Length 11;
Pred. No. 0.013;
0; Mismatches 1; Indels
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PRIOR FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
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CCATION: (6)...(6)
COTHER INFORMATION: norvaline-(CO)
US-09-909-164-19
; OTHER INFORMATION: norvaline-(CO)
JS-09-909-164-14
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LOCATION: (1)...(1)
COTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
                                                              Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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FRATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
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CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE PALENTIN VERBION 3.1
SEQ ID NO 43
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: June 3, 2004, 12:57:16
Job time: 33.7333 secs
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NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
FRATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (8)..(8)
OTHER INFORMATION: D-amino acid
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                                                                                                                                                                                                     TYPE: PRT ORGANISM: artificial sequence
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APPLICANT: Lim Wilby, Marguerita
APPLICANT: Lim Wilby, Marguerita
APPLICANT: Lim Wilby, Marguerita
APPLICANT: Lim Wilby, Marguerita
APPLICANT: Lim Wilby, Marguerita
APPLICANT: Lim Wilby, Colie E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEFATITIS C
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 00/220,101
PRIOR PILING DATE: 2003-03-23
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTHARE: Patentin version 3.1
SEQ ID NO 24
LENGTH: 11
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Publication No. US20020068702A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Corves International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
APPLICANT: Brunck, Terence K
APPLICANT: Brunck: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
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91.7%; Score 44; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 1; Indels
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Publication No. US20020068702A1
GENERAL INFORMATION:
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NAME/KEY: MISC_FEATURE
LOCATION: (6). -(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KSY: NOD RES
LOCATION: (1)...(1)
OTHER INFORMATION:
ACETYLATION
FEATURE:
NAME/KEY: NOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
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LOCATION: (8)..(9)
COTHER INFORMATION: D-amino acids
US-09-909-164-24
     ; OTHER INFORMATION: D-amino acid
US-09-909-164-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: artificial sequence
                                                                           Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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Gaps ; 0

Length 11;

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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M protein - protein search, using sw model

June 3, 2004, 11:35:47; Search time 9 Seconds (without alignments) 117.567 Million cell updates/sec tun on:

US-09-909-164-43 48 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 EEVVPXGXSYS 11 scoring table: ;equence:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

dinimum DB seq length: 0 daximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:* Jatabase

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		ıcal		hypothetical prote	hypothetical prote	ATP-dependent DNA	ö	tolB protein - Hae	hypothetical prote	hypothetical prote	3-phosphoshikimate	zinc finger protei	bacteriocin BCN5 -	DNA-binding protei					a)	hypothetical prote	periplasmic sorbit	ATP-dependent DNA	o)	type II secretion	٣	ical	_	able beta-ga	I) ABC t
SUMMARIES	ΩI	130	37	A42452	49	23	m	KLJS	F64064	E75619	T24111	D82163	822293	A30481	A34203	E69342	875817	503833	815299	AF0767	AG2945	C98337	AH2679	C82900	C84239	F97461	T05331	S15009	C95978	D82352
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d	ery			70.8																				64.6						
	Score	36	35	34	34	34	34	33	33	32	32	32	32	32	32	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31
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hypothetical prote	leucine-tRNA ligas	leucyl-tRNA synthe	leucine-tRNA ligas	probable sulfate p	sulfate permease -	hypothetical prote	hypothetical prote	isoleucine-tRNA li	K-Cl cotransport p	K-Cl cotransport p	K-Cl cotransport p	probable chitinase	K-Cl cotransport p	conserved hypothet	hypothetical prote
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31	31	31	31	31	31	m	m	m	m	m	e	m	m	m	m

ALIGNMENTS

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hypothetical 367K protein - Cenarchaeum symbiosum
C;Species: Cenarchaeum symbiosum
C;Species: Cenarchaeum symbiosum
C;Species: Cenarchaeum symbiosum
C;Accession: T31308
R;Schleper, C.; DeLong, E.F.; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V.
A;Schleper, C.; DeLong, E.F.; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V.
A;Fitle: Genomic analysis reveals chromosomal variation in natural populations of the ur
A;Accession: T31308
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RESULT 2

Gaps ö 72.9%; Score 35; DB 2; Length 225; 54.5%; Pred. No. 7; ive 3; Mismatches 2; Indels Query Match Best Local Similarity 54.5 Matches 6; Conservative

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1 EEVVPXGXSYS 11 : | | | | ; |: 32 DEVVPNGKTYA 42 à 占 us-09-909-164-43.rpr

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Cispecies: Brucella melitensis
Cispecies: Brucella melitensis
Cibate: 0.1-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
Cibate: 0.1-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
Cibate: AF2286
RibelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, R.; DelVecchio, V.G.; Kapatral, V.; B.Zer, P.H.; Hagius, S.; O'Callaghan, D.; Letes Froc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                             ATF-dependent DNA helicase BME10275 [imported] - Brucella melitensis (strain 16M)
C,Species: Brucella melitensis
C,Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Status: preliminary
A,Molecule type; DWA
A,Residues: 1-1028 «KUR»
A,Cross-references: GB:AE008917; PIDN:AAL51457.1; PID:gl7982167; GSPDB:GN00190
A,Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trans-regulatory splicing protein - simian immunodeficiency virus SIVcpz N;Alernate names: anti-repression trans-activator; art protein; rev protein; C;Species: simian immunodeficiency virus SIVcpz A;Note: host Pan troglodytes (chimpanzee) (c;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999 C;Accession: S09988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: AIDS trans-regulatory splicing protein, transcription regulation; Keywords: AIDS; immunodeficiency; splicing protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Residues: 1-124 <HUE>
;Cross-references: EMBL:X52154; NID:958866; PIDN:CAA36405.1; PID:9763085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 1028;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                     Indels
                                     ٠<u>.</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB;
Pred. No. 59;
2; Mismatches
Pred. No. 13;
1; Mismatches
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.8%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 70.8
Best Local Similarity 54.5
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EEVVPXGXSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 EKIVPPGARYS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 ETVPAGGNYS 116
                                                                                                     2 EVVPXGXSYS 11
                                                                                                                                                                    22 EVAPAGASYN 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EVVPXGXSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: AF3286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
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                                                                                                                                                                    셤
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                                                        V1 protein - tobacco yellow dwarf virus (strain Australia)
(5) Species: tobacco yellow dwarf virus
(5) Species: tobacco yellow dwarf virus
(5) Species: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
(5) Accession: A42452
(5) Accession: A42452
(6) Accession: A42452
(7) Accession: A24452
(7) Accession: A2452
(7) Accessi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: D69493
R;Klenk, H.D.; Clayton, R.A.; Tomb, J.P.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson F;Klenk, H.D.; Clayton, R.A.; Tomb, J.P.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.P.; McDonald, E. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaech A;Reference number: A69250; MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE000968; GB:AE000782; NID:g2689291; PIDN:AAB89307.1; PID:g264859
C;Superfamily: Archaeoglobus fulgidus hypothetical protein AF1949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein AF1949 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 04-Mar-2000
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34536
R;Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, October 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 8.3;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein DKFZp434C031.1 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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Pred. No. 4.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.8%;
Local Similarity 60.0%;
les 6; Conservative
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Status: preliminary
Molecule type: mRNA
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Query Match Best Local S Matches 6

Query Match

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R.Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardeon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, E. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

J. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Alture 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301
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C;Species: Rattus norvegicus (Norway rat)

C;Species: P3-dan-1998 #sequence_revision 06-Peb-1998 #text_change 20-Sep-1999

C;Accession: S22293; 178656

R;Mitchelmore, C.; Traboni, C.; Cortese, R.

R;Mitchelmore, C.; Traboni, C.; Trab
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A;Cross-references: GB:AE004251; GB:AE003852; NID:G9656248; PIDN:AAF94882.1; GSPDB:GN001
A;Experimental source: serogroup 01; strain N16961; biotype El Tor
C;Genetics:
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C;Superfamily: 3-phosphoshikimate 1-carboxyvinyltransferase; 3-phosphoshikimate 1-carbox
                                                                                                                                                                                                                                                                                             Ajectory, C. Mander: 219842
Aj.Reference number: 219842
Aj.Reference number: 219842
Aj.Recession: 174111
Aj.Reterence preliminary; translated from GB/EMBL/DDBJ
Aj.Rolecule type: DNA
Aj.Reterences: EMBL: 281109; PIDN:CAB03241.1; GSFDB:GN00023; CESP:RIODI2.10
Aj.Experimental source: clone R10D12
                                                                                                                      Species: Caenorhabditis elegans
Spate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
Accession: T24111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3-phosphoshikimate 1-carboxyvinyltransferase VC1732 [imported] - Vibrio cho
C.Species: Vibrio cholerae
C.Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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Pred. No. 62;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 425;
                                                                                                     hypothetical protein R10D12.10 - Caenorhabditis elegans
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Pred. No. 62;
2; Mismatches
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50.0%;
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nes 5; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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A;Gene: CESP:R10D12.10
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A;Molecule type: DNA
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Best Local &
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D82163
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SyMhite, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           '....catus.pum.catus.
',Status: preliminary
',Status: preliminary
',Residecule type: DNA
',Residecule type: DNA
',Residecule type: DNA
',Residecule type: DNA
',Residecule type: DNA
',Residecule type: DNA
',Residecule type: DNA
',Experimental source: strain 1479
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NiMolecule type: DNA
NiSesidues: 1-27 <#HI>
A;Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12657.1; PID:g6460953; TICR:DRB00
A;Experimental source: strain Rl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4, Description: involved in transport of colicins and phages across the cell envelope, pl
Date: 18-Aug-1995 #sequenciere.

"Accession: F64064; UC5213

"Palaischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, J. Cacayone, J.D.; Scott, U.S.; Scott, U. D.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Science, 269, 496-512, 1995

1, Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.Title: Whole-genome random sequencing and assembly of Haemophilus Influenzae Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tisen, K.; Sikkema, D.J.; Murphy, T.F.
Sene 178, 75-81, 1996
Ayfitler: Isolatrion and characterization of the Haemophilus influenzae tolQ, tolR, tolA tiReference number: JC5212; MUID:97080550; PMID:8921895
                                                                                                                                                                                                                                                                                                                                                                                                                             1, Status: nucleic acid sequence not shown; translation not shown
1, Molecule type: DNA
1, Molecule type: DNA
1, Molecule type: DNA
1, Molecule type: DNA
1, Cross-references: GB:142023; NID:g1573348; PIDN:AAC22040.1; PID:g1573352;
1, Experimental source: strain Rd KW20
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;Superfamily: Deinococcus radiodurans megaplasmid hypothetical protein DRB0013
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Species: Deinococcus radiodurans
Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 32;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 68.8%; Score 33; DB 2; Length 427; Best Local Similarity 60.0%; Pred. No. 38; Matches 5; Conservative 1; Mismatches 3; Indels
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Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 OVVPSGNGYS 112
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Gaps

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A,Cross-references: GB:AE001054; GB:AE000782; NID:g2689377; PIDN:AAB90501.1; PID:g26498
C;Superfamily: uncharacterized conserved protein
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                          Length 2717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 123; 27;
                          Score 32; DB 2; Length 271
Pred. No. 4.5e+02;
1; Mismatches 2; Indels
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Pred. No. 27;
2; Mismatches
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ne: 10 secs
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50.0%;
                          Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 50.v.
S. Conservative
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                                                                                                                            3 VVPXGXSYS 11
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Job time
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R;Baldwin Jr., A.S.; Leclair, K.P.; Singh, H.; Sharp, P.A.
Mol. Cell. Bio.1 10; 1466-141, 1990
A;Title: A large protein containing zinc finger domains binds to related sequence elemen A;Reference number: A34779; WID:90205817; PMID:2108316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,'N',1074-1168,'K',1170-1225,'V',1227-1434,'N',1436-1607,'I',1609-10
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Cibate 22-Un-1990 #text_change 20-Sep-1999
Cipate 22-Un-1990 #sequence_revision 22-Jun-1990 #text_change 20-Sep-1999
Cipates 22-Un-1990 #sequence_revision 22-Jun-1990 #text_change 20-Sep-1999
Rifen, C.M.; Maniatis, T.
Rifen, C.M.; Maniatis, T.
Rifen, C.M.; Maniatis, T.
Rifen, C.M.; Maniatis, T.
Rifen, A.; Faterence number: A34203; MUID:90169514; PMID:2106471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Species: Clostridium perfringens
); Species: Clostridium perfringens
); Date: 31-Mar-1992 #text_change 24-Nov-1999
); Accession: A30481; S03779
); Garnier, T.; Cole, S.T.
Bacteriol. 168, 1189-1196, 1986
); Title: Characterization of a bacteriocinogenic plasmid from Clostridium perfringens
); Reference number: JT0354; MUID:87057020; PMID:2877971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nolecule type: DNA
Residues: 1-890 cGAR>
Cross-references: GB:M32882; GB:J03309; NID:g150738; PIDN:AAA98249.1; PID:g150739
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A;Status: nucleic acid sequence not shown
A;Molecule type: mRNT
A;Residues: 1.670 <MUT>
A;Cross-references: EMBL:X54250; NID:g57519; PIDN:CAA38151.1; PID:g57520
A;Cross-references: EMBL:X54250; NID:g57519; PIDN:CAA38151.1; PID:g57520
C;Superfamily: HIV-EP2 enhancer-binding protein
C;Superfamily: HIV-EP2 enhancer-binding protein
C;Superfamily: DNA binding; transcription regulation; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Genome: plasmid
C;Superfamily: Clostridium perfringens plasmid pIP404 bacteriocin BCN5
C;Keywords: bacteriocin
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A;Molecule type: mRNA
A;Residues: 801-1072, N',1074-1168, 'K',1170-1225,'V',1227-1434,
A;Cross-references: GB:M32019
C;Superfamily: HIV-RP2 enhancer-binding protein
C;Superfamily: HIV-RP2 enhancer-binding protein
C;Keywords: DNA binding; transcription regulation; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 32; DB 2; Length 890
Pred. No. 1.4e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                      2; Indels
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                                                                                                                                                                                                    66.7%; Score 32; DB 2; 66.7%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                   1; Mismatches
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                   376 VVPAGLTYS 384
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Residues: 1-2717 <FAN>
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Copyright (c) 1993 - 2004) M protein - protein search, using sw model tun on: June 3, 2004, 11:32:06 ; S
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US-09-909-164-43 48 1 EEVVPXGXSYS 11 Perfect score:

BLOSUM62 Scoring table: sequence:

Gapop 10.0 , Gapext 0.5

141681 segs, 52070155 residues

searched:

141681 otal number of hits satisfying chosen parameters:

finimum DB seq length: 0 faximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_42:* Jatabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	ption		fusop		archaeoglob	homo sapien	_		-	_		_	salmonella	burkholderi	lactococcus						streptococc	streptococc	schizosacch		homod	田山田	homo		oryctolagus	rattus norv	-	-		homo sapien
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SUMMARIES	ΙD	A10A HUMAN	CARB FUSIN	Y11K_TYDVA	YJ49 ARCFU	GSR2 HUMAN	REV SIVCZ	TOLE HAEIN	AROA VIBCH	BCNS_CLOPE	ZEP1 HUMAN		RFBB_SALTY	THD1 BURCE	SYL LACLA	SYL_STRA3	SYL_STRMU	SYL_STRP3	SYL STRP8	SYL STRPN	SYL_STRPY	SYL STRR6	SULH SCHPO	SYI TETTH	S127 HUMAN	S127 MOUSE	S124 HUMAN	S124 MOUSE	S124 RABIT	S124 RAT	S125 MOUSE	S125 HUMAN	S125 RAT	S126_HUMAN
	DB	-	-	Н	н	-		-	н	-	Н	П					Н	н	Н						Н							Н	-	ч
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	% Query Match	75.0	72.9	70.8	70.8	70.8	68.89	68.8	66.7	66.7	66.7	64.6	64.6	64.6	64.6	64.6	4.	64.6	64.6	64.6	64.6	64.6	4	4	64.6	64.6		•	•	•	•	64.6	•	4.
	Score	36	33	34	34	34	33	33	32	32	32	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31
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SEQUENCE OF 337-1499 FROM N.A. TISSUE-Brain;

Q924n4 mus musculu Q9uhf0 homo sapien Q8unid torynebacte Q8u492 pyrococcus Q8hu2 halobacteri Q97hu2 halobacteri Q97hu2 halobacteri Q97hu3 halobacteri Q97hb6 methanosarc Q8ptb0 methanosarc Q8ptb0 methanosarc Q8ptb0 methanosarc
S126 MOUSE TYNK HUMAN PURO PYRFU PURO PYRFU PURO HALNI PURO MYCLE PURO MYCLE PURO MYCTU PURO METAA PURO METAA SCOA HELPU
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bata N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soaree M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunbaratne P.H.,
Richards S., Worley K.C., Hale S., Gazcia A.M., Gay L.J., Hulyk S.W.,
Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Hallon D.K., Woung A.C., Shevchenko Y., Bouffard G.G.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard
Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Reneral A., Schein J.E., Jones S.J.M., Marra M.A.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                       "A novel maternally expressed gene, ATP10C, encodes a putative aminophospholipid translocase associated with Angelman syndrome."; Nat. Genet. 28:19-20(2001).
                 A10A HUMAN STANDARD; PRT; 1499 AA.

060312; 096914;
30-MAY-2000 (Rel. 39, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Potential phospholipid-transporting ATPase VA (RC 3.6.3.1) (ATPVA)
(Aminophospholipid translocase VA).

ATP10A OR ATP10C OR ATPVC OR KIAA0566.
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          maps
                                                                                                                                                                                                                                                                                                                                                                                                                                      [2] SEQUENCE FROM N.A. MEDMed=11353404; MEDLINE=21313119; PubMed=11353404; MEDLINE=21313119; Kim S.-J., Cook E.H. Jr., Ledbetter D.H.; Herzing L.B.K., Kim S.-J., Cook E.H. Jr., Ledbetter D.H.; The human aminophospholipid-transporting ATPase gene ATP10C maadjacent to UBE3A and exhibits similar imprinted expression."; Am. J. Hum. Genet. 68:1501-1505(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Skin;
MEDLINE-22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [3]
SEQUENCE FROM N.A.
HUMAN
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N

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Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,

RA Nomura N., Ohara O.; Miyajima N., Tanaka A., Kotani H.,

RY Prediction of the coding sequences of unidentified human genes. IX.

RY The complete sequences of 100 new CDNA clones from brain which can

RY The complete sequences of 100 new CDNA clones from brain which can

RY Code for large proteins in vitro.";

CODE FORTIVITY. ATP + H(2)O = ADP + phosphate.

CO -1 - CANALYTIC ACTIVITY: Widely expressed, with highest levels in

Kidney, followed by lung, brain, prostate, testis, ovary and

CO -1 - SIBGELIULAR LOCATION: Integral membrane protein (By similarity).

CO -1 - DISEASE: Defects in ATP10A are a cause of Angelman syndrome (AS)

(MIM.105830); also known as 'happy puppet syndrome'. As is

CO -1 - DISEASE: Defects in ATP10A are a cause of Angelman syndrome

CO -1 - ANGAGERIUM, microcephaly, ataxia, frequent jerky limb movements

CO -1 - ANGAGERIUM, microcephaly, ataxia, frequent jerky limb movements

CO -1 - ANGAGERIUM, and and hands, hypotonia, hyperactivity,

CO -1 - ANGAGERIUM, a great propensity for protruding the tongue ('tongue

CO -1 - SIMIARRIY: Belongs to the cation transport ATPases family (P-type

ATPASES). Subfamily IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R MIN; 105830; -.
R GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0004012; F:phospholipid-translocating ATPase activity; NAS.
R GO; GO:0008360; P:regulation of cell shape; NAS.
R InterPro; IPR001757; ATPase E1-E2.
R InterPro; IPR005339; Flippase.
R InterPro; IPR005339; Flippase.
R Pfan; PF00702; Hydrolase; 1.
R PRINTS; PR00119; CATATPASE.
R TIGRRAMS; TIGR01494; ATPASE-Pitpid; 1.
R PROSTITE; PS001184; ATPASE E1-E2; 1.
R Hydrolase; Transmembrane; Phosphylation; Magnesium; ATP-binding; M Multigene family.
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98290545; PubMed=9628581;
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TRANSMEM
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last ancharation update)
Car-bamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB ON ENVALS.
Pusobacterium nucleatum (subsp. nucleatum).
Bacteria, Pusobacteria; Fusobacteria; Fusobacteriacese; ô POTENTIAL. CYTOPLASMIC (POTENTIAL). PHOSPHORYLATION (BY SIMILARITY). MAGNESIUM (BY SIMILARITY). MAGNESIUM (BY SIMILARITY). Score 36; DB 1; Length 1499; Pred. No. 13; 0; Mismatches 3; Indels Q -> R (IN REF. 4). MW; D4996A4D0635A68D CRC64; EXTRACELLULAR (POTENTIAL). EXTRACELLULAR (POTENTIAL). EXTRACELLULAR (POTENTIAL) POTENTIAL. EXTRACELLULAR (POTENTIAL) CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL) . CYTOPLASMIC (POTENTIAL). PRT; 1058 AA. fhe large (or ammonia) chain to synthes: similarity). -!- SIMILARITY: Belongs to the carB family. POTENTIAL. POTENTIAL. POTENTIAL POLY-GLU 167687 Query Match
Best Local Similarity 72.7
Matches 8; Conservative STANDARD; 469 EEVVPRGGSVS 479 1 EEVVPXGXSYS 11 388 38 1499 AA; NCBI_TaxID=76856; SEQUENCE FROM N.A 1171 1193 1200 1268 427 1031 1035 1223 FUSNN DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN DOMAIN TRANSMEM DOMAIN DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN DOMAIN SEQUENCE DOMAIN MOD RES METAL METAL TRANSMEM TRANSMEM CARB FUSIN ठे 셤

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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                   EMBL; AEC10554; AAL94625.1; ALT_INIT.

R HAMAP; MF 01210, -: 1.

R InterPro; IPR006493; CPase_L.

R InterPro; IPR005493; CPase_L.

R InterPro; IPR005493; CPase_L.

R InterPro; IPR005491; CPase_L.

R InterPro; IPR00481; CPase_L.

R InterPro; IPR00481; CPase_L.

R Pfam; PF02286; CPSase_L.

R Pfam; PF02286; CPSase_L.

R Pfam; PF02187; CPSase_L.

R Pfam; PF02142; MGS; 1.

R Pfam; PF02142; MGS; 1.

R PROSTTE; PS00866; CPSASE.

R PROSTTE; PS00866; CPSASE.

R ATP-binding; Manganese; Complete protecome.

M ATP-binding; Manganese; Complete protecome.

T DOMAIN.

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ATP (POTENTIAL).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).
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MEDLINE=91188538; PubMed=1546458; MerinE=91188538; PubMed=1546458; Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.; The nucleotide sequence of the infectious cloned DNA component tobacco yellow dwarf virus reveals features of geminiviruses infecting monocotyledonous plants."; Virology 187:633-642(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 1; Length 1058; Pred. No. 16; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tobacco yellow dwarf virus (strain Australia) (TYDV).
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NCBI_TaxID=31599;
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01-JUL-1993 (Rel. 26, Last sequence update)
01-CT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
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or send an email to license@18b-sib.ch).
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SERAINA-C1-6 ( DSM 4304 / ATCC 49558;

MEDLINE-96049343; PubMed-9389475;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Katchum K.A., DodGon R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., McRanney K., Adams M.D., Loftus B.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Rikness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., Mowell L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Rujii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Nature 390:364-370(1997).
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                                                                                                                                                                                                                                                                                                                                                              70.8%; Score 34; DB 1; Length 102; 60.0%; Pred. No. 2.2; tive 2; Mismatches 2; Indels
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                                                                                                                                                             PRR, A42452, A42452.
InterPro; IPR002621, Gemini mov.
Pfam, PF01708, Gemini mov, 1.
Hypothetical protein.
SEQUENCE 102 AA; 11178 MW; A40ECF1E0AF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
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141 161 POTENTIAL.
165 AA; 17588 MW; BBC17054810ADBF8 CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein AF1949.
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PIR; D6493; D69493.
                                                                                                                                    EMBL; M81103; AAA47947.1; -.
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Best Local Similarity 60.0
Matches 6; Conservative
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028330;
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MEDLINE=22388257; PubMed=12477932;
A Strausberg R.L. Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Diatchenow C., Marushan K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Robert S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Wuzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Fahey J., Helton E., Ketteman M., Madan A., Rodriques S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rhiching M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length
Human and mouse cDNa sequences.",
11 proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (oct-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBUNIT: Interacts with HSV-1 early proteins ICP22 and ICP0.
-!- SUBCELLULAR LOCATION: Muclear.
-!- TISSUE SPECIFICITY: Expressed at high levels in heart and pancreas, moderate levels in placenta, liver, skeletal muscle, and kidney, and low levels in brain and lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEDLINE=99214318; PubMed=10196275;
Bruin R., Fineschi B., Ogle W.O., Roizman B.;
Bruin R., Fineschi B., Ogle W.O., Roizman B.;
A novel cellular protein, p60, interacting with both herpes simplex virus 1 regulatory proteins ICP22 and ICP0 is modified in a cell-type-specific manner and is recruited to the nucleus after infection.";
J. Virol. 73:3810-3817(1999).
                                                                                                                                                                                                                                                                                                                                                                                               NEDLINE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=20175410; PubMed=10708517;
Smith J.S., Tachibana I., Pohl U., Lee H.K., Thanarajasingam U.,
Specifier B.P., Ucki K., Billings S., Ramaswamy S., Mohrenweiser H.W.,
Schatthauer B.W., Louis D.N., Jenkins R.B.;
"A transcript map of the chromosome 19q-Arm glioma tumor suppressor
                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                 GSRZ HUMAN STANDARD; PRT; 478 AA.
QSNZMS; QSBTC6; QSHAX6; QSNPP1; QSNPR4; QSUFI2;
16-OCT-2001 [Rel. 40, Created)
16-OCT-2001 [Rel. 40, Last sequence update)
10-OCT-2003 [Rel. 42, Last annotation update)
Glioma tumor suppressor candidate region gene 2 protein (p60).
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Andreu N., Estivill X., Escarceller M., Sumoy L.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
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60 EESIPDGASY 69
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SEQUENCE FROM N.A.
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- S (IN REF. 2; AAH04229).

D - H (IN REF. 3).

PEGNILADREKSFORRNMIEPRERAKFKRYKVKLVEKAP-
REQ - - VLTVSCROAPCPVMTPSLLEVPPRGYGRHHGCP-
WAGFVGPMFG (IN REF. 5).

ECNILADREKSPORRNMIEPRERAKFKRKYKVKLVEKRAFR
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(Rel. 15, Last sequence update)
(Rel. 41, Last annotation update)
(Anti-repression transactivator protein) (ART/TRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IQL -> RGQHSFETGSRAFRGGI (IN REF. 7F18923E348CB52B CRC64;
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Viruses; Rētroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11723;
-!- SIMILARITY: Belongs to the GLTSCR2 family.
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GO; GO:0005622; C:intracellular; NAS.
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EMBL, BC004229, AAH04229.1; --
EMBL, BC010095, AAH10095.1, --
EMBL, AF296124, AAG30413.1, --
EMBL, AF296336, CAB94787.1, --
EMBL, AL122063; CAB59242.1, --
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VARIANT 389 389 R
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Genew; HGNC:4333; GLTSCR2
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01-AUG-1990
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P17280;
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Sen K., Sikkema D.J., Murphy T.F.;
"Isolation and characterization of the Haemophilus influenzae tolQ,
tolR, tolA and tolB genes.";
Gene 178:75-81(1996).
-!- FUNCTION: Involved in the tonB-independent uptake of proteins (By
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PEfam, PR00424, 1.
Transcription regulation, AIDS, Phosphorylation, Nuclear protein.
SEQUENCE 124 AA, 13701 MW, FS877DIBDF65A7B2 CRC64;
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Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Haemophilus.
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similarity LOCATION: Periplasmic (Potential).
similarity: Belongs to the tolb family.
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TOLB HARIN STANDARD, PRT; 427 AA.

LD 70LB HARIN STANDARD, PRT; 427 AA.

QC P44677; P94811;

QC 1.NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 42, Last annotation update)

DT 01-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                   EMBL; X52154; CAA36405.1; -. PIR; S09988; VKLJSI. HIV; X52154; REV$CPZ.
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TOLB OR HI0382.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=E1 Tor N16961 / Serotype O1;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.P., Bisen J.A., Nolson W.C., Clayton R.A., Gwinn M.L.,
Heidelberg J.P., Bisen J.A., Nolson W.C., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                 Periplasmic; Signal; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 406:477-483(2000).
-1- CATALTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = -1- CATALTIC ACTIVITY: Carboxyvinyl)-3-phosphoshikimate.
-1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
29-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)
enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase)
AROA OR VC1732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
VCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                            68.8%; Score 33; DB 1; Length 427; 60.0%; Pred. No. 17; 3; Indels ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i. SUBENIT: Monomer (By similarity).
-i. SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-i. SIMILARITY: Belongs to the EPSP synthase family.
                                                                                                                                                                                                TOLB PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                         HAMAP, MF_00671; -; 1.
InterPro; IRN07195; TolB_N.
Bam, PR04052; TolB_N; 1.
Transport; Protein Transport;
                                                                                                                                                                                                                                                                                                                                                                                  44967 MW;
                                          EMBL; U32722; AAC22040.1; -.
EMBL; U32470; AAC44597.1; -.
PIR; F64064; F64064.
                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
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                                                                                                                                                                                   237
322
326
326
427 AA;
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Best Local Similarity
                                                                                            HSSP; P19935; 1CRZ
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                                                                                                             rigR; HI0382;
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VARIANT
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09KRB0;
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AROA VIBCH
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                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Garnier T., Cole S.T., "Complete nucleotide sequence and genetic organization of the bacteriocinogenic plasmid, pIP404, from Clostridium perfringens."; plasmid 19:134-150(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CPN50;
MEDLINE=87057020; PubMed=2877971;
Garnier T., Cole S.T.;
"Characterization of a bacteriocinogenic plasmid from Clostridium perfringens and molecular genetic analysis of the
                                                                                                                                         TIGR; VC172; --
HAMAP; MF 00210; -; 1.
HAMAP; MF 00210; -; 1.
HAMAP; MF 00210; -; 1.

HAMAP; MF 00210; -; 1.

PRO0196; BESP synth.

ProDom; P0010867; BESP synthse; 1.

PROSITE; PS00104; BESP SYNTHARE; 1.

PROSITE; PS00104; BESP SYNTHARE 1; 1.

PROSITE; PS00885; BESP SYNTHARE 1; 1.

Aromatic anino acid bioSynthesis; 1.

Aromatic anino acid bioSynthesis; 1.

SEQUENCE 426 AA; 46101 MW; 38852D6483BFE1C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium perfringens.
Plasmid pIP404.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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                                                                                                                                                                                                                                                                                                                                      66.7%; Score 32; DB 1; Length 426; 60.0%; Pred. No. 27; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   890 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Microbiol. 2:607-614(1988).
-!- FUNCTION: MAY FUNCTION AS AN IONOPHORE.
-!- INDUCTION: By UV irradiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bacteriocin-encoding gene.";
J. Bacteriol. 168:1189-1196(1986)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CPN50;
MEDLINE=88336297; PubMed=2901768;
                                                                                                             EMBL; AE004251; AAF94882.1; -. PIR; D82163; D82163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                     223 EFVIPAGOSY 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1988 (Rel. 06, C
01-JAN-1988 (Rel. 06, L
01-OCT-1994 (Rel. 30, L
Bacteriocin BCNS.
                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGXSY 10
                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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Matches
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PSTRUCTURE BY NAR OF 2087-2142.

WEDLINE=9223684; PubMed=1567844;

Conichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E.,

Conemborn A.M.;

"High-resolution solution structure of the double Cys2His2 zinc
"High-resolution solution structure of the double Cys2His2 zinc
"High-resolution solution structure of the double Cys2His2 zinc
"High-resolution solution structure of the double Cys2His2 zinc
"High-resolution solution structure of the double Cys2His2 zinc
"High-resolution solution structure of the double Cys2His2 zinc
"In High-resolution structure of the double Cys2His2 zinc
"In ADDITON: HIR PROMOTERS SUCH AS THOSE OF SV40, CWV, OR HIVI.
"C OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I
OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I
IN T-CELL ACTIVATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Zinc finger protein 40 (Human immunodeficiency virus type I enhancer-binding protein 1) (HIV-EP) (Major histocompatibility complex binding protein 1) (MBP-1) (Positive regulatory domain II binding factor 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "High-resolution three-dimensional structure of a single zinc finger from a human enhancer binding protein in solution."; Biochemistry 29:9324-9334(1990).
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PRDII-BFI).
HIVEPI OR ZNR40.
HOMO sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                             66.7%; Score 32; DB 1; Length 890; 66.7%; Pred. No. 59;
                                                                                                                                                                                                                                                                                           96699 MW; F4E5E8971C31C6C6 CRC64;
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MEDLINE=91064333; PubMed=2248949;
Omichinski J.G., Clore G.M., Appella E., Sakaguchi K.,
Gronemborn A.M.;
                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                            HYDROPHOBIC.
                                                                                                                          EWBL; M14481; AAA98248.1; -.
EWBL; M32882; AAA98249.1; -.
PTR; A30481; A30481.
ThterPro; IPR003349; Peptidase_M14.
InterPro; IPR003346; SH3 bac.
Pfam; PF00246; Zn carbopept; 1.
SWART; SM00287; SH3b; 3.
Antibiotic; Bacteriocin; Plasmid, DOMAIN
                                                                                                                                                                                                                                                                                                                                                 Local Similarity 66.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                         170 EVVPGGFTY 178
                                                                                                                                                                                                                                                                                                                                                                                                        2 EVVPXGXSY 10
                                                                                                                                                                                                                                                                                               SECUENCE 890 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZBP1_HUMAN .
P15822;
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Matches
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SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X14524; CAA32666.1; -. PIR; S03833; S03833.
MEROPS; C07.001; -.
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 EEVVPAG.37
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P26391;
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                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstanten the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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**RANSPACT 100497; ---

**RANSPACT 100497; ---

**RANSPACT 100497; ---

**RANSPACT 100407; ---

**RAMP 194540; ---

**RAMP 1940344; C:nucleus; TAS.**

**RAMP 1960357; **RE C2H2, 5.**

**RAMP 1960356; **AEC 2H2, 5.**

**RAMP 1960356; **RE C2H2, 1; 4.**

**RAMP 196036; **AEC 2H2, 5.**

**RAMP 196036; **RE C2H2, 1; 4.**

**RAMP 196036; **AEC 2H2, 1; 4.**

**RAMP 196036; **RE C2H2, 1; 4.**

**RAMP 196036; **AEC 2H2, 1; 4.**

**RAMP 196036; **RE 2H2, 1; 4.**

**RAMP 196036; **RE 2H2, 1; 4.**

**RAMP 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036; **RE 206036
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SUBCELLULAR LOCATION: Nuclear.
INDUCTION: BY mitogens and photol ester.
DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein 1 in hypovirulence-associated ds-RNA genetic element (Contains: P29 proteinseel.
Cryphonectria parasitica (Chesnut blight fungus) (Endothia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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2095
2108
2116
2124
2124
2135
AA, 297217 MW, D45D3CA951FEAS61 CRC64,
                                                                                                                            ZINC-FINGER IN-BETWEEN.
SIMILARITY: STRONG, TO HIVEP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X51435; CAA35798.1; -.
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Conservative
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PDB; 3ZNF; 15-JAN-92.
PDB; 4ZNF; 15-JAN-92.
PDB; 1BBO; 31-OCT-93.
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nes 6; Conserv
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AC P10941—CRYPA
AC P10941—1989
DT 01-JUL-1989
DT 01-JUL
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STRAIN=LT2;
MEDLINE=91260454; PubMed=1710759;
MEDLINE=91260454; PubMed=1710759;
Jiang X.-M., Neal B., Santiago F., Lee S.J., Romana L.K., Reeves P.R.;
Structure and sequence of the rfb (O antigen) gene cluster of
Salmonella serovar typhimurium (strain LT2).";
Mol. Microbiol. 5:695-713(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=602;
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85.7%; Pred. No. 34;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002704; Peptidase_C7.
Pfam; PF01830; Peptidase_C7; 1.
Probom; PD040949; Peptidase_C7; 1.
Hypothetical protein; Hydrolase; Thiol protease.
SEQUENCE 319 AA; 35443 MW; A1P5F775F9AECE7A CRC64;
                                                                                                                                                                                                                                                                                               in the cytoplasm.
-!- SIMILARITY: Belongs to peptidase family C7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
dTDP-Glucose 4,6-dehydratase (EC 4.2.1.46).
Salmonella typhimurium.
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us-09-909-164-43.rsp

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EMBL; U40630; AAA83215.1; -. HSSP; P04968; 1TDJ.
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Matches 6; Conservative
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Q9CHB6;
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                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from threonine in a two-step reaction. The first step is a dehydration of threonine, followed by rehydration and liberation of ammonia.

-!- CATALYTIC ACTIVITY: 1-threonine = 2-oxobutanoate + NH(3).

-!- COFACTOR: Pyridoxal phosphate.

-!- STATHWAY: Isoleudine biosynthesis; first step.

-!- SUBMINIT: Homotetramer (By similarity).

-!- SIMILARITY: Belongs to the serine/threonine dehydratase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                  -i- PATHWAY: DTDP-L-RHAMMOSE BIOSYNTHESIS WITHIN THE O ANTIGEN
BIOSYNTHESIS PATHWAY OF LIPOPOLYSACCHARIDE BIOSYNTHESIS.
-i- SIMILARITY: BELONG TO THE SUGAR EPIMERASE FAMILY. DTDP-GLUCOSE DEHYDRATASE SUBFAMILY.
-!- CATALYTIC ACTIVITY: dTDP-glucose = dTDP-4-dehydro-6-deoxy-D-glucose + H(2)0.
-!- COFACTOR: NAD.
-!- PATHWAY: num.
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TIGRPAMS; TIGR01181; dTDP gluc dehyt; 1.
Lipopolysaccharide biosynthesis; Lyase; NAD; Complete proteome;
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Burkholderiaceae; Burkholderia.
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Last annotation update)
biosynthetic (EC 4.3.1.19) (Threonine
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SEQUENCE 361 AA, 40718 MW, 3A574B4D917EBC57 CRC64;
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Pred. No. 38;
2; Mismatches
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PDB; IKEU; 25-JAN.02.
PDB; IKEW; 25-JAN.02.
PDB; KRW; 25-JAN.02.
PDB; IKEW; SGI0345; rfbB.
InterPro; IPR005888; dTDP_gluc_dehyt.
InterPro; IPR001599; Epimerase_Dh.
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EMBL; AE008792; AAL21001.1; -.
PIR; S15299; S15299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last seq 28-FBB-2003 (Rel. 41, Last ann Threonine dehydratase biosynth
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Best Local Similarity 50.0
Matches 5, Conservative
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278 DEIVPKATSY 287
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,

Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,

Weissenbach J., Ehrlich S.D., Sorokin A.;

"The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis IL1403.",

Genome Res. 11:731-753(2001).

-! CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +

diphosphate + L-leucy1-tRNA(Leu).

-! SUBCELLUIAR LOCATION: Cytoplasmic.

-! SIMILARITY: Belongs to class-I aminoacy1-tRNA synthetase family.
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FIRA, H86726; H86726.
FAMAPP, MF 000499; -1.
InterPro; IPR001300; LRNA-synt_la.
InterPro; IPR001412; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_l.
FIRA, PR00133; LRNA-synt_l.
FRINTS; PR00335; TRNA-SYNTHIEU.
TIGRFAMS; TIGR00396; leus, Dact, l.
PRINTS; PR00385; TRNA-SYNTHIEU.
TIGRFAMS; TIGR00396; leus, Dact, l.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae, Lactococcus.
NCBI_TaxID=1360;
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LeOCT-2001 (Rel. 40, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
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60.0%; Pred. No. 54;
tive 1; Mismatches
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Leu-tRNAsyntla.

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STRAIN=22222988; PubMed=12200847;
MEDLINE=22222988; PubMed=12200847;
Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S., Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C., Radure D., Edorova M.B., Scanlan D., Khouri H., Mulligan S., Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M., Iacobini B.T., Brettoni C., Galli G., Marlani M., Vegni F., Maione D., Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STEAIN=NEM316 / Serotype III;
MEDLINE=22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
                                                                                                                                                                Gaps
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-!- CATALYTIC ACTIVITY: AFF + L-leucine + tRNA(Leu) = AMP + diphosphate + L-leucyl-tRNA(Leu).
-!- SUBCELLUIAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                         SYL_STRA3 STANDARD; PRT; 833 AA.

98E3V2; 9BEXO2;
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome sequence of Streptococcus agalactiae, a pathogen causing
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                                                                                                                  64.6%; Score 31; DB 1; Length 829; 66.7%; Pred. No. 91; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus agalactiae (serotype III), and
Streptococcus agalactiae (serotype V).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                   51 "HIGH" REGION.
613 "KMSKS" REGION.
612 ATP (BY SIMILARITY).
93791 MW; POFOA43014F6C389 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invasive neonatal disease.";
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168 EEVLPDGTS 176
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TIGR, SAG2057; -.
HAMAP, MF_00049; -; 1.
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                                                                                               612 6
829 AA;
Complete proteome.
SITE 40
SITE 609
BINDING 612
SEQUENCE 829 AA;
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SYL STRA3
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   InterPro; IPR002300; ERNA-synt_1.
InterPro; IPR001412; ERNA-synt_1.
InterPro; IPR001412; ERNA-synt_1.
InterPro; IPR001008; ValRS IleRS_edit.
Pfan, PF00133; ERNA-synt_1; 1.
PRINTS; PR001036; IEUS_bact; 1.
PR0SITE; PS00178; AA_TRNA_LIGASE I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Complete proteome.
41 52 "HIGH" REGION.
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Pred. No. 91;
1; Mismatches 2; Indels
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ATP (BY SIMILARITY).
; 2C6F281AE3D3A896 CRC64;
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614 "K
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93966 MW;
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833 AA;
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Mus musculus (Mouse),
bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.1%; Score 37; DB 11; Length 471; 60.0%; Pred. No. 14; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.; Strausberg R.; Submitted (WAR-2002) to the EMBL/GenBank/DDBJ databases. Submitted (WAR-2002) to the EMBL/GenBank/DDBJ databases. MGD; MGI:2154441; Gltscr2. MGD; MGI:2154441; Gltscr2. Hypothetical protein. SEQÜÜENCE 471 AA; 54506 MW; EODA685C374A9760 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Bypothetical protein (Fragment).
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Last sequence update)
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Q7ZTH8
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Q8CLLD1
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                                 PRELIMINARY;
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TISSUE-Liver;
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Q8VD18
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01-MAR-2002 (
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Copyright (c) 1993 - 2004 Compugen Ltd
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SEQUENCE FROM N.A.
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SETAIN=C57BL/6J; TISSUE=Pituitary;
MEDLINE=22354BL/6J; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
BMBL; AK077341; BAC5660.1;
SEQUENCE 484 AA; 55792 MW; BB67949BCBE92D44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasamoto S.,
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MEDININE-2222144; PubMed=12240834;

A Watanabe A., Iriquchi M., Kawashima K., Kimura T., Kishida Y.,

A Watanabe A., Iriquchi M., Kawashima K., Kimura T., Kishida Y.,

Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N.,

Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

T. Complete genome structure of the thermophilic cyanobacterium

Thermosynachococus elongatus BP-1.";

DNA Res 9:123-130(2002).

I DNA Res 9:123-130(2002).

R GO; GO:0016021; Fitransporter activity; IEA.

R GO; GO:0005215; Fitransporter activity; IEA.

R GO; GO:0006310; Pitransporter activity; IEA.

R InterPro; IPR001036; Acrifvin_res.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Pred. No. 14;
2; Mismatches 2; Indels
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 24, Last annotation update)
Multidrug efflux transporter.
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Pfam; PF00873; ACR tran; 1.
PRINTS; PR00702; ACRIFLAVINRP.
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Best Local Similarity 60...
Best Local Similarity 60...
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239 EVIPAGASYN 248
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SEQUENCE 1044 AJ
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                              Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.1%; Score 37; DB 11; Length 484; 60.0%; Pred. No. 14; 2; Indels ative 2; Mismatches 2; Indels
                                    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to glioma tumor suppressor candidate region gene 2.
GLTSCR2 OR AMS3641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QBBK35;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UIN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to glioma tumor suppressor CANDIDATE region gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last amoniation update)
51milar to gliona tumor suppressor CANDIDATE region gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R., Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases EMBL, BC017637, AAH17637.1; -. MGD; MGI:2154441; Gltscr2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            484 AA; 55835 MW; BBB45F3B4BE02A36 CRC64;
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Salivary gland;
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Best Local Similarity
Matches 6; Conserv
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GLTSCR2.
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Gaps

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Q8BK35

Q8BK35

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Indels
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=226900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C55268ACB7225995 CRC64;
                                                                                                                                                                                      01-JTN-2003 (TrEMBLrel. 24, Created)
01-JTN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter substrate-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
   5
                                                                                                                                                          344 AA
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   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 423.87-91(2003).
EMBL; AE017015; AAP12123.1; -.
InterPro; IPR000437; Prok lipoprot S.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
                                                                                                                                                          PRT;
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STRAIN=AV19 / DSM 6324 / JCM 9639;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60.0
Best Local 6; Conservative
   6; Conservative
                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                         : | | | | | : |:
32 DEVVPNGKTYA 42
                                     1 EEVVPXGXSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 EEIAPLGLSY 161
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                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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SEQUENCE 344 AA
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NCBI_TaxID=2320;
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01-JUN-2002
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Q8TX62;
                                                                                                                                                          Q815A7
Q815A7;
   Matches
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Q8TX62
                                                                                                                         RESULT 8
Q815A7
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                                                                                                                                                                                                         Swanson R.V.;
Swanson R.V.;
Genomic analysis reveals chromosomal variation in natural populations
of the uncultured psychrophilic archaeon Cenarchaeum symbiosum.";
J. Bacteriol. 180:5003-5009(1998).
GENBL: AF083079: AAC62699.1;
PIR: T31308; T31308
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; F:transporter activity; IEA.
InterPro; IPR000515; BPD transporter
InterPro; IPR000515; BPD transporter
InterPro; IPR000515; BPD transporter
Swanson: Swanson: Wando.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots; asterids; lamiids, Solanales, Solanaceae, Solanum.
                                                             Archaea; Crenarchaeota; Thermoprotei; Cenarchaeales; Cenarchaeaceae; Cenarchaeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Milligan S.B., Gasser C.S.,

MEDLINE-95375233; PubMed=7647301;

MEDLINE-95375233; PubMed=7647301;

MIlligan S.B., Gasser C.S.,

Invalure and regulation of pistil-expressed genes in tomato.";

Plant Mol. Biol. 28:691-711(1995).

R EMBL; U20592; AAA80497.1; -.

R PR; S57310; S57810.

GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.

R PROSTER PRO0129; Kunitz_legume.

R PART; SM00452; Kunitz_legume; 1.

PRODOM; PD000891; Kunitz_legume; 1.

R SMART; SM00452; STI; 1.

R PROSTER; PS00283; SOYBEAN KUNITZ; 1.

R HYPOChetical protein; Signal.

T SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 1; Length 3472;
Pred. No. 2.1e+02;
3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                      SWART; SM00320; WD40; 2.
PROSTIE: PS00402; BPD_TRANSP_INN_MEMBR; 1.
HYDOCHetical protein.
SEQUENCE 3472 Aa; 367058 MW; 37P80707030F9355 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 UNKNUWW.
25188 MW; 1074C261D20CFDAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein precursor.
Lycopersicon esculentum (Tomato).
01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.9%; Score 35; DB 10;
54.5%; Pred. No. 17;
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                                                                                                                                                                           MEDLINE=98422450; PubMed=9748430;
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ilarity 54.5%;
Conservative
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2294 EDVIPRGISFS 2304
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                                                         Cenarchaeum symbiosum.
                                     Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
6; Conserv?
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Best Local Similarity
                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                        NCBI_TaxID=46770;
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RESULT 7

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Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22008415; PubMed=12721630;
Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
Overbbeck R., Kyrpides N.;
Genome sequence of Bacillus cereus and comparative analysis with
Bacillus anthracis.";
   Gabs
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MEDIUR=2192647; bubMed=11930014;
Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
Malykh A.G., Koonin E.V., Kozyavkin S.A.;
"The complete genome of hyperthermophile Methanopyrus kandleri AV19
and monophyty of archaeal methanogens.";
Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
InterPro. IREO10627.1; -.
InterPro. IREO10627, UPF0047.
Pronom; PD005232; UPF0047; 1.
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Pred. No. 28;
1; Mismatches 3; Indels
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC014009; AAH14009.1; -.
EMBL; BC007248; AAH07248.1; -.
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Q9E1X6
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fagales; Betulaceae; Betula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0008843 Frendochitinase activity; IEA.
GO; GO:0016798; Frendochitinase activity, acting on glycosyl bonds; IEA.
GO: GO:0016798; Frendohydrate metabolism; IEA.
InterPro; IPR001223; Glyco_hydro_18.
PEGP: PR001239; Glyco_hydro_18.
PEM: PF00704; Glyco_hydro_18; I.
PROSITE; PS01095; CHITINASE_18; I.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillovaara-Teijo M., Korhonen M.S., Palva T.E., Kangaejarvi J., Submitred (JAN-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AJ279692; CAB66334.1; -- HSSP; P23472; 2HVM.
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99CSO; Q96IT7;
01-DBC-2001 (TrEMBLrel. 19, Created)
01-DBC-2001 (TrEMBLrel. 19, Last sequence update)
01-DBC-2002 (TrEMBLrel. 22, Last annotation update)
Glioma tumor suppressor candidate region gene 2 (Fragment).
Homo sapiens (Human).
                                                                                          70.8%; Score 34; DB 17; Length 143; 60.0%; Pred. No. 18; ative 1; Mismatches 3; Indels
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                                                             143 AA; 15734 MW; 4C8B28A1FBBEDD0B CRC64;
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                                                                                                                                                                                                                                                                                                01-OCT-2000 (TIEMBLIEL. 15, Created)
01-OCT-2000 (TIEMBLIEL. 15, Last sequence update)
01-OCT-2003 (TIEMBLIEL 25, Last annotation update)
Acidic endochitLinase (EC 3.2.1.14) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
TIGRFAMS; TIGRO0149; TIGRO0149; 1.
PROSITE; PSO1314; UPP0047; 1.
COMPLETE PINEFOO4681; UPP0047; 1.
COMPLETE PINTEGEOME.
SEQUENCE 143 AA; 15734 MW; 4C8
                                                                                        Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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75 EELVPQGAGY 84
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TISSUE=Lung, and Skin;
Strausberg R.;
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SEQUENCE FROM N.A.
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Q9M3T4;
01-OCT-2000
01-OCT-2000
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AC 096CS
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AC 096CS
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OC BUKAT
OC MAMMA OC MAMMA (1]
RN SEQUE
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STRAIN=MAFP301099;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
MEANDER T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kiyokawa C., Kohara M., Marsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takanohi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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                                                                                                                                       70.8%; Score 34; DB 4; Length 479; 60.0%; Pred. No. 67; 3; Indels ative 1; Mismatches 3; Indels
NON TER 1 1 SEQUENCE 479 AA; 54529 MW; 0A6C3A8B476F7E8F CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Ceroopithecine herpesvirus 7.
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable DNA ligase.
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PROSITE; PS00697; DNA_LIGASE_A1; 1.
PROSITE; PS50160; DNA_LIGASE_A3; 1.
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Query Match

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Beet Local Similarity 60.00,
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Best Local Similarity 60.v
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Search completed: June 3, 2004, 11:57:34
Job time : 30.8667 Becs
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QREWD4
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STRAIN-16M / ATCC 23456 / Biotype 1;

WEDLINE=20020109; PubMed=1175668;

A DelVecchio V.G., Kapatral V., RedKar R.J., Patra G., Mujer C., Los T.,

La l'vanova N., Anderson I., Bhattacharyva A., Lykidis A., Raznik G.,

La lvanova N., Anderson I., Bhattacharyva A., Lykidis A., Raznik G.,

A Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman B.,

Selkov B., Elzer P.H., Hagjus S., O'Callaghan D., Letesson J.-J.,

Haselkorn R., Kyrpides N., Oventheek R.,

The genome sequence of the facultative intracellular pathogen

Brucella malitensis.";

The genome sequence of the facultative intracellular pathogen

Tr Brucella malitensis.";

Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).

Brucella malitensis.";

Brucella malitensis.";

C GO, GO:0005524; F.AIP binding; IEA.

GO, GO:0005524; F.AIP binding; IEA.

GO, GO:0005524; F.AIP bending; IEA.

GO, GO:0005524; F.AIP dependent helicase activity; IEA.

GO, GO:000
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                                                                                     GEQUENCE FROM N.A.

Gray W.L., Starnes H.B., White M.W., Ashburn C.V., Mahalingam R.;

"Complete Sequence of the Simian Varicella Virus Genome.";

Submitted (WAR-2001) to the EMBL/GenBank/DDBU databases.

EMBL; AF275548; AAG27217.1; -..

GO, GO:0019012; P:10A packaging; IEA.

GO, GO:006123; P:10A packaging; IEA.

InterPro; IPR007640; Herpes_UL17.

Hypothetical protein.

SEQUENCE 678 AA; 75850 MW; A17B09E30512FE3C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brucella melitensis.
Barceria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Brucellaceae, Brucella.
NCBI TaxID=29459;
                                                                                                                                                                                                                                                                                                                                                     Query Match 70.8%; Score 34; DB 12; Length 678; Best Local Similarity 50.0%; Pred. No. 98; Matches 5; Conservative 2; Mismatches 3; Indels
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
NCBI_TaxID=35245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ATP-dependent DNA helicase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1028 AA.
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MEDLINE=2254719; PubMed=12466555;
MEDLINE=2254719; PubMed=12466555;
Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K., Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
"The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans.";
Nucleic Acids Res. 30:5293-5300(2002).
EMBL, ARD0417; BAC44062.1;
InterPro; IPR008985; Cord, like lec gl.
InterPro; IPR008985; Cord, like lec gl.
InterPro; IPR008985; Lipoprotein.17.
Pfam, PG44000; Lipoprotein.17; 3.
Complete proteome.
SEQUENCE 1123 AA, 123636 MW; A4D707330B3DB4AC CRC64;
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                                                                                                                                                                               Mycoplasma penetrans.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBL_TaxID=28227;
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                      OSEWD4;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
XYPE 2560 paralog, 57%.
   PRT; 1123 AA
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PRELIMINARY;
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Abb80536 Hepatitis
Abb80542 Hepatitis
Abb80543 Hepatitis
Abb80543 Hepatitis
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virucide.
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WO200208251-A2
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(c) 1993 - 2004 Compugen Ltd.
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Listing First 45 summaries
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Gapop 10.0 , Gapext 0.5
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43. geneseqp2000s:*
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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Pred. No. 0.0045;
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RESULT 4

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Score 49; DB 5; Pred. No. 0.0045;

94.2%;

Query Match Best Local Similarity

"Norvalyl carbonyl forming keto-amide linkage with

residue

Misc-difference

Modified-site

note=

/note= "C-terminal amide" 'note= "D-form residue"

WO200208251-A2

31-JAN-2002

19-JUL-2001; 2001WO-US023169. 21-JUL-2000; 2000US-0220101P.

'note= "N-terminal acetyl"

Location/Qualifiers

Modified-site

Synthetic

virucide.

Modified-site

Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide;

C virus NS3/NS4a serine protease inhibitor peptide

Hepatitis

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'note= "Norvalyl carbonyl forming keto-amide linkage with
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lty useful for treating disorders associated with hepatitis C
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Best Local Similarity
Matches 10; Conserv
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Modified-site
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                                                                                                                                                                                                                                                                                                        Synthetic.
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                                                                                                                                                                                                                                                        virucide.
ABB80555
ID ABB80555
                                                                          ABB80555;
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Brunck TK;

(CORV-) CORVAS INT INC Lim-Wilby M, Levy OE,

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                                                                                                                                                                                                                                                                                                                                                                              Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #38.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 64; 69pp; English.
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Best Local Similarity
Matches 10; Conserv
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Gaps

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ABB80523 standard; peptide; 11 AA.

RESULT 5

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EEVVPXGSHYS

(first entry)

08-OCT-2002

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Modified-site
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                                         31-JAN-2002
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                                 /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #17
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Pred. No. 0.007
0; Mismatches
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                 'note= "N-terminal acetyl"
                                                                           'note= "C-terminal amide"
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                                                          'note= "Oxymethionine"
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cocation/Qualifiers
                                                                                                                                                                                Brunck TK;
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                                                                                                                                            21-JUL-2000; 2000US-0220101P
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                                                                                                                                                                                                                                                                                                                                                                         10; Conservative
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                                                                                                                                                                               Levy OE,
                                                                                                                                                               (CORV-) CORVAS INT INC
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Best Local Similarity
Matches 10; Conserv
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ABB80537
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                virus
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                                                                                                                                                                                                                                                                                                                                                                                           ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #40.
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Pred. No. 0.0072;
0; Mismatches 1; Indels
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11
/note= "C-terminal amide"
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Best Local Similarity 90.9
Matches 10; Conservative
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Lim-Wilby M, Levy OE,
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                                                                                                                                                      Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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Pred. No. 0.0072;
0; Mismatches 1; Indels
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                                                                                                         Brunck TK
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                               19-JUL-2001; 2001WO-US023169
                                                       21-JUL-2000; 2000US-0220101P
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                       Levy OE,
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                                                                              (CORV-) CORVAS INT INC
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Modified-site
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         31-JAN-2002
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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Pred. No. 0.0072;
0; Mismatches 1; Indels
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Brunck TK;
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                                                                                                                                                                                                                                              Claim 17; Page 64; 69pp; English
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                                                           WPI; 2002-361643/39.
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Length 11; Indels

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carbonyl forming keto-amide linkage with
pharmaceutical composition comprising the peptide as an active ingredient
is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #11
                                                                              Score 48; DB 5;
Pred. No. 0.0072;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "N-terminal acetyl"
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                                                                                                                                                                                                                                                                 ABB80531 standard; peptide; 11
                                                                                 92.3%;
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ilarity 90.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           residue 7"
                                                                                                                  Conservative
                                                                                                                                                1 EEVVPXGXHYS 11
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Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
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Modified-Bite
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                                                The sequence represents a peptide compound of the invention having hepatities C virus (RCV) protease inhibitory activity. The peptides of the invention are alpha -ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                   Gaps
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0.0072;
thes 1; Indels
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                      Claim 17; Page 65; 69pp; English.
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ilarity 90.9%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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les 10; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB80532;
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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Pred. No. 0.0072;
0; Mismatches 1; Indels
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ABB80549

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                     carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                   Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #28
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                                                                                                                                                                                                                                                                                                                                                                /note= "Norvalyl
residue 7"
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ABB80548 standard; peptide; 11
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Similarity 81.8%;
9; Conservative
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                                                                                                                                                                                "Norvalyl carbonyl forming keto-amide linkage with 9 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
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                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
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                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #29.
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Pred. No. 0.29;
0; Mismatches
                                                                                                                                                          'note= "N-terminal acetyl"
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                                                                                                                                  Location/Qualifiers
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81.8%;
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Best Local Si
Matches 9
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21-JUL-2000; 2000US-0220101P.
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                             Key
Modified-site
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Synthetic.
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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"

/note= "C-terminal amide"

note= "N-terminal acetyl"

Location/Qualifiers

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                          Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
Lim-Wilby M, Levy OE, Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 65; 69pp; English.
                                                                                                  WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                       protease.
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ö Query Match 76.9%; Score 40; DB 5; Length 11; Best Local Similarity 81.8%; Pred. No. 0.29; Matches 9; Conservative 0; Mismatches 2; Indels

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Gaps

1 EEVVPXGTDYS 11

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Sequence 11 AA;

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Sequence 3, Appli
Sequence 6771, Ap
Sequence 182, App
Sequence 182, App
Sequence 6, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                6, Appli
19, Appli
66, Appli
66, Appl
66, Appl
56, Appl
8, Appli
10, Appli
4, Appli
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Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                              Sequence 21444, A
Sequence 4794, Ap
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26615,
                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                            June 3, 2004, 11:36:47; Search time 11.7333 Seconds (without alignments) 48.399 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5
Sequence 5
Sequence 5
Sequence 8
Sequence 1
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Sequence 7
Sequence 9
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                     Issued Patents AA:*
... /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
... /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
... /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
... /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
... /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
... /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
... /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                             09-252-991A-21444
                                                                                                                                                          otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3-08-530-010-5
3-08-530-010-7
3-08-530-010-9
                                                                                                                                          389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                  ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                 M protein - protein search, using sw model
                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                               US-09-909-164-44
52
1 EEVVPXGXHYS 11
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                  'itle:
'erfect score:
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                                                                                                  equence:
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                                                 un on:
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No.
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RESULT 2
US-09-114-001C-4794

| US-09-114-001C-4794 |
| Sequence 4794, Application US/09134001C |
| Patent No. 6380370 |
| GENERAL INFORMATION |
| TICLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS |
| TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS |
| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS |
| CURRENT FILING DATE: 1994-08-13 |
| CURRENT FILING DATE: 1997-11-08 |
| PRIOR FILING DATE: 1997-11-08 |
| PRIOR FILING DATE: 1997-08-14 |
| NUMBER OF SEQ ID NOS: 5674 |
| LENGTH: 1037 |
| TYPE: PRI
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        Sequence 9, Appli
Sequence 11, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 9, Appli
Sequence 11, Appli
Sequence 12, Appli
Sequence 3250, Ap
Sequence 7284, Ap
Sequence 15, Appl
Sequence 15, Appli
Sequence 605, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
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Pred. No. 18;
0; Mismatches 3; Indels
US-08-484-101B-7

US-08-484-101B-9

US-08-484-101B-1

US-08-714-524D-3

US-08-714-524D-5

US-08-714-524D-9

US-08-714-524D-9

US-08-714-524D-9

US-08-714-524D-9

US-09-134-001C-3950

US-09-134-001C-4185

US-09-328-352-7284

US-09-328-352-7284

US-09-348-352-7284

US-09-348-352-7284

US-09-348-352-7284

US-09-348-352-7284

US-09-348-357-15

US-09-342-647-4

US-08-489-0358-8065

US-09-342-647-4

US-08-459-065-2

US-09-342-647-4
                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-21444
                                                                                                                                                                                                                                                                                                                                                                                                                      73.1%;
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 70.v
   1 EEVVPXGXHY 10
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Pred. No. 14;
1; Mismatches 2; Indels
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MEDIUM TYPE: Diskette
COMPUTER: DIskette
COMPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Keser, Matthew R.
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STREET: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09215096; Patent No. 6008194
GENERAL INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                    TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: aingle
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      ...crowody: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 163590
US-08-879-995A-3
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STRANDEDNESS: sing
TOPOLOGY: linear
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARENT NO. 2521/99
PARENT NO. 2521/90:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: APPLICATION NUMBER: US/09/252,991A
CURRENT PPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26615
LENGTH: 277
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                                                                                                                                                                                             0; Gaps
                                                                                                                Query Match 69.2%; Score 36; DB 4; Length 1037; Best Local Similarity 63.6%; Pred. No. 56; Matches 7; Conservative 1; Mismatches 3; Indels
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Pred. No. 21;
0; Mismatches 4; Indels
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Patent No. 5985606

GENERAL INFORMATION:
APPLICANT: Hilman, Jennifer L.
APPLICANT: Hal, Preeti
APPLICANT: Raser, Matthew R.
TILE OF INVENTION: HYMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94304
COMPUTER READABLE PORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPREATING SYSTEM: DOS
SOFTWARE: FastSERO for Windows Version 2.0
SOFTWARE: FastSERO for Windows Version 2.0
SOFTWARE: Herewith
TPLING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -09-252-991A-26615
Sequence 26615, Application US/09252991A
Patent No. 6551795
           , ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26615
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Best Local Similarity 63.6%;
Matches 7; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                199 KEVVSNGLHYS 209
                                                                                                                                                                                                                                                                       1 EEVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 EETVPGGGHTS 58
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178 IVPHGGHY 185
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                                                                                                                                                                                                                                                    BSULT 6
S-09-107-532A-6771
Sequence 6771, Application US/09107532A
Sequence 6771, Application US/09107532A
Batent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
                                                                                   ö
                                                                                   Gaps
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                                  Score 34; DB 3; Length 126;
Pred. No. 14;
1; Mismatches 2; Indels
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63.5%; Score 33; DB 4; Length 63;

Best Local Similarity 45.5%; Pred. No. 10;

Matches 5; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSES: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <UDKNOWN>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: UNJY 2, 1997
APTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 60/051571
FILING DATE: UNJY 2, 1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: GTC-012
TELEPHONE: (781)893-5007
TELEPRAK: (781)893-5007
TELEPRAK: (781)893-5007
TELEPRAK: (781)893-507
TELEPRAK: (781)893-507
TELEPRAK: (781)893-507
TELEPRAK: (781)893-507
TELEPRAK: (781)893-507
TELEPRAK: (781)893-507
TELEPRAK: (781)893-607
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;
; LOCATION: (B) LOCATION 1...63
; SEQUENCE DESCRIPTION: SEQ ID NO: 6771:
JS-09-107-532A-6771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 63 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
COUNTRY: USA
                                         65.4%;
                                    Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                            28 EQVVPGGGH 36
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S-09-215-096-3
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Sequence 182, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSES: Human Genome Sciences, Inc.
ATREET: 9410 Few West Avenue
COUNTRY: USA
ZIP: 2080 Feete, 3.50 inch, 1.4Mb storage
COUNTRY: USA
ZIP: 2080 Feete, 3.50 inch, 1.4Mb storage
COUNTRY: USA
ZIP: 2080 Feete, 3.50 inch, 1.4Mb storage
COMPUTER: READABLE FORM:
MADIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFFICATION: A35
RICHARD AND AND AND APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFFICATION NUMBER: B3440P2
FILING DATE:
APPLICATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: B3440P2
TELECOMMUNICATION INPORMATION:
NAME: (301) 309-8614
TELECOMMUNICATION INPORMATION:
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TELECOMMUNICATION I
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Sequence 182, Application US/09536784

Patent No. 6573082
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
SIRRET: 9410 Key West Avenue
CITY. Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 89; 2; Indels
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HV vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA::
RPELICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 63.5%;
Best Local Similarity 62.5%;
Matches 5; Conservative
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein US-08-961-083-182
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Gaps

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RESULT 7 US-08-961-083-182

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ADDRESSEE: No. 59898890 No. 5989889disk of No. 5989889th America, Inc. STREET: 405 Lexington Avenue CITY: New York
          ADDRESSEE: No. 58211040 No. 5821104disk of No. 5821104th America, Inc. STREET: 405 Lexington Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB 2; Leus-Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Rey, Michael
APPLICANT: Rey, Michael
APPLICANT: Golightly, Elizabeth
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES
TITLE OF INVENTION: HAVING TRIPEPTIDE AMINOPEPTIDASE
TITLE OF INVENTION: ACTIVITY
NUMBER OF SECURNICES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,118
FILIGO DATE: 19-MAR-1997
CLASSIFICATION: 47=
                                                       CITY: NY
COMPUTE: NY
CONDITY: US
CONDITY: US
CONDITY: Disched

ZIP: 10174

ZIP: 10174

COMPUTER READABLE FORM:
MEDIUM TYPE: Disched
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTERED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,119
FILING DATE: 19-MAR-1997
CLIASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Ellas J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4107.204-US
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION OF TO NO. 10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INPORMATION POR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 600 amino acide TYPE: amino acid STRANDEDNES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-821-119-19
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 VPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 VPKGWHYS 38
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| Sequence 6, Application US/09468656A
| Sequence 6, Application US/09468656A
| Sequence 6, Application US/09468656A
| Sequence 6, Application US/09468656A
| GENERAL INFORMATION:
| APPLICANT: Johnson, Leslie S.
| TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
| TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structural
| TITLE OF INVENTION: MOTIES
| FILE REFERENCE: 465201-444
| CURRENT APPLICATION NUMBER: 1999-12-02
| PRIOR APPLICATION NUMBER: 60/113,048
| PRIOR FILING DATE: 1998-12-21
| NUMBER OF SEQ ID NOS: 14
| SEQ ID NOS: 14
| SEQ ID NO 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.5%; Score 33; DB 4; Length 484; 62.5%; Pred. No. 97;
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US-08=821-119-19
i Sequence 19, Application US/08821119
patent No. 5821104
i GENERAL INFORMATION:
APPLICANT: Holm, Kaj Andre
APPLICANT: Ramussen, Grethe
APPLICANT: Halkier, Torben
i APPLICANT: Lehnbeck, Jan
TITLE OF INVENTION: Tripeptidyl Aminopeptidase
i NUMBER OF SEQUENCES: 23
            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: 0CT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGESTRATION NUMBER: 41,971
FELECOMMUNICATION INFORMATION:
TELEFROME: (301) 309-8504
TELEFROME: (301) 309-8512
INFORMATION FOR SEQ ID NO: 182:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 182: US-09-536-784-182
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT; ORGANISM: Streptococcus pneumoniae US-09-468-656A-6
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Best Local Similarity 62.5
Matches 5; Conservative
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184 IVPHGDHY 191
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US-08-961-083-56
                                                                                           US-09-536-784-66
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Sequence 66, Application US/08961083
Sequence 66, Application US/08961083
Sequence 66, Application US/08961083
Sequence 66, Application
APPLICANT: Choi et. al.
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Huan Genome Sciences, Inc.
STREET: 9410 Key West Avenue
STREET: 9410 Key West Avenue
STREET: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 63.5%; Score 33; DB 3; Length 763; Best Local Similarity 62.5%; Pred, No. 1.6e+02; Matches 5; Conservative 1; Mismatches 2; Indels
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1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                                                Score 33; DB
Pred. No. 1.26
0; Mismatches
       4107.400-US
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 410°
TELECOMUNICATION INPORATION:
TELEBRAX: 212-867-0123
TELEFAX: 212-876-9655
TELEFAX: 212-876-9655
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 600 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 763 amino acids amino acids
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                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal IS-08-821-118-2
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Gaps

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3 VVPXGXHY 10

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US-09-536-784-66

1 Sequence 66, Application US/09536784

1 Sequence 66, Application US/09536784

1 Patent No. 657302

2 GENERATION: Streptococcus pneumoniae Antigens and Vaccines TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452

CORRESSES: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STREET: 9410 Key West Avenue

CITY: Rockville

STREET: 9410 Key West Avenue

CITY: Rockville

STREET: 9410 Key West Avenue

COMPUTER: NEADALE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: READALE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: PREADALE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: PREADER: SOSTEN MEDOS VETSION 6.2

SOFTWARE: ASOTEN MEDOS VETSION 6.2

SOFTWARE: 30-0ct.1997

CLASSIFICATION NUMBER: 08/961,083

PRIOR APPLICATION NUMBER: 08/961,083

FILING DATE: OCT-30-1997

TELECOMUNICATION INFORMATION:

MEDIESTRATION NUMBER: 41,971

TELECOMUNICATION INFORMATION:

TELECOMUNICATION INFO
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APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: Streptococcus pneumoniae Antigens and Vaccines
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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COMPUTER RADABLE FORM:
MEDIUM TYRE: Diskette, 3.50 inch, 1.4Mb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein SEQ ID NO: 66: US-09-536-784-66
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Patent No. 6159469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 763 amino acids
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Best Local Similarity 62.5%;
Matches 5; Conservative
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184 IVPHGDHY 191
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COMPUTER: HP Vectra 448/33

COMPUTER: HP Vectra 448/33

COMPUTER: MADOS VARIENCE CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR AND
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STRANDEDNESS: single

TOPOLOGY: linear

HOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 56:

US-09-536-784-56

Query Matches

S; Conservative

T; Mismatches

Qy

S; Pred. No. 1.78+02;

Matches

S; Conservative

Up

S; NPKGXHY 10

S; Mismatches

S; Indels

O; Gaps

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Search completed: June 3, 2004, 12:03:09

JOB time: 12.8 secs
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Sequence
Sequence
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Sequence
Sequence
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13. (2012 6/ptodata/1/pubpaa/USO7_BUB_PEP:*

14. (2012 6/ptodata/1/pubpaa/USO6_BUB_PEP:*

15. (2012 6/ptodata/1/pubpaa/USO6_BUB_PEP:*

15. (2012 6/ptodata/1/pubpaa/USO7_NEW_PUB_PEP:*

15. (2012 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

15. (2012 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

15. (2012 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16. (2012 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

17. (2012 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18. (2012 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

19. (2012 6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

enCore version 5.1.6
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US-09-909-164-34

US-09-909-164-39

US-09-909-164-39

US-09-909-164-17

US-09-909-164-15

US-09-909-164-15

US-09-909-164-15

US-09-909-164-25

US-09-909-164-25

US-09-909-164-42

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                                                                                                                                                                                                                                                                                                                                                                             1155919 segs, 281338677 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                  - protein search, using sw model
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Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Applic
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ALIGNMENTS

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RESULT. 164-30
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Length 11;

DB 12;

94.2%; Score 49;

Query Match

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NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
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NAME/KEY: MISC_FEATURE
LOCATION: (8). (9)
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LOCATION: (11)...(1
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US-09-909-164-39
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                                                     SEQ ID NO 38
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                                                                                                                                                                                                            Sequence 34, Application US/09909164

Sequence 34, Application US/09909164

Sequence 34, Application US/09909164

Sequence 34, Application US/09909164

Sequence 34, Application No. USZ020068702A1

APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Willby, Marguerita
APPLICANT: Lim-Willby, Marguerita
APPLICANT: Brunck, Terence K

TITLE OF INVEXTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT FILING DATE: 2003-03-25

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1
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APPLICANT: Corvas International, Inc.
APPLICANT: Lim-wilby, Marguerita
APPLICANT: Lim-wilby, Marguerita
APPLICANT: Levy, Oddle B
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE REPERBNCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRICE APPLICATION TWEER: 60/220,101
PRICE APPLICATION TWEER: 60/220,101
Best Local Similarity 90.9%; Pred. No. 0.0038; Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps
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LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MISC FEATURE
LOCATION: (9). (9)
OTHER INFORMATION: D-amino acid
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OTHER INFORMATION: ACETYLATION
PEATURE:
NAME/KEY: MOD_RES
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OTHER INFORMATION: AMIDATION
FEATURE:
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US-09-909-164-38
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LENGTH: 11
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Sequence 39, Application US/09909164
Publication No. US2020068702A1
Publication No. US2020068702A1
APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
ITILE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS (CURRENT PILLOR DATE: 2003-03-25
PRIOR REPLICATION NUMBER: 60/220,101
PRIOR PILLING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTHARE: Patentin version 3.1
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                                                         OTHER INFORMATION: 11-mer synthesized according to example 1
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94.2%; Score 49; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0038;
Matches 10; Conservative 0; Mismatches 1; Indels
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OTHER INFORMATION: norvaline-(CO)
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                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MISC FEATURE
LOCATION: (8). 7(8)
OTHER INFORMATION: D-amino acid
                                                                                                                NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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OTHER INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
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OTHER INFORMATION: AMIDATION
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LOCATION: (11). (11)
OTHER INFORMATION: AMIDATION
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APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Lovy, Odile E
APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT PILING DATE: 2003-03-25
PRIOR PLILNG DATE: 2003-03-25
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTION VERSION 3.1
SEQ ID NO 15
LENGTH: 11
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ORCANISM: artificial sequence
PERTURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
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FERTURE:
FORTURE:
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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    CURRENT APPLICATION NUMBER: US/09/909,164
                          CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
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NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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NAME/KEY: MISC_FEATURE

LOCATION: (8)...(8)

OTHER INFORMATION: D-amino acid
US-09-909-164-11
                                                                                          NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
ERNOTH: 11
                                                                                                                                                                                      TYPE: PRT ORGANISM: artificial sequence
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NAME/KRY: MOD_RES
NACATION: (11).
OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/0990164
Publication No. US20020068702A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEFATITIS C
FILE REFERENCE: IN101192-US
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2003-03-25
PRIOR PILIAGE OF THE SECOND-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VERSION 3.1
LENGTH: 11
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APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
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                                                                    Score 49; DB 12; Length 11;
Pred. No. 0.0038;
0; Mismatches 1; Indels
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LOCATION: (1)...(1)
COTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline (CO)
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Publication No. US20020068702A1
GENERAL INFORMATION:
; OTHER INFORMATION: D-amino acids JS-09-909-164-39
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OTHER INFORMATION: D-amino acid
FEATURE:
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90.9%;
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                                                                    Query Match 94.2%;
Best Local Similarity 90.9%;
Matches 10; Conservative
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OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.9
Matches 10; Conservative
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US-09-909-164-25;
Squarce 25 Application US/09909164;
Publication No. US20020068702A1;
Publication No. US20020068702A1;
Publication No. US20020068702A1;
Publication No. US20020068702A1;
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
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ORGANISM: artificial sequence
PERTURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
PEATURE:
                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: 11-mer synthesized according to example 1 FRATURE:
NAME/KRS: MOD RES
LOCATION: (1)...(1)
FEATURE:
FEATURE:
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Pred. No. 0.006
0; Mismatches
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
SOFTWARE: Patentin version 3.1
SEQ ID NO 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
FRATURE:
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CHER INFORMATION: D-amino acid

US-09-909-164-21
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FRATURE:
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ORGANISM: artificial sequence
PEATURE:
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.9
Matches 10, Conservative
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US-09-909-164-16

Sequence 16, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION: No. US20020068702A1

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Brunck, Terence K

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: IN0192-US

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT PILING DATE: 2003-03-25

PRIOR FILING DATE: 2003-07-21

NUMBER OF SEQ ID NOS: 62

SEQ ID NO 16

LENGTH: 11

LENGTH: 11
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Sublication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Torence X
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
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                                                                                                92.3%; Score 48; DB 12; Length 11; 90.9%; Pred. No. 0.006; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MISC_FEATURE
LOCATION: (6)._(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
         i OTHER INFORMATION: norvaline-(CO)
US-09-909-164-15
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; OTHER INFORMATION: D-amino acid
US-09-909-164-16
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LOCATION: (1) ...(1)
OTHER INFORMATION: ACETYLATION
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LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
FEATURE:
                                                                                                   Query Match 92.3
Best Local Similarity 90.5
Matches 10; Conservative
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Best Local Similarity
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Matches
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-wilby, Marguerita

APPLICANT: Lim-wilby, Marguerita

APPLICANT: Lim-wilby, Marguerita

APPLICANT: Levy, Odile E

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT FILING DATE: 2000-07-21

PRIOR FILING DATE: 2000-07-21

PRIOR FILING DATE: 2000-07-21

SOFTWARE: Patentin version 3.1

SEQ ID NO 28

LENGTH: 11

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APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Hunck, Terence K
TILLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILLE REPERENCE: IN0192-US
CURRENT APPLICATION WUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 44
LENGTH: 11
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ORGANISM: artificial sequence
PERATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
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NAME/KEY: MOD RES
COCHION: (11)...(11)
COCHIEN: INFORMATION: AMIDATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (8)...(9)
OTHER INFORMATION: D-amino acids
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Publication No. US20020068702A1
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NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: artificial sequence
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CTHER INFORMATION: Met(0)
US-09-909-164-44
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LOCATION: (1)..(1)
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Sequence 42, Application US/09909164
Publication No. US20020068702A1
GENERAL INPORMATION:
APPLICANT: Lim-wilby, Marguerita
APPLICANT: Lim-wilby, Marguerita
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APPLICANT: Lim-wilby, Marguerita
APPLICANT: Lim-wilby, Marguerita
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OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
                                                                                                                                                                                                                                                                                                                Length 11;
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                                                                                                                                                                                                                                                                                                           Score 48; DB 12;
Pred, No. 0.006;
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                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
         OTHER INFORMATION: norvaline-(CO) FEATURE:
                                                                                            NAME/KEY: MISC_FEATURE
LOCATION: (8)...(8)
OTHER INFORMATION: D-amino acid
JS-09-909-164-25
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.9
Matches 10, Conservative
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APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
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APPLICANT: Lim-Wilby, Marguerita
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APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICANTON NUMBER: 60/220,101
PRIOR PELING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: 11-mer synthesized according to example 1
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Job time: 33.7333 secs
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LOCATION: (6)...(6)
CTHER INFORMATION: norvaline-(CO)
US-09-909-164-31
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OTHER INFORMATION: ACETYLATION
FEATURE:
   Publication No. US20020068702A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: artificial sequence
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Best Local Similarity 81.8%;
Matches 9; Conservative
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OTHER INFORMATION: AMIDATION
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US-09-164-29
Sequence 29 Application US/09909164
Sequence 29 Application US/09909164
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Levy, Odile E
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OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                Score 40, DB 12, Length 11;
Pred. No. 0.24;
0, Mismatches 2; Indels
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Pred. No. 0.24
0; Mismatches
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US-09-909-164-31
; Sequence 31, Application US/09909164
                                                                                                                                                                                            NAWE/KEY: MISC_FEATURE
1.CCATION: (6)..(6)
1.CTHEN INFORMATION: norvaline-(CO)
US-09-909-164-28
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LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
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; OTHER INFORMATION: D-amino acid
US-09-909-164-29
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LOCATION: (1) ...(1)
OTHER INFORMATION: ACETYLATION
OTHER INFORMATION: ACETYLATION
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81.8%;
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Best Local Similarity 81.8%;
Matches 9; Conservative
                                                     NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
FEATURE:
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NAME/KEY: MOD RES
LOCATION: (11)...(11)
CTHER INFORMATION: AMIDATION
FEATURE:
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Best Local Similarity 81.6
Matches 9; Conservative
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NAME/KEY: MISC_FEATURE
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Score 40; DB 12; Length 11; Pred. No. 0.24; 0; Mismatches 2; Indels

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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M protein - protein search, using sw model

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June 3, 2004, 11:35:47 ; Search time 9 Seconds (without alignments) 117.567 Million cell updates/sec

US-09-909-164-44 52 1 EEVVPXGXHYS 11 itle: erfect score:

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283366 segs, 96191526 residues earched: otal number of hits satisfying chosen parameters:

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ost-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	T02590	A72207	E69086	AF3286	536851	A42452	A25905	C75538.	T28717	A69284	T46758	F89892	五97985	VKLJSI	D82618	AE2001	A48702	S69046	G86430	S38143	C95136	B95136	E98004	G95115	C97985	D98004	H95115	D97985	A70939
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225	286	311	322	364	369	374	425	454	519	536	627	969	701	716	738	
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30	31	32	33	34	35	36	37	38	6	40	41	42	43	44	45	

ALIGNMENTS

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ö Gaps ô Query Match
67.3%; Score 35; DB 2; Length 233;
Best Local Similarity 60.0%; Pred. No. 9.8;
Matches 6; Conservative 1; Mismatches 3; Indels

1 EEVVPXGXHY 10 : || | || 99 90 QAVVPKGRHY 99 d ઠે

ft.SH proteinase activity modulator HflK - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Dates: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Dates: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: A72207
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.N.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.,

Nature 399, 323-329, 1999
A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A,Reference number: A72200; MUID:99287316; PMID:10360571
A,Reference number: A72200; MUID:99287316; PMID:10360571
A,Rolecule type: DNA
A,Molecule type: DNA
A,Rossiques: 1-308 cARN>
A,Rossiques: 1-308 cARN>
A,Experimental Source: Strain MSB8
A,Experimental source: strain MSB8
C,Genetics: A,Gene: TM1822
C,Superfamily: erythrocyte band 7 integral membrane protein

Gaps ; 0 Query Match 67.3%; Score 35; DB 2; Length 308; Best Local Similarity 75.0%; Pred. No. 13; Matches 6; Conservative 0; Mismatches 2; Indels

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3 VVPXGXHY 10 VVPSGIHY 48

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A Molecule type: DNA

A Residues: 1-1396 cxLL>

A; Cross-references: EMBL:X69460; NID:g15415; PIDN:CAA49220.1; PID:g15416

A; Cross-references: EMBL:X69460; N. Bayev, A.A.

R; Kaliman, A.V.; Kryukov, V.M.; Bayev, A.A.

Nucleic Acids Res. 16, 6230, 1988

Nucleic Acids Res. 16, 6230, 1988

A; Title: The nucleotide sequence of bacteriophage T5 DNA at the region between early and A; Reference number: S01982; MUID:88289370; PMID:3267228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: tobacco yellow dwarf virus
C;Species: tobacco yellow dwarf virus
C;Date: 15-Jan.1993 #sequence_revision 15-Jan.1993 #text_change 08-Oct-1999
C;Date: 15-Jan.1993
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
Virology 187, 633-642, 1992
A;Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yell
A;Reference number: A42452; MUID:92188538; PMID:1546458
R;Kaliman, A.V.; Kulshin, V.E.; Shlyapnikov, M.G.; Ksenzenko, V.N.; Kryukov, V.M. FEBS Lett. 366, 46-48, 1995
A;Title: The nucleotide sequence of the bacteriophage T5 ltf gene.
A;Reference number: 865934; MUID:95309401; PMID:7788514
A;Accession: 865934
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C;Species: Bos primiganius taurus (cattle)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
C;Accession: A25905
F;Kotani, H.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 83, 7074-7078, 1986
A;Title: Structure and gene organization of bovine neuromedin K precursor.
A;Reference number: A25905, MUID:86313713; PMID:3462746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB: M81103; NID: 9335283; PIDN: AAA47947.1; PID: 9335284
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Pred. No. 6.5;
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(7)
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Pred. No. 68;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: translation not shown
A;Molecule type: DNA
Mesidules: 934-985, A;Residules: 934-986 <KA2>
A;Cross_references: EMBL:X07559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: ltf
C;Keywords: late protein; tail fiber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
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Best Local Similarity 50.0
Page 5; Conservative
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A, Residues: 1-126 < KOT>
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A; Residues: 1-102 < MOR>
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A;Title: The agenome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                         C. Accession: E69086
R. Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Quit, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. ki, S.; Gurch, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A. Pacteriol. Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A. Paccession: E69086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A)Status: preliminary, nucleic acid sequence not shown, translation not shown
A;Molecule type: DNA
A;Residues: 1-560 cMTH
A;Cross-references: GB:AE000923; GB:AE000666; NID:g2622766; PIDN:AAB86115.1; PID:g262277
A;Experimental source: strain Delta H
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1028 4KUR>
A;Coss-references: GB:AE008917; PIDN:AAL51457.1; PID:g17982167; GSPDB:GN00190
A;Experimental source: strain 16M
                                                                                                                                                                                                                                                    cell division protein - Methanobacterium thermoautotrophicum (strain Delta H) C,Species: Methanobacterium thermoautotrophicum C,Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L-shaped tail fiber protein - phage T5
N;Alternate names: ltf protein
N;Alternate names: ltf protein
C;Species: phage T5
C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 17-Nov-2000
C;Accession: S65934; S01984; $36851
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45.5%; Pred. No. 16;
ive 4; Mismatches 2; Indels
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A;Gene: MTH1642 C;Superfamily: cell division protein MJ0174

5; Conservative

Query Match Best Local Similarity Matches 5; Conserv

|::|| | |:: EDLVPMGSHHT 108 1 EEVVPXGXHYS 11

ò g DB 2; 49;

2; Mismatches Score 35; Pred. No.

6, Conservative

Query Match Best Local Similarity Matches 6; Conserv

C;Genetics: A;Gene: BMEI0275 A;Map position: I

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67.38;

Score 34; DB 2; Length 126; Pred. No. 8.2; 1; Mismatches 2; Indels

65.4%;

6; Conservative

Query Match Best Local Similarity Matches 6; Conserv

28 EQVVPGGGH 36

1 EEVVPXGXH 9

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coenzyme F420-quinome oxidoreductase (EC 1.6.5.+) 56K chain - Archaeoglobus fulgidus
NyAlternate names: sarcosine oxidase alpha chain soxA homolog
C;Species: Archaeoglobus fulgidus
C;Daccession: A62284; S45665;
C;Accession: A62284; S45665;
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
S;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: A69284
A;Status: nucleic acid sequence not shown; translation not shown
A;Accession: A69284
A;Kusow, J.; Linder, D.; Stetter, K.O.; Thauer, R.K.
Bir. J. Biochem: 223, 503-511, 1994
A;Title: F(420)H(2): quinone oxidoreductase from Archaeoglobus fulgidus. Characterizatio
A;Reference number: 845665; MUID:94333340; PMID:8055920
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Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000
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C)ates: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: F8982
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.;
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Pred. No. 62;
0; Mismatches 2; Indels
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Best Local Similarity 45.5%; Pred. No. 39;
Matches 5; Conservative 3; Mismatches
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nes 6; Conservative
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Matches
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                                                                                                                                                                                                                                                                                                                                                                           ypothetical protein - Deinococcus radiodurans (strain R1)
(Species: Deinococcus radiodurans
(Species: Deinococcus radiodurans
(Species: O3-bec-1999 #sequence_revision 03-bec-1999 #text_change 28-Jul-2000
(Accession: C7558
(Multe, O.) Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; White, O.) Eisen, J.A.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma (Smith, H.O.; Venter, J.C.; Fraser, C.M.
(Smith, H.O.; Venter, J.C.; Fraser, C.M.
(File Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.) Accession: C75538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .Molecule type: DNA.
.;Residues: 1-279 «WHI.»
.;Cross-references: GB:AE01889; GB:AE000513; NID:g6457944; PIDN:AAF09867.1; PID:g645795
.;Experimental source: strain R1
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Space: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
Accession: T28717
                                                                                                Gaps
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65.4%; Score 34; DB 2; Length 279; 75.0%; Pred. No. 19; 2; Indels tive 0; Mismatches 2; Indels

Query Match Best Local Similarity 75.0 Matches 6; Conservative

100 VPLGRHYS 107

4 VPXGXHYS 11

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Superfamily: Deinococcus radiodurans hypothetical protein DR0271

", Map position: 1

;Status: preliminary

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Query Match 65.4%; Score 34; DB 2; Length 495; Best Local Similarity 50.0%; Pred. No. 36; Matches 5; Conservative 2; Mismatches 3; Indels

1 : | | | | | 1 218 ENIVPTGKHH 227 1 EEVVPXGXHY 10

≿

XESULT 10 169284

imap position: 5 Ajintrons: 37/2; 90/1; 113/1; 183/3; 356/3; 380/3; 428/2

Gene: CESP:F10D2.3

Graves, T.; Wohldmann, P.; Gillam, B.
ubmitted to the EMBL Data Library, September 1997
Uppescription: The sequence of C. elegans cosmid F10D2.
Uppercession: 228717

\times translated from GB/EMBL/DDBJ
\times molecule type: DNA
\times idea: 1-495 <GRA>

pothetical protein F10D2.3 - Caenorhabditis elegans

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Cydecession: T46758
R;Spellerberg, B.; Rozdzinski, E.; Martin, S.; Weber-Heynemann, J.; Schnitzler, N.; Luet R;Spellerberg, B.; Rozdzinski, E.; Martin, S.; Weber-Heynemann, J.; Schnitzler, N.; Luet R;Spellerberg, B.; Rozdzinski, E.; Martin, S.; Weber-Heynemann, J.; Schnitzler, N.; Luet A;Title: Lmb, a protein with similarities to the LraI adhesin family, mediates attachmen A;Reference number: 224091; MUID:99115568; PMID:9916102
A;Accession: T46758
A;Accession: T46758
A;Accession: T46758
A;Residues: L-822 <- SPE.
A;Molecule type: DNA
A;Residues: L-822 <- SPE.
A;Accession: Teferences: EMBL:AF062533; NID:94249622; PIDN:AAD13797.1; PID:94249624
A;Experimental source: strain R268
C;Superfamily: Streptococcus agalactiae hypothetical 92.4K protein
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ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; I
A;Molecule type: protein
A;Residues: 2,'X',4,'X',6-7,'X',9-10,'XX',13-14 <XUN>
A;Residues: 2,'X',4,'X',6-7,'X',9-10,'XX',13-14 <XUN>
A;Note: the authors could not distinguish between glutamate and cysteine for residues 5-C;Superfamily: glutamate synthase small chain
C;Keywords: oxidoreductase
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C;Superfamily: AIDS trans-regulatory splicing protein
C;Keywords: AIDS; immunodeficiency; splicing protein; transcription regulation
                                                                                                                                           63.5%;
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55.6%;
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Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                      Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      107 ETVPAGGNYS 116
                                                                                                                                                                                                                                                                                                                  2 EVVPXGXHYS 11
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A,Molecule type: DNA
A,Residues: 1-156 <SIM>
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A;Note: host Pan troglodytes (chimpanzee)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: 809988
R;Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
Nature 345, 356-359, 1990
A;Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A;Reference number: 809983; MUD:90259077; PMID:2188136
A;Accession: 809988
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C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C;Accession: 187985
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C;Accession: 1
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C;Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain; biotin
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A;Molecule type: DNA
A;Residues: 1-1057 «KUR»
A;Cross-references: GB:BA000018; PID:g13701002; PIDN:BAB42298.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-46 <XUR>
A;Cross-references: GB:AE007317; PIDN:AAK99713.1; PID:g15458516; GSPDB:GN00174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein spr0909 [imported] - Streptococcus pneumoniae (strain R6)
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
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A,Molecule type: DNA
A,Residues: 1-124 < HUE>
A,Cross-references: EMBL:X52154; NID:958866; PIDN:CAA36405.1; PID:9763085
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Matches 5; Conserv
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A;Introns: 27/1
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A.Gene: spr0909
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A, Cross-references: GB:AE004014; GB:AE003849; NID:G9107044; FIDN:AAP84752.1; GSPDB:GN00 A, Gross-references: GB:AE004014; GB:AE003849; NID:G9107044; FIDN:AAP84752.1; GSPDB:GN00 A, Gross-references: GB:AE0040, B.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Astingson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Carraro, D.M.; Carrar, Jas-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. asbmitted to GenBank, June 2000

**Abuthors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frobindso, M.A.; Madeira, M.M.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Markins, J.D.; Junqueira, M.M.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Markins, J. R.; Madeira, A.N.; Marino, C.L.; Marques, M.V.; Markins, J. F. G.; Numes, L.R.; Oliveira, A.N.; Acliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.Y.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasai, A, M. Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.D.; A, Acharis, annotation
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                                                          Gaps
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Score 33; DB 1; Length 124;
Pred. No. 13;
1; Mismatches 3; Indel8
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SLS1_YARLI
TOLB HABEN
YL15_VIBPA
DHP1_SCHPO
PDRB_YEAST
A10A_HUYAN
POLG_PERVM
ILLIA_BOVIN
ILLIA_CAPHI
ILLIA_CAPHI
ILLIA_SHEEP
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=RIMD 2210633 / Serotype O3:K6;
MEDLINE=22508454; PubMed=1262039;
MEDLINE=22508454; PubMed=1262039;
MARKING K., Oshima K., Kurckawa K., Yokoyama K., Uda T., Tagomori K.,
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasuunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
Genome sequence of Vibrio parahemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
Lancet 36:743-749(2003).

-I. CATALTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate.
-I. PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
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10-007-2003 (Rel. 42, Last sequence update)
10-007-2003 (Rel. 42, Last ennotation update)
10-007-2003 (Rel. 42, Last annotation update)
3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase)
4ROA OR VB1020.
Vibrio parahaemolyticus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
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InterPro; IRRO01986; ERSP synth.
PEAM; PF00275; ERSP synthase; 1.
PROSITE; PS00104; EPSP SYNTHASE 1; 1.
PROSITE; PS00885; ERSP SYNTHASE 2; 1.
Aromatic amino acid blosynthesis; Transferase; Complete proteome.
SEQUENCE 426 AA; 46094 MW; 373D39CC5BA1P70F CRC64;
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-:- SUBUNIT: Monomer (By similarity).
-:- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-:- SIMILARITY: Belongs to the EPSP synthase family.
-:- SIMILARITY: Belongs to the EPSP synthase family.
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Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
A chang Y.-Q., Miao Y.-G., Rang W.-Y. Chen R.-S., Shen Y., Chen Z.,
Yuan Z.-H., Zhao G.-P., Qu D., Danchin A.-Y., Wen Y.-M.;
Genome-based analysis of virulence genes in a non-biofilm-forming
IT Genome-based appldermidis strain (ATCC 12228).";
Mol. Microbiol. 49:157-1593 (2003).
C.-I. CATALYITC ACTIVITY: 2 APP + L-glutamine + CO(2) + H(2)O = 2 ADP +
phosphate + L-glutamate + carbamoyl phosphate.
C.-I. CATALYITC ACTIVITY: 2 APP + L-glutamine (By similarity).
C.-I. COFACTOR: Binde 3 manganese inns per subunit (By similarity).
C.-I. PATHWAY: Arginia biosynthesis.
C.-I. PATHWAY: Arginial biosynthesis.
C.-I. PATHWAY: Composed of two chains; the small (or glutamine) chain
promotes the hydrolysis of glutamine to ammonia, which is used by
the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBD outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pfam; Proz142; MGS; 1.
PRINTS: PRO0098; CPSASE.
TIGRPAMS: TIGR01369; CPSASE.
TIGRPAMS: TIGR01369; CPSASE.
PROSITE; PS00866; CPSASE.1; 2.
PROSITE; PS00866; CPSASE.2; 2.
Arginine biosynthesis; Prinidine biosynthesis; Ligase; Repeat; Arginine biosynthesis; Complete proteome.
ATP-binding; Manganese; Complete proteome.
ATP-binding; Manganese; Complete proteome.
A101 CARROXFHOSPHATE SYNTHETIC DOMAIN.
A102 546 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                               15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP (POTENTIAL).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Firmicutes, Bacillales, Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the carB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AE016746; AA004476.1; -.
HANAP, MF 0210; -; 1.
INCEPPO; IPR006575; CRAL L glu.
INCEPPO; IPR006493; CPASE L.
INCEPPO; IPR006493; CPASE L.
INCEPPO; IPR006491; CPASE L.
INCEPPO; IPR006491; CPASE L.
INCEPPO; IPR006491; CPASE L.
INCEPPO; IPR006591; CPASE L.
INCEPPO; IPR00169; SHPFOC ASILE.
PÉRM; PP00289; CPSSSS L.
PÉRM; PP00289; CPSSSS L.
PÉRM; PP02787; CPSSSS L.
                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis.
                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=ATCC 12228;
Pubmed=12950922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
                                                                                                                                                                                                                                                                                                                    OR SE0879.
                                                            CARB STAEP
Q8CPJ4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NP_BIND
NP_BIND
METAL
METAL
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DOMAIN
DOMAIN
REPEAT
RESULT 2
CARB STAEP
                                                                       HE TO THE STANDARD BEAR AND DESCRIPTION OF STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STANDARD BEAR AND STAND
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RA Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
Rapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
Battecharyya A., Bartman A., Garchier W., Grechkin G., Zhu L.,
A Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
A Larsen N. D'Souza M., Walunas T., Pusch G., Haselkorn R.,
Ronstein M., Kyrpides N., Overbeek R.;
Ronnene sequence and analysis of the oral bacterium Fusobacterium
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT "Genome sequence and analysis of the oral bacteriol. 184:2005-2018[002].
J. Bacteriol. 184:2005-2018[002].
J. CATALYITC ACTIVITY: 2 AFF H.-Glutamine + CO(2) + H(2)O = 2 ADP +
D'ORDATYA: Arginine biosynthesis.
J. CORACTOR: Binds 3 manganese ions per subunit (By similarity).
J. PATHMAY: Arginine biosynthesis.
J. PATHMAY: Arginine biosynthesis.
J. STHIMATIY: Belongs to the carB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNBL outstation the Buropean Bioinformatics plaintenation. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (RC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB OR FN0422.
                                                                                                                                                                                                                                                     ö
                                                                                                                                                                Score 36; DB 1; Length 1057; Pred. No. 14; Mismatches 3; Indels
300 300 MANGANESE 2 (BY SIMILARITY).
820 820 MANGANESE 3 (BY SIMILARITY).
832 832 MANGANESE 3 (BY SIMILARITY).
1057 AA; 117391 MW; 89447708DBICAES9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusobacterium nucleatum (subsp. nucleatum).
Bacteria, Fusobacteria, Fusobacterales, Fusobacteriaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AE010554; AAL94625.1; ALT_INIT.
HAWAP; MF 01210; -; 1.
Interpro; IPR006275; CarA L glu.
Interpro; IPR005493; CPase L.
Interpro; IPR005493; CPase L. D3.
Interpro; IPR005491; CPase L. D3.
Interpro; IPR005491; CPase L. D3.
Interpro; IPR005491; CPase L. N.
Interpro; IPR005491; CPase L. D3.
Interpro; IPR004362; MGS like.
Pfam; PF00289; CPGase L. Chain; 2.
Pfam; PF02787; CPGase L. D3; 2.
Pfam; PF02787; CPGase L. D3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00098; CPSASE.
TIGRFAMS; TIGR01369; CPSaseII_lrg; 1.
                                                                                                                                                                            69.2%;
                                                                                                                                                                                                              63.68;
                                                                                                                                                                    Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                189 KEVVSNGLHYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                      1 EEVVPXGXHYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARB FUSIN
                                                                 METAL
SEQUENCE
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CARE_FUSNN
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                                                                                                                                                                                                                                                                      0; Gaps
PROSITE; PS00866; CPSASE 1; 2.
PROSITE; PS00867; CPSASE 2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
ATP-binding; Manganese; Complete proteomer
DOMAIN 402 546 OLIGOMERIZATION DOMAIN.
DOMAIN 547 929 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                              ATP (POTENTIAL).
ATP (POTENTIAL).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriophage T5.
Viruses; deDNW viruses, no RNA stage; Caudovirales; Siphoviridae;
T5-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaliman A.V., Kryukov V.M., Bayev A.A.;
"The nucleotide sequence of bacteriophage T5 DNA at the region between early and late genes.";
Nucleic Acids Res. 16:6230-6230(1988).
-!- FUNCTION: Nonessential protein that mediates binding to the polymannose O antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleotide sequence of the bacteriophage T5 ltf gene."; Lett. 366:46-48(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDILINE=55309401; PubMed=7789514;
MEDILINE=53309401; PubMed=7789514;
MEDILINE=5309401; Kulshin V.E., Shlyapnikov M.G., Ksenzenko V.N.
Kryukov V.M.;
                                                                                                                                                                                                                                           Score 35; DB 1; Length 1058;
Pred. No. 23;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                            ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                         01-07N-1990 (Rel. 13, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
L-shaped tail fiber protein (LTF protein).
                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1396 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=88289370; PubMed=3267228;
                                                                                                                                                                                                                                             67.3%;
                                                                                                                                                                                                                                                        Local Similarity 60.0
                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                      190 EIVPNGLNYS 199
                                                                                                                                                                                                                                                                                               2 EVVPXGXHYS 11
                                                                                                                                                                                                           832
                                                                                                                              153
302
302
284
298
300
300
820
832
832
1058 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              P13390; 048502;
                                                                                                                                                                                         METAL
METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                    VLTF BPTS
                                                                                                                    REPEAT
NP_BIND
NP_BIND
METAL
                                                                                                                                                                                                                                           Query Match
                                                                                          DOMAIN
REPEAT
                                                                                                                                                                                 METAL
                                                                                                                                                                                                                                                                                                                                                           ESULT 4
                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92188538; PubMed=1546458;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
The nucleotide sequence of the infectious cloned DNA component of
tobacco yellow dwarf virus reveals features of geminiviruses
infecting monocotyledonus plants.";
Virology 187:633-642(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
ammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoídea,
Bovidae, Bovinae, Bos.

NCBI_TaxID=9913,
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                                                                                                                 67.3%; Score 35; DB 1; Length 1396; 50.0%; Pred. No. 31; tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 1; Length 102;
Pred. No. 3.4;
2; Mismatches 2; Indels
                                              986 986 V -> A (IN REF. 2).
1396 AA; 147989 MW; 18CD2192F65FFFC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A42452; A42452.
InterPro; IPR002621; Gemini mov.
Pfam; PF01708; Gemini mov; I.
Mypotherical protein.
SEQUENCE 102 AA; 11178 MW; A40ECFIEOAF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-CTT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurokinin B precursor (NKB) (Neuromedin K).
                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.4%;
                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                               1360 KTIPAGDHYS 1369
                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                     2 EVVPXGXHYS 11
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Late protein.
CONFLICT 986 98
SEQUENCE 1396 AA;
                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=31599;
                                                                                                                                                                                                                                                                                                                                                                             Y11K TYDVA
P31619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TKNK BOVIN
ID TKNK BOVIN
AC P08858;
                                                                                                                      Query Match
                                                                                                                                                                       Matches
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EMBL; X69460; CAA49220.1; -. EMBL; AJ001191; CAA04591.1; -. PIR; S01982; S01982.

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RESULT 8
CARB STAAW
ID CARB STAAW
AC P58940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
DOMAIN
REPEAT
REPEAT
NP BIND
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
SECURICE FROM N.A.
SECURICE FROM N.A.
MEDLINE-86313713; PubMed=3462746;
Kotani H., Hoshimaru M., Nawa H., Nakanishi S.;
Kotani H., Hoshimaru M., Nawa H., Nakanishi S.;
"SETUCTURE and gene organization of bovine neuromedin K precursor.";
"SETUCTURE and gene organization of bovine neuromedin K precursor.";
"SETUCTION: Tachykinins are active peptides which excite neurons,
evoke behavioral responses, are potent vasodilators and
secretagogues, and contract (directly or indirectly) many smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=MuSO / ATCC 700699, and N315;
STRAIN=MuSO / ATCC 700699, and N315;
STRAIN=MuSO / ATCC 700699, and N315;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui I., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M14351; AAA30723.1; -.
EMBL; M14348; AAA30723.1; JOINED.
EMBL; M14348; AAA30723.1; JOINED.
EMBL; M14349; AAA30723.1; JOINED.
EMBL; M14350; AAA30723.1; JOINED.
EMBL; M14369; AAA30723.1; JOINED.
EMBL; M14369; AAA30723.1; JOINED.
EMBL; M14369; AAA30723.1; JOINED.
EMBL; M14369; Neurokinin; J.
EMBL; M14348; AAA30723.1; JOINED.
EMBL; M14349; AAA307257.1; JOINED.
EMBL; M14349; AAA307723.1; JOINED.
EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMIDATION (G-96 PROVIDE AMIDE GROUP) 446EF433498EC059 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
phosphate syntherase ammonia chain)
CARB OR PYRAB OR SAV1203 OR SA1046,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain N315).
Bacteria, Firmicutes; Bacillales; Staphylococcus.
[1]
                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the tachykinin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 AA; 13871 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amidation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STAAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC DOT DOT DOT SERVING OS SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SER
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                                                                                                                                   Lancet 357:1225-1240(2001).

-!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + Dosphate + L-glutamate + carbamoyl phosphate.

-!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + Dosphate + L-glutamate + carbamoyl phosphate.

-!- PATHWAY: Arginine biosynthesis.
-!- PATHWAY: Pyrimidine biosynthesis, first step.
-!- PATHWAY: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; "Whole genome sequencing of meticillin-resistant Staphylococcus aurens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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ATP (POTENTIAL).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00098; CPSASE.
TIGRFAMs; TIGR01369; CPSASE.1.
PROSITE; PS00866; CPSASE 1; 2.
PROSITE; PS00867; CPSASE 1; 2.
PROSITIC; PS00867; CPSASE 2; 2.
ARGININE blosynthesis; Pyrimidine biosynthesis; Ligase; Repeat; ATP-binding; Manganese; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 1; Length 1057;
Pred. No. 38;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1057 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
-!- SIMILARITY: Belongs to the carB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP003361; BAB57365.1; -...
EMBL; AP003361; BAB42298.1; -...
FISP; P00968; 1050.
HAMAP; MF 01210; -; 1...
InterPro; IPR006575; CarA L glu.
InterPro; IPR006548; CPase L D2.
InterPro; IPR005499; CPase L D3.
InterPro; IPR005481; CPase L D3.
Pfam; PP02788; CPSase L D2; 2.
Pfam; PP02788; CPSase L D2; 2.
Pfam; PP02789; CPSase L D3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.4%;
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Les 6, Conservative
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                                                                                                                                                                                                                                                     MEDLINE-22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Manganese; Complete proteome.

1 401 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.

102 546 OLIGOMERIZATION DOMAIN.

47 929 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

10 1057 ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (POTENTIAL).

ATP (POTENTIAL).

ANGANESE 1 (BY SIMILARITY).

MANGANESE 1 AND 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamcyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamcyl-phosphate synthetase ammonia chain).
CARB OR PYRAB OR WW1086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0098; CPSASE.
TIGREAMS; TIGR01369; CPSASE.
FROSTIE; PS00865; CPSASE.1; 2.
PROSTIE; PS00867; CPSASE.2; 2.
Arginine blosynthesis; Pyrimidine blosynthesis; Ligase; Repeat; ATP-binding; Manganese; Complete proteome.
                                                                                                                                                                                                         Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 1; Length 1057;
Pred. No. 38;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW; DBE3B09F9BC6F152 CRC64;
                                                                                      Staphylococcus aureus (strain MM2).
Bacteria, Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF 01210; -; 1.
InterPro; 1PR006275; CarA L glu.
InterPro; 1PR006479; CPase L D2.
InterPro; 1PR005480; CPase L D2.
InterPro; 1PR005480; CPase L D3.
InterPro; 1PR005481; CPase L D3.
InterPro; 1PR005481; CPase L D3.
InterPro; 1PR005481; CPase L D3.
InterPro; 1PR00482; MGS 11%e.
Pfam; PP02784; CPSase L Chain; 2.
Pfam; PP02784; CPSase L D3; 1.
Pfam; PP02784; CPSase L D3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AP004825; BAB94951.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117185
                                                                                                                                                                                                                                                    359:1819-1827 (2002)
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546
1057
210
352
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300 30
820 82
832 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                      NCBI_TaxID=196620;
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NP_BIND
NP_BIND
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Nature 345:356-356.1950).

Nature 345:356-356.1950).

Nature 345:356-356.1950).

NAGATIVE REPRESSION OF GAG AND ENV PRODUCTION.

SUBCELLULAR LOCATION: Nuclear; accumulates in the nucleoli.

PTM: Phosphoproteein whose state of phosphorylation is mediated by a specific serine kinase activity present in the nucleus.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90259077; PubMed=2188136;
Huet T., Cheynier R., Meyerhans A., Roelants G., Wain-Hobson S.;
"Genetic organization of a chimpanzee lentivirus related to HIV-1.";
Nature 345:356-359(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Transcription regulation; AIDS; Phosphorylation; Nuclear protein.
SEQUENCE 124 AA; 13701 MW; F5877D1BDF65A7B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                     01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-BEB-2003 (Rel. 41, Last annotation update)
REV protein (Anti-repression transactivator protein) (ART/TRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Pred. No. 6.8;
1; Mismatches 3; Indels
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Mallory M.J., Strich R.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
Viruses, Retroid viruses, Retroviridae, Lentivirus.
VCBI_TaxID=11723,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UMBI_YEAST STANDARD; PRT; 460 AA. Q03010; PST30; OU-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 110-0CT-2003 (Rel. 42, Last annotation update) NMBI OR WIM3 OR YPI139C OR LPI7C.
                                                                                                                                                                                                                            124 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X52154; CAA36405.1; -.
PIR; S09988; VKLJSI.
HIV; X52154; REV$CPZ.
InterPro; IPR00625; REV_protein.
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Best Local Similarity 60.0.
Local 6, Conservative
                                                                                                                                                                                                                            STANDARD;
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                                             190 EIVSNGLHYS 199
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2 EVVPXGXHYS 11
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SEQUENCE FROM N.A.
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                                                                                                                                                                                         REV_SIVCZ
ID REV_SIVCZ
AC P17280;
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UME1 YEAST
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Multidrug resistance-like ATP-binding protein mdlB
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InterPro; IPR001140; ABC TM_transpt.
InterPro; IPR003439; ABC_transporter.
Pfan; PR00664; ABC_membrane; 1.
Pfan; PF00005; ABC_tran; 1.
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P36148;
01-JUN-1994 (Rel. 29, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66827 MW;
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Best Local Similarity 50...
5; Conservative
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                          MDLB OR BBP42
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SEQUENCE
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YK47 YEAST
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RA MUDINE=9731321; PubMed=9169875;

RA Bussey H., Stoorms R.K., Ahmed A., Albermann K., Allen E., Ansorge W., RA Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V., R., Brietein D., Bowmann S., Bruckner M., Carpenter J., Cherry J.M., RA Chung E., Churcher C.M., Coster F., Davis K., Davis R.W., Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A., RA Duncan M., Floeth M., Fortin N., Frises H.J. D., Fritz C., Goffeau A., RA Hall J., Hebling U., Heamann K., Hilbert H., Hiller L.W., RA Hall J., Hebling U., Lashkari D., Lew H., Lin A., Lin D., Louis E.J., RAM OC., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J., RAM Mueller Auer S., Namath A., Nentwich U., Oefner P., Pearson D., RA Mueller Auer S., Namath A., Nentwich U., Oefner P., Pearson D., RA Scherens B., Schramm S., Schrame M., Schraff M., Schramm S., Schrame M., Schraff M., Tettelin H., RA Wing Y., Wandler R., Wandler R., Wandler R., Wandler R., Wedler R., Wedler R., Wedler R., Minnett E., RA Zhong W.W., Zollner A., Vo D.H., Hani J., Wedler B., Wedler H., Winnett E., Runker B., Struck R., Mandler B., Wedler R., Mandler R., Wedler R., Radler R., Wenner B., Struck R., Landler R., Wedler R., Radler R., Wenner B., Struck R., Landler R., Wedler R., Radler R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- FUNCTION: TRANSCRIPTIONAL MODULATOR WITH ROLES IN MEIOTIC REGULATION AND SILENCING: NEGATIVE REGULATOR OF MEIOSIS.
-i- SIMILARITY: CONTAINS 4 WD repeats.
-i- SIMILARITY: STRONG, TO YEAST WIMI AND WIM2.
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GO; GO:0003714; F:transcription co-repressor activity; IDA.
GO; GO:0003714; F:transcription of meiosis; IGI.
InterPro; IPR00105; WD40.
Pfam; PF00400; WD40; 3.
SMART; SM00320; WD40; 4.
PROSITE; PS00679; WD REPEATS 1; FALSE NEG.
PROSITE; PS00679; WD REPEATS 2; FALSE NEG.
PROSITE; PS50294; WD REPEATS REGION; FALSE NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.5%; Score 33; DB 1; Length 460; 62.5%; Pred. No. 26; ive 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regulation, Melosis, Repeat; WD repeat.
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Last sequence update)
Last annotation update)
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GermOnline; 144121; -.
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460 AA;
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TRANSFAC; T04309;
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10-OCT-2003
10-OCT-2003
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MDLB BUCBP
ID MDLB BUCBP
AC Q89A96;
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                                                                                                                                                                                               MEDLINE-22426901; PubMed=1252265;
MEDLINE-22426901; PubMed=1252265;
Van Ham R.C.H.J., Kamerbeek J. Palacios C., Rausell C., Abascal F.,
Van Ham R.C.H.J., Kamerbeek J., Jimenez L., Poetigo M., Silva F.J.,
Bastolla U., Fernandez J.M., Jimenez L., Poetigo M., Silva F.J.,
Tamames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;
Reductive genome evolution in Buchnera aphidicola.";
Proc. Natl. Acad. Sci. U.S.A. 100:881-586(2003).
--- SIMILARI LOCATION: Integral membrane protein (Potential).
--- SIMILARITY: Belongs to the ABC transporter family. MDR subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Buchnera aphidicola (subsp. Balzongia pistaciae).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
NCBI_TaxID=135842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=S288c;
van Vliet-Reedijk J.C., Planta R.J.;
van Vliet-Reedijk J.C., Planta R.J.;
submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: STRONG, TO YEAST YBL011W.
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01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 83.6 kDa protein in CCP1-MET1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PESCO 220 ABC TMIF; 1.
PROSITE; PSO0211; ABC TRANSPORTER 1; FALSE NEG.
PROSITE; PSO093; ABC TRANSPORTER 2; 1.
ATP-binding; Transport; Transmembrane; Complete proteome.
TRANSMEM 26 46
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Pred. No. 3
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SEQUENCE
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                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch.
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                                                                                                                                                                                                                                                                                                                   GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0004366; F:glycerol-3-phosphate O-acyltransferase acti. . .; IDA.
GO; GO:0008654; P:phospholipid biosynthesis; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DECLEMENT 2210633 / Serotype 03:K6;

MEDLINE=22508454; PubMed=12620733;

MEDLINE=22508454; PubMed=12620733;

MEDLINE=22508454; PubMed=12620733;

MAKINO K., OBHIMA K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome Sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. Cholerae.";

Lancet 361:743-749(2003).

-! FUNCTION Has an important function as a repair enzyme for

-! FUNCTION Has an important function as a repair enzyme for

-! FUNCTION Has an important function as a repair enzyme for

-! FUNCTION contains that have been inactivated by oxidation. Catalyzes the

reversible oxidation-reduction of methionine sulfoxide in proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to methionine (By similarity).
-!- CATALYTIC ACTIVITY: Protein L-methionine + oxidized thioredoxin = protein L-methionine S-oxide + reduced thioredoxin.
-!- SIMILARITY: Belongs to the merA Met sulfoxide reductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Peptide methionine sulfoxide reductase msrA (EC 1.8.4.6) (Protein-
methionine-S-oxide reductase) (Peptide Met(O) reductase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Protecobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio. NCBI_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.5%; Score 33; DB 1; Length 743; ilarity 75.0%; Pred. No. 43; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 55 POTENTIAL.
69 85 POTENTIAL.
502 524 POTENTIAL.
539 555 POTENTIAL.
743 AA, 83644 MW, 84B9946ES5B82FIS CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 AA
                                                                                                                                                                                                                                                                                                                                                                                             InterPro, IPRO02123, Acyltransferase
Pfam, PF01553, Acyltransferase, 1.
SMART; SM00563, PlBC, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane
                                                                                                                                                                                                                    EMBL; Z28292; CAA82146.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio parahaemolyticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 VVPCGLHY 301
                                                                                                                                                                                                                                            PIR; S38143; S38143.
GermOnline; 140046; -
SGD; S0001775; GPT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VVPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
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MSRA_VIBPA
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
GMP synthase [glutamine-hydrolyzing] subunit B (EC 6.3.5.2) (GMP
                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mechanobacterium thermoautotrophicum.
Archaea, Buryarchaeota, Methanobacteria, Methanobacteriales,
Mechanobacteriaceas, Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF_00345; -; 1.

InterPro__IPR001674; GMP_synth_C.

Pfam; PR00958; GMP_synt_C; 1.

ITGRPAMs; IIGR00884; guaA_Cterm; 1.

Iigase; GMP_biosynthesis; Purine biosynthesis; ATP-binding; Complete protecome.
                                                                                                                                                                                                                             Query Match 61.5%; Score 32; DB 1; Length 212; Best Local Similarity 55.6%; Pred. No. 19; Astches 5; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GMP-BINDING (BY SIMILARITY).
                                                                                                            Pram; PF01625; PMSR; 1.
Oxidoreductase; Complete proteome.
ACT SITE 51 51 BY SIMILARITY.
SEQUENCE 212 AA; 23616 MW; 1967AFEC3C735EC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP (BY SIMILARITY).
F2DCF6ED202CAEC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     308 AA.
or send an email to license@isb-sib.ch/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000850; AAB85215.1; ALT_INIT.
HSSP; P04079; 1GPM.
                                              EMBL; AP005074; BAC58569.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 35 A
308 AA; 34403 MW;
                                                                    HAMAP; MF_01401; -; 1.
InterPro; IPR002569; PMSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                      171 EIVPAGPYY 179
                                                                                                                                                                                                                                                                                                                          2 EVVPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GUAAB OR MTH710.
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GAAB METTH
ID GAAB METTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthetase)
                                                                       HAMAP; MF
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C.1-PHOSPHATE GROUP OF THE SUBSTRATE.

C.1-PHOSPHATE GROUP OF THE SUBSTRATE.

SCHIFF-BASE WITH DIHYDROXYACETONE-P.

ENSENTIAL FOR ENHANCED ACTIVITY OF THE

BAZYME TOWARD FRUCTOSE 1,6-BISPHOSPHATE

AS COMPAED WITH FRUCTOSE 1-PHOSPHATE.

WW. FC8B45666821E2BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning and characterization of a full-length cDNA coding for ovine aldolase B from fetal mesonephros.";
Biochim. Biophys. Acta 1219:523-227 (1994).
-!- CALALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone phosphate + D-glyceraldehyde 3-phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PATHWAY: Glycolysis; sixth step.
-!- SUBUNIT: Homotetramer (By similarity).
-!- MISCELLANEOUS: In vertebrates, three forms of this ubiquitous glycolytic enzyme are found, aldolase A in muscle, aldolase B in liver and aldolase C in brain.
-!- SIMILARITY: Belongs to class I fructose-bisphosphate aldolase
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Fructose-bisphosphate aldolase B (EC 4.1.2.13) (Liver-type aldolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Mesonephros;
MEDIINE=9436863; PubMed=8086469;
Gianquinto L., Pailhoux E.A., Bezard J., Servel N., Kirszenbaum M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Netazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, Bovidae, Caprinae, Ovis.
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61.5%; Score 32; DB 1; Length 308; 63.6%; Pred. No. 29; ive 0; Mismatches 4; Indels
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PIR; S47540; 547540.
HSSP; PO0883; 1A0.
InterPro; IPRO00741; Aldolase I.
Bfam; PF00274; Glycolytic_enzy; 1.
PRODIT: PS001128; Aldolase I; 1.
PROSITE; PS00158; ALDOLASE_CLASS I; 1.
Lyase; Schiff base; Glycolysis; Multigene family.
INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                 363 AA
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                                                                     7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                         216 EEVVESGLHES 226
                                                                                                                                       1 EEVVPXGXHYS 11
   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             ALFB SHEEP
P52210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                     Matches
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Gaps

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189 EVIPDGSH 196
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Searched:

Database

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029966 archaeoglob

02972 streptococc

0864u1 streptococc

086281 streptococc

080282 streptococc

0805924 streptococc

080591 streptococc

080591 streptococc

080591 streptococc

080591 streptococc

080591 streptococc

080592 sulfolobus

080592 sulfolobus

080593 sylella fas

08063 sylella fas

081031 bos taurus

9rxn9 deinococcus
Q9hlh8 thermoplasm
O16912 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.; Strausberg R.; Strausberg R.; Strausberg (JUN-2002) to the EMBL/GenBank/DDBJ databases.

BMBL; BC032195, AAH32195.1; -.

MGD; MGI:191724; Tada31.

GO; GO:0030374; F:ligand-dependent nuclear receptor transcrip.

GO; GO:0005515; F:protein binding; IPI.

SEQUENCE 413 AA; 46621 NW; ASBRAIDC70CDA0D5 CRC64;
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Pred. No. 2.7;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
1-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to expressed sequence AI987856.
TADA31 OR 1110004819RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                Q57489
Q9PC35
Q87D36
Q8I033
                                                                                                                                                                                                                                                                                                                                                                                       Q8YWP1
Q867A5
Q8HXY9
Q7VP43
Q9UEE9
Q8IGN5
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Q96YH5
QBCYU7
Q9XST4
                                                       029966
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Q8NZ82
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099XV4
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000404
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       Local Similarity 63.6
les 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
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     01-NOV-1996
01-NOV-1996
01-OCT-2003
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Matches 7
       Q8K289
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                                                                                                                        June 3, 2004, 11:35:06; Search time 29.8667 Seconds (without alignments) 116.206 Million cell updates/sec
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Q46486
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Q98317
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Q9XEE
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Gapop 10.0 , Gapext 0.5
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1: SP_archea:*
2: sp_bacteria:*
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4: sp_human:*
5: sp_human:*
6: sp_mammal:*
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sp_plant:*
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sp_virus:*
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52
1 EEVVPXGXHYS 11
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Q9LW50
ID Q9LW9
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A chen Z., Wen Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Oin Z.,
A chen Z., Wen Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Oin Z.,
A chen Z., Wen Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Oin Z.,
Chen Z., Wen Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Oin Z.,
Chen Z., Wen Y., Rey L., Chen Z., Lu C., Chen Z., Lu C., Colous J., Ficysteaine-type endopeptidase activity; IEA.
Colous J., Ficysteaine-type endopeptidase activity; IEA.
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MEDILINE=20194806; PubMed=10735689,
MEDILINE=20194806; PubMed=10735689,
Tauch A., Krieft S., Kalinowski J., Puhler A.;
Trauch A., Corynebacterium striatum M82B is composed of DNA segments
incitally identified in soil bacteria and in plant, animal, and human
pathogens.",
Mol. Gen. Genet. 253:1-11(2000).
EMBL; AF024666; AAG03390.1; -.
GO; GO:0046861; Cextrachromosomal DNA; IEA.
Hypothetical protein; Plasmid.
SEQUENCE 208 Aa; 23012 MW; FISO4BEIECDE85A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                   SPECIES=C.xerosis; STRAIN=M82B; MEDLINE=S6117603; PubMed=S559800; MEDLINE=S6117603; PubMed=S559800; Tauch A., Kassing F., Kalinowski J., Publer A.; Troch A., Kassing F., Kalinowski J., Publer A.; The Corynebacterium serosis composite transposon In5432 consists of the videntical insertion sequences, designated IS1249, flanking the errthromycin resistance gene ermCX."; plasmid 34:119-131(1995).
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                                                                          Corynebacterium xerosis, and Corynebacterium striatum.
Corynebacterium striatum.
Bacteria, Actinobacteria, Actinobacteridae; Corynebacterineae; Co
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
Carbamoyl-phosphate synthase large chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.2%; Score 36; DB 2; 50.0%; Pred. No. 15; ative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1057 AA
Hypothetical protein (GcrA)
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Best Local Similarity 50.0
Matches 5; Conservative
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130 DVIPEGKHYA 139
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Bukaryopyta; Tracheophyta;
Bukaryopyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BY4; TISSUBE-Leaf;
STRAIN=BY4; TISSUBE-Leaf;
STRAIN=BY4; TISSUBE-Leaf;
MEDLINE=952.76459; PubMed=7756828;
MEDLINE=952.76459; PubMed=7756828;
MEDLINE=952.76459; PubMed=7756828;
MEDLINE=952.76459; PubMed=7756828;
MEDLINE=952.76259; PubMed=7756828;
MEMBL; D38126; BAA07324.1; -...
EMBL; D38126; BAA07324.1; -...
EMBL; D38126; BAA07324.1; -...
RSP; O800337; 26C5.
RRSP; O800337; 26C5.
RRSP; O800337; TO2590; Piregulation of transcription, DNA-dependent; IEA.
GO; GO:00003700; Firranscription of transcription, DNA-dependent; IEA.
RD; GO:0001370; Firranscription of transcription, DNA-dependent; IEA.
RD; GO:000142; TFERP.
RRNINTS; PRO0367; ETHRSPELEMNT.
RPINTS; PRO0367; ETHRSPELEMNT.
RRART; SMO0380; AP2; 1.
SMART; SMO0380; AP2; 1.
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Pred. No. 88;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                    1057 AA; 117391 MW; 8944D7D8DB1CAE59 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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InterPro; IPR005481; CPase L.N.
InterPro; IPR00432; MGS like.
InterPro; IPR00432; MGS like.
InterPro; IPR00432; MGS like.
Pro0289; CPSase L. Chain; 2.
Pfam; PP0278; CPSase L. D2; 2.
Pfam; PP0218; CPSase L. D3; 1.
Pfam; PP02142; MGS; 1.
Pran; PR02142; MGS; 1.
PRINTS; PR0098; CPSASE L.
PROSITE; PS00866; CPSASE 1; 2.
PROSITE; PS00867; CPSASE 1; 2.
PROSITE; PS00839; THIOL_PROTEASE HIS; 1.
COMPLETE PROCESOME.
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01-OCT-2000 (TrEMBLrel. 15, Created)
                                                                                                                                                                                                                                                                                                                                                                     63.2%;
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Best Local Similarity 60...
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                        Query Match 69.2
Best Local Similarity 63.6
Matches 7; Conservative
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67.3%;
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Matches 5; Conservative
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Best Local Similarity
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Q9X2E2
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                                                                                                                                                                                              Bukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids, lamids, Solanales, Solanaceae; Nicotlana.
NCSI_TaxID=4096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=11082930; PubMed=11214968; Kaneko T., Sasamoto S., Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawamane A., Idesawa K., Kohara M., Marsumoto M., Matsumoto A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takarohi C., Yamada M., Tabata S.; Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Sugimoto M., Masoritic Bathata S.; Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama Makayama S., Makayama Makayama S., Makayama Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makayama S., Makaya
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-20399450; PubMed=10945353;
Kitajima S., Koyama T., Ohme-Takagi M., Shinshi H., Sato F.;
Kitajima S., Koyama T., Ohme-Takagi M., Shinshi H., Sato F.;
Kitajima S., Koyama T., Ohme-Takagi M., Shinshi H., Sato F.;
Characterization of gene expression of NBERRB, transcription factors
of basic PR genes from Nicotiana sylvestris.";
Plant Cell Physiol. 41:817-824 (2000).
HSSP, 080337, 20cc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001471; FERF.
Pfam; PF00847; AP2-domaIn; 1.
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EMBL; AP03300; BAB4970.1; -.

GO; GO:0005746; C:mitochondrial electron transport chain; IEA.

GO; GO:0005489; F:electron transporter activity; IEA.

GO; GO:0005489; F:electron transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.3%; Score 35; DB 10; Length 237; 60.0%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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ProDom; PD001423; TF ERF; 1.
SMART; SM00380; AP2; 1.
SMART; SM00380; AP2; 1.
SEQUENCE 237 AA; 26243 MW; 01EC3EEB51E46298 CRC64;
01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Ethylene-responsive element binding factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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InterPro; IPR002326; Cyt C1.
Easi, PP0012167; Cytcochrome C1; 1.
PRINTS; PR00603; CYTOCHROME C; 1.
PROSITE; PS00190; CYTOCHROME C; 1.
                                                                                                                                                               Nicotiana sylvestris (Wood tobacco)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 60.0
Matches 6; Conservative
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SEQUENCE 285 AA
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198HU6
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STRAIN=MBB / DSM 3109;

MEDLINE=929287316;

MEDLINE=929287316;

MEDLINE=929287316;

MEDLINE=929287316;

MEDLINE=10 H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

A. McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

A. Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria from Genome sequence of Thermotoga maritima.";

In Nature 399:323-329(1999).

R. REBL; ARD10819; AAD16885.1; -.

R. TIGR, TM1822; -.
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                                                        Gaps
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Bacteria, Thermotogae, Thermotogales, Thermotogaceae, Thermotoga.
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Viruses, dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
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16; Length 285
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                                                        2; Indels
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Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
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SWART; SMO0244; PHB; 1.
Protease; Complete proteome.
SEQUENCE 308 AA; 34778 MW; ADE03603E5101A9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrENBLrel. 12, Last sequence update) 01-UNY-2003 (TrENBLrel. 24, Last annotation update) TRSH protease activity modulator HFLK.
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  35;
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                                                           2; Mismatches
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GO; GO:0016020; F:peptidase activity; IEA.
Interpro; IPR001107; Band_7.
Interpro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
     Score 35;
Pred. No.
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sequence of Methanobacterium thermoautotrophicum
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01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
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tes 5; Conservative
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01-MAR-2001
01-OCT-2003
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Q7XTG3;
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Q9E1X6
ID Q9E1X1
AC Q9E1X1
DT 01-MA1
DT 01-MA1
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MEDLINE=98037514; PubMed=9371463;
Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
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MEDLINE=95138034; PubMed=7836307;
Henrich B., Binishofer B., Blaesi U.;
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J. Bacteriol. 177:723-732(1995).
                                                                                                                                                             SECUENCE FROM N.A.
MEDLINE=93231558; PubMed=8472961;
Fremaux C., De Antoni G., Raya R., Klaenhammer T.;
"Genetic organization and sequence of the region encoding integr functions from Lactobacillus gasseri temperate bacteriophage phiadn.";
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Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
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Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          34703 MW; 9FF271SEE43561C7 CRC64;
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01-7579;
01-73A-1998 (TEWBLrel. 05, Last sequence update)
01-JAN-1998 (TEWBLrel. 05, Last sequence update)
01-JUN-2003 (TEWBLrel. 24, Last annotation update)
01-JUN-2003 (TEWBLrel. 24, Last annotation update)
MTH1642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
    [2]
SEQUENCE FROM N.A.
MEDLINE=99384014; PubMed=10452953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                67.3%;
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Best Local S
Matches 6
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FUGG. PROM N.A.

Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.O., Zhu G.F., Tu Y.F., Shao S.Y., Rang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Mang L.J. Ding C.W., Sheo H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Feng Q., Chen E., Fan D.L., Weng Q.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhao L., Lu Y.Q., Yu S.L., Liu X.H., Lu Y.C., Li Y., Zhang Y.C., Li Y., Zhang Y., Lu Y.Q., Yu S.L., Liu X.H., Zhou B., Chen Z.H., Hao P., Zhang Y., Guan J.P., Hong G.F., Shang R.Q. Guan J.P., Hong G.F., Shang X.Q. Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Hong G.F., Shang X.Q., Gatan J.P., Shang X.Q., Shang X.Q., Gatan J.P., Shang X.Q., Shang X.Q., Shang 
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OJ991214_12.4.
Oryza sativa (Rice).
Bukaryota, Virighjantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bhrhartoideae; Oryzeae; Oryza.
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45.5%; Pred. No. 46;
tive 4; Mismatches 2; Indels
"Complete genome sequence of Methanobacterium thermoautotro deltaH: functional analysis and comparative genomics.";
J. D. Bacteriol. 179:1735-7155(1997).

EMBL; AEG00023; AAB86115.1; -.

PIR; E69086; E69086.

GO; GO:0005634; Cinucleus; IEA.

R O; GO:00005634; Cinucleus; IEA.

R O; GO:0000510; P:cytokinesis; IEA.

R InterPro; IPR005144; RRF1_2.

R InterPro; IPR005144; RRF1_3.

R InterPro; IPR005145; PelA.

R Pfam; PF03464; RRF1_2.

R Pfam; PF03464; RRF1_2; I.

R Pfam; PF03465; RRF1_3; I.
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SEQUENCE 360 AA; 40814 MW; 2A000CB4B3CEF469 CRC64;
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(TrEMBLrel, 16, Last sequence update)
(TrEMBLrel, 25, Last annotation update)
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SEQUENCE FROM N.A.
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MEDLINE-20196006; PubMed=10731132;

MEDLINE-20196006; PubMed=10731132;

MEDLINE-20196006; PubMed=10731132;

MEDLINE-20196006; PubMed=10731132;

MEDLINE-20196006; PubMed=10731132;

MEDLINE-20196006; PubMed=10731132;

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                                                                                                                                                                       Gray W.L., Starnes H.B., White M.W., Ashburn C.V., Mahalingam R.;
"Complete Sequence of the Simian Varicella Virus Genome.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR273348; AAG2727.1; -
EMBL; AR273348; PAG2727.1; -
EMBL; PEDNA Packaging; IEA.
GO; GO:00013012; C:virion; IEA.
GO; GO:0001302; PEDNA packaging; IEA.
InterPro; IPR007640; Herpes_UL17; -
Pfam; PPG4559; Herpes_UL17; -
Pfam; PPGAFS9; Herpes_UL17; -
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CG30437 OR CG10398 OR CG10408.
Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Bukaryota, Endopterrygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.3%; Score 35; DB 12; Length 678; 50.0%; Pred. No. 90; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   75850 MW; A17B09E30512FE3C CRC64;
     Cercopithecine herpesvirus 7.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
NCBI_TaxID=35245;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Best Local Similarity 50.0.
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Hypothetical protein.
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QBIME6;
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Revale C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Buracon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busem D.A.,

A carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.W.,

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A Routen M., Strong R., Svirskas R., Tector C., Tyler D.,

A Williams S.W., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

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Matara S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Calong M., Dryddale R., Bammert D., Frise E., de Grey A., Harris N., Krommiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Shu S., Smutniak F., Whitfield E., "Abnotation of Drosophila melanogaster genome.", J. Lewis S.E.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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EMBL; AE003786; AAN16124.1; -.
FlyBase; FEgn0050437; CG30437.
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PROSITE; PS00080; MULTICOPPER OXIDASE2; 1.
SEQUENCE 855 AA; 94532 MW; 39BD5A516D6312DB CRC64;
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Last annotation update)
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01-MAR-2002 (TYEMBLrel. 20,
01-MAR-2002 (TYEMBLrel. 20,
01-OCT-2003 (TYEMBLrel. 25,
ATP-dependent DNA helicase.
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Beet Local Similarity 66.70,
Beet Local Similarity 66.70,
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TIGRFAMS; TIGR00915; 2A0602; 1.

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                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SETRAILING A JACC 23456 / Biotype 1;
MEDLINE-20020109; Pubbed=1175668;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
Ivanova N., Anderson I., Bhatracharya A., Lykidis A., Reznik G.,
Ivanova N., Anderson I., Bhatracharya A., Lykidis A., Mazur K.,
Selkov B., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
"The genome sequence of the facultative intracellular pathogen
Brucella melitensis.";
Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
PRES. ARD09470; ARIS1457.1;
PIR; AF3286; AF3286
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Marbins=2225144; PubMed=12240834;
Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Marsuno A., Nakazaki N., Kiyokawa C., Sodimoto M., Matsumoto M., Marsuno A., Tabata S.;
"Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 16; Length 1028;
Pred. No. 1.4e+02;
2; Mismatches 3; Indels C
                         Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
NCBI_TaxID=29459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1028 AA; 112996 MW; A752B7042572E219 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Symechococcus elongatus (Thermosymechococcus elongatus)
Bacteria; Cyanobacteria; Chrococcales; Symechococcus.
                                                                                                                                                                                                                                                                                                                                     GO; 00:00524; F:ATP binding; IEA.
GO; 00:00524; F:ATP binding; IEA.
GO; 00:00526; F:ATP dependent helicase activity; IEA.
GO; 00:001676; F:nucleic acid binding; IEA.
GO; 00:001641; F:nucleic acid binding; IEA.
GO; GO:001615; F:nucleic acid binding; IEA.
InterPro; IPR001608; Aldehyde_dehydr.
InterPro; IPR001410; DEAD.
InterPro; IRR001650; Helicase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OBDIHO;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Multidrug efflux transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res. 9:123-130(2002).

BMB1, AP005374; BAC09170.1; --
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0005215; F:transporter activity; IEA.
GO; GO:0005215; F:transport! IEA.
InterPro; IPR001036; Acrflvin_res.
InterPro; IPR004764; HAE1.
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PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
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SMART; SM00490; HELICC; 1.
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les 6, Conservative
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                 Brucella melitensis.
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REDILINE=22827954; PubMed=1210271;

MEDLINE=22827954; PubMed=1210271;

MEDLINE=22827954; PubMed=1210271;

MEDLINE=22827954; PubMed=1210271;

MEDLINE=22827954; PubMed=1210271;

MEDLINE=22827954; PubMed=1210271;

MATTIS D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

MACHIAN M., Ackin R., Temple L., James K., Harris B., Quail M.A.,

Achtman M., Ackin R., Temple L., James K., Harris B., Quail M.A.,

Achtman M., Ackin R., Collins M., Cronin A., Davis P., Doggett J.,

MALLI Goble A., Hamlin M., Hauser H., Drwod S., Jagels K.,

Leather S., Monle S., Norberczak H., O'Neil S., Ormond D., Price C.,

Leather S., Monle S., Norberczak H., O'Neil S., Ormond D., Price C.,

Mabbinowitsch E., Rutter S., Sanders M., Squares S., Stevens K.,

Munin L., Whitehead S., Barrell B.G., Maskell D.J.;

Matter analysis of the genome sequences of Bordetella pertussis,

Mat. Genet. 35:32-40(2203).

MEDLI BX640440: CAR31621.1; -.
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
NCBI_TaxID=518;
                                                    Length 1044;
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Complete proteome.
SEQUENCE 1044 AA; 113205 MW; 00E9C13F0F636D2F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                  Last annotation update)
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation updat
                                                    67.3%; Score 35; DB 16;
63.6%; Pred. No. 1.4e+02;
iive 1; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                    Putative enoyl-CoA hydratase.
                                               Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
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Matches 6; Conserv
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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
                                                                                                                                                                                                                                                 Abb80537 Hepatitis
Abb80560 Hepatitis
Abb80527 Hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus, HCV, serine protease; inhibitor; alpha-ketoamide; virucide.
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                       Abb80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80550 RABB80550 RABB80550 RABB80550 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB8055 ABB8055 RABB8055 RABB8055 RABB8055 RABB8055 RABB8055 RABB
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/note= "C-terminal amide"
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ABB 0554
ABB 0550
ABB 0550
ABB 0520
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Misc-difference
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Modified-site
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 ABB80548;
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ABB80548
 Abb80548 Hepatitis
Abb80557 Hepatitis
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Abb80551 Hepatitis
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               GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: geneseqp1980s:*

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invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 otide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
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virucide.
                                                                                                                                                                                                                                                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #27.
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                                                                                            Length 11;
                                                                                                                 1; Indels
                                                                                           Score 47; DB 5;
Pred. No. 0.012;
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                                                                                          Match 94.0%;
Local Similarity 90.9%;
es 10; Conservative
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                                                                                                                                                                                    Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C ^{\circ}
                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #36
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Pred. No. 0.012;
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                                                                                                                                                                                                                                                                            'note= "N-terminal acetyl"
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                                                                                     ABB80556 standard; peptide; 11 AA.
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90.9%;
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Best Local Similarity
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activity usefu
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                                                                                                               ABB80556;
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EEVVPXGSDYS 11

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus

RESULT 4

Length 11;

DB 5; 0.012;

Score 47; Pred. No.

94.0%;

Query Match Best Local Similarity

Sequence 11 AA;

note= "Norvalyl carbonyl forming keto-amide linkage with

residue 7"

Misc-difference

Modified-site

/note= "C-terminal amide" note= "D-form residue"

WO200208251-A2

31-JAN-2002

'note= "N-terminal acetyl"

Location/Qualifiers

Key Modified-site

Synthetic

Modified-site

Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.

Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #31

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'note= "Norvalyl carbonyl forming keto-amide linkage with
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virucide.
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                                                                                                                                                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #37
                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "N-terminal acetyl"
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                           ABB80557 standard; peptide; 11 AA.
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BB80557
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Brunck

Levy OE,

Lim-Wilby M,

(CORV-) CORVAS INT INC

19-JUL-2001; 2001WO-US023169. 21-JUL-2000; 2000US-0220101P.

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Best Local Similarity 90.9
Matches 10; Conservative
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Gaps

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DB 5; Length 11; 0.012; 1; Indels

Score 47; DB: Pred. No. 0.013 0; Mismatches

94.0%;

Query Match
Best Local Similarity 90.5
Matches 10; Conservative

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EEVVPXGSDYS 11 1 EEVVPXGXDYS 11

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ABB80551 standard; peptide; 11 AA.

ESULT 5

(first entry)

08-OCT-2002

ABB80551;

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                                    /note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"
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virucide.
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                        'note= "N-terminal acetyl"
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Location/Qualifiers
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The sequence represents a peptide compound of the invention having the peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of an endicament to treat disorders associated with NCV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treat disorders associated with hepatitis C virus
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ity useful for treating disorders associated with hepatitis C virus
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                                 /note= "C-terminal amide"
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           /note= "D-form residue"
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                                                                                                       19-JUL-2001; 2001WO-US023169
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Best Local Similarity 90.9
Matches 10; Conservative
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Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                            ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #23
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                                                                                                                                                                                                                                                                                                                      Score 46; DB 5; Length 11;
Pred. No. 0.02;
0; Mismatches 1; Indels
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/note= "C-terminal amide"
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                                                                                Brunck TK;
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                                                                                                                                                                           Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; peptide; 11
                                                                                                                                                                                                                                                                                                                       92.0%;
90.9%;
           19-JUL-2001; 2001WO-US023169
                                  21-JUL-2000; 2000US-0220101P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     residue 7"
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Best Local Similarity 90.9
Matches 10; Conservative
                                                                                OE,
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                                                      (CORV-) CORVAS INT INC
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                                                                                                      WPI; 2002-361643/39.
                                                                                Levy
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                                                                                                                                                                                                                                                                                                 Sequence 11 AA;
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                                                                                                                              Novel peptide
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Modified-site
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                                                                              Lim-Wilby M,
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                                                                      Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
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Pred. No. 0.02;
0; Mismatches
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                  Brunck TK;
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                                                                                                                                                                  Claim 17; Page 65; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                           92.0%;
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nes 10; Conservative
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                  Levy OE,
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                                                    WPI; 2002-361643/39.
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                  Lim-Wilby M,
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                                The sequence represents a peptide compound of the invention having the peptides of virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat alsorders associated with HCV protease. A pharmacceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                            Score 46; DB 5; Length 11;
Pred. No. 0.02;
0; Mismatches 1; Indels
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            Claim 17; Page 64; 69pp; English
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                                                                                                                                                           92.0%;
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                                                                                                                                      Sequence 11 AA;
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ABB80533
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus

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                                            Gaps
                                                                                                                                                                                                                                   Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
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Best Local Similarity
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Sequence 11 AA;
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protease.
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ABB80538 standard; peptide; 11 AA.
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                        ABB80538;
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                                                                                                                                                                                                                                                       /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                 Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                        Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #42.
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Pred. No. 0.02
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                                                                                                                                                                                                                                'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                       'note= "D-form residue"
                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brunck TK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-2000; 2000US-0220101P
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Best Local Similarity 90.5
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                   Misc-difference
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                                                                                                                                               Synthetic.
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                                                                                                                              /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
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Pred. No. 0.02;
0; Mismatches 1; Indels
                                                                                                     'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                      /note= "C-terminal amide"
                                                                                                                                                                                                  'note= "D-form residue"
                                                                                                                                                                                                                            'note= "D-form residue"
                                                                                                                                                                        note= "Oxymethionine"
                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                        19-JUL-2001; 2001WO-US023169.
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                            Key
Modified-site
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3, 2004, 11:48:24

Search completed: June Job time: 45.9333 secs

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OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 76, Appl
Sequence 82, Appl
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14, Appli
43, Appli
4318, Ap
2, Appli
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14, Appli
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1. /ogn2_6/ptodata/2/iaa/5A_COMB.pep:*

2. /ogn2_6/ptodata/2/iaa/5B_COMB.pep:*

3. /ogn2_6/ptodata/2/iaa/6A_COMB.pep:*

3. /ogn2_6/ptodata/2/iaa/6B_COMB.pep:*

3. /ogn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

3. /ogn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

3. /ogn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-134-000C-4318
US-08-459-066-2
US-08-413-814-86
US-09-617-594A-2
US-09-617-594A-2
US-09-621-976-4604
US-09-621-976-4604
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-08-926-8423-20
-08-926-842B-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         389414 seqs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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50
1 EEVVPXGXDYS 11
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Match Length DB
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Sequence:
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No.
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Sequence 25088, A Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 3, Appli Sequence 2, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 7, Appli	CES RELATING TO TICS AND THERAPEUTICS	gth 181; Indels 0; Gaps 0;	
US-09-252-991A-25088 US-09-040-799-3 US-09-093-448-1 US-09-093-448-3 US-09-093-448-3 US-09-093-448-3 US-09-813-555-1 US-09-813-555-3 US-09-813-555-3 US-09-523-2638-4 US-09-523-2638-16 US-09-523-2638-16 US-09-523-2638-17 US-09-523-2638-17 US-09-523-2638-17 US-08-13-17-17 US-08-11-17-17 US-08-11-17-17-17 US-08-11-17-17	ALIGNMENTS US/09134000C US/09134000C Stand et al CACID AND AMINO ACID SEQUENCES F COCOCCUS FAECALIS FOR DIAGNOSTICS E. US/09/134,000C US 60/055,778 13.1	Score 37; DB 4; Len Pred. No. 5.1; 0; Mismatches 3;	SED ANTIBODIES BUTH KURTZ Mackiewicz E 8, LLP e - 46th Floor
44444444444444444444444444444444444444	lcation US/0 Loctte-Stamm NUCLETC AC NUCLETC AC 796-032 US 1097-0815 11997-0815 11997-0815 Version 3.1	74.0%; 70.0%; ative 10 154	action US/08569: NN: CON: HUMANISED CON: 95 DDRESS: 95 DDRESS: 06180377ris, 1 A. 6180377ris, 1 A. Floppy disk I.PC compatible
	1000C-4848 4848, Appl. 100CF-4848 100CF-4848 100CF-4848 100CF-4848 100CF-4848 100CC-4848 100CC-4848 100CC-4848 100CC-4848 100CC-4848	atch 3al S 7 1	147-76 16 Applic No. 6180377 No. 6180377 No. 6180377 No. 6180377 No. 6180377 No. 6180377 No. 6180377 No. 6180377 No. 6180377 No. 6180377 No. 6180377 No. 6180377 No. 6180377 No. 6180377 No. 618037 No
0 0 0 0 H 0 W 4 W 9 W 9 W 9 W 9 W 9 W 9 W 9 W 9 W 9	RESULT 1 US-09-134-00 Sequence 4 Patent No. Patent No. PAPLICANT APPLICANT TITLE OF TITLE OF TITLE OF FILE REFE CURRENT A CURRENT A CURRENT A PRIOR APP PRIOR APP PRIOR APP PRIOR APP PRIOR APP PRIOR APP PRIOR APP PRIOR APP PRIOR APP TOURIER OF SOFTWARE: TYPE: PR CORDINISA	Query Best 1 Matche	RESULT 2 US-08-569-1, Sequence (Patent No GENERAL (TITLE (T
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RESULT 4
US-09-134-001C-5124
Sequence 5124, Application US/09134001C
; Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-5124
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55.6%;
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Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
ZIP: 19103
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PREDED FORM:
MEDIUM TYPE: PROPRY AIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/569,147
FILING DATE: DATE: DATE: DATE: TAUGHT AND POST STATE ATTONIN FORMATION:
NAME: TTULING DATE: 35,719
REPRENCE/POCKET NUMBER: 35,719
TELEPHONE: (215) 568-3100
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TELEPHONE: (215) 568-3100
TELEPHONE: MANDER: SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/569,147
FILLING DATE: 25-March-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INNORMATION:
    NAME: Trujillo, Doreen Yatko
    REGISTRATION NUMBER: 35,719
    REPERRANG/DOCKET NUMBER: 35,719
    REPERRANG/DOCKET NUMBER: 35,719
    TELECOMMUNICATION INNEMATION:
    TELECHONE: (215) 568-3100
    TELEFHONE: (215) 568-3100
    INFORMATION: POR SEQ ID NO: 76:
    SEQUENCE CHARACTERISTICS:
    LENGTH: 140 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.0%; Score 33; DB 3; Length 140; 75.0%; Pred. No. 24; cive 0; Mismatches 2; Indels
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Pred. No. 24;
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Patent No. 6180377
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CORRESPONDENCE 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6180377ris, LLP
ADDRESSEE: No. 6180377ris, LLP
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-147-76
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Best Local Similarity 75.0°
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Best Local Similarity 75.0
Matches 6; Conservative
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GENERAL INCORNATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: UNDERE: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
SPRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
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PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR PLOR DATE: 1997-11-08
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Sequence 14, Application US/09830217

Patent No. 6521441

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides

FILE REFERENCE: PRACHER:

CURRENT APPLICATION NUMBER: US/09/830,217

CURRENT PILING DATE: 2001-04-24

PRIOR APPLICATION NUMBER: POT/US99/06199

PRIOR PILING DATE: 1998-03-18

PRIOR PILING DATE: 1998-04-01

PRIOR PILING DATE: 1998-05-07

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 14

LIENGTH: 301
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Pred. No. 38;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
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; Patent No. 6632937
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340 Kingsland Street

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Sequence 4318, Application US/09134000C

Sequence 4318, Application US/09134000C

Batent No. 6617156

GENERAL INFORMATION:

APPLICATY: Lyn. DOUGETE-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTERCOCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ENTERCOCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: UNMER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

FRIOR PELLING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SEQ ID NO 4318

LENGTH: 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                 APPLICANT: Swanson, Ronald V.
APPLICANT: Reddman, Robert A.
APPLICANT: Reddman, Robert A.
APPLICANT: Reddman, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP. 002A
CURRENT APPLICATION NUMBER: 1899-09-29
FRIGH REPLICATION NUMBER: 60/102,294
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 3472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | LOCATION: (2).7(2)
| CTHER INFORMATION: Amino acid 2 is Xaa wherein Xaa = any amino acid.
US-09-134-000C-4318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.0%; Score 32; DB 4; Length 3472; 45.5%; Pred, No. 1.5e+03; Live 3; Mismatches 3; Indels
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APPLICANT: Choi, Gil Ho
APPLICANT: Choi, Gil Ho
APPLICANT: Nuss, Donald Lee
TITLE OF INVENTION: Genetically Engineered Transmissible
TITLE OF INVENTION: Hypovirulence
NUMBER OF EGUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
62.0%; Score 31; DB 4; Length 303;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 3; Mismatches 3; Indels
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Patent No. 5866405
                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 45.5-
Then 5; Conservative
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2294 EDVIPRGISFS 2304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MISC_FEATURE
SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-408-020-4
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GENERAL INFORMATION:
APPLICANT: Choi, Gil Ho
APPLICANT: Choi, Gil Ho
APPLICANT: Choi, Gil Ho
APPLICANT: Nuss, Donald Lee
TITLE OF INVENTION: Hypovirulence
ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 31; DB 2; Length 62;
Pred. No. 3.3e+02;
0; Mismatches 1; Indels
                                                                                                                                             COMPUTER KELLELE FORDAGISK

CONTUTER: Ploppy disk

CONTUTER: IBM PC COMPALIBLE

CONTUTER: IBM PC COMPALIBLE

CONTUTER: IBM PC COMPALIBLE

CONTUTER: PATEMICATION

CONTUTER: PATEMICATION

APPLICATION NUMBER: US/08/459,146

FILING DATE: 02-UJN-1995

CLASSIFICATION DATA:

APPLICATION NUMBER: US 07/832,117

FILING DATE: 06-FEB.199

ATTORNEY/AGENT INFORMATION:

NAME: REPRENCE/DOCKET NUMBER: 9589

TELEPCOMMUNICATION INFORMATION:

TELEPRAM: (201) 235-6208

TELEPAK: (201) 235-6208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,065
FILING DATE: 02-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Endothia parasitica (Cryphonectria ORGANISM: parasitica)
STRAIN: EP713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08459065
Patent No. 5882642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 622 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 85...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 02-JUN-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
STREET:
CITY: Nutley
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 EEVVPAG 37
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                                                                   COUNTRY: U
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US-08-459-146-2
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Sequence 2, Application US/09617594A

Patent No. 6541458

GENERAL INFORMATION:
GENERAL TRICANT: Addonmet, et al.
TITLE OF INVENTION: FELINE CALICIVIRUS GENES AND VACCINES IN PARTICULAR RECOMBINANT
TITLE OF INVENTION FELINE CALICIVIRUS GENES AND VACCINES IN PARTICULAR RECOMBINANT
FILE REPRESENCE: 1454313-3151.1
CURRENT APPLICATION NUMBER: 05/09/617,594A
CURRENT PILING DATE: 2000-07-14
PRIOR PELING DATE: 2000-03-30
PRIOR PELING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: France 00 01761
PRIOR APPLICATION NUMBER: France 99 09421
PRIOR APPLICATION NUMBER: FIRE 2000-02-11
PRIOR APPLICATION NUMBER: FIRE 2000-03-30
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: FIRE 2000-03-30
PRIOR PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: FIRE 2000-03-30
PRIOR APPLICATION NUMBER: FIRE 2000-03-30
PRIOR APPLICATION NUMBER: FIRE 2000-03-30
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4.5e+02;
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Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: VAN DER OSTEN, CLAUS
APPLICANT: HALKLER; TORDEN
APPLICANT: HALKLER;
APPLICANT: BAUDITZ, PETER
APPLICANT: BAUDITZ, PETER
TITLE OF INVENTION: PETER RAMP
TITLE OF INVENTION: PETER RAMP
TITLE OF INVENTION: PETER RAMP
TITLE OF INVENTION: POTER RAMP
CURRENT APPLICATION NUMBER: US / 08/963, 951
CURRENT FILING DATE: 1997-11-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PARISEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4604, Application US/09621976

Sequence 4604, Application US/09621976

Patent No. 6639063

GENERAL INPORMATION:
APPLICANT: Dumes Milne Edwards, J.B.
APPLICANT: JONET, S.
APPLICANT: Glordano, J.Y.
FILLE REFERENCE: ESTS and Encoded Human Proteins.
FILLE REFERENCE: GENERIC 648PR2

CURRENT APPLICATION NUMBER: US/09/621,976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGANISM: Enterococcus faecalis US-08-963-851-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Feline calicivirus
US-09-617-594A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        428 EELTPAG-DYS 437
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US-09-621-976-4604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Brocker, Helmut
APPLICANT: Blocker, Helmut
APPLICANT: Blocker, Helmut
APPLICANT: Color, Paul M
APPLICANT: Color, Paul M
APPLICANT: Goldberg, Steven L
APPLICANT: Goldberg, Steven L
APPLICANT: Goldberg, Steven L
APPLICANT: Goldberg, Steven L
APPLICANT: Mueller, Joachim
APPLICANT: Medien Goldberg, Steven L
APPLICANT: Medien Goldberg, Steven L
APPLICANT: Heldenbach, Hans
APPLICANT: Heleropolykeide compounds
FILE REFERENCE: POT/US 99/23535
CURRENT FILING DATE: 1999-10-07
FILE REFERENCE: POPPLICATION NUMBER: DE 198 46 493.2
EARLIER APPLICATION NUMBER: DE 198 46 493.2
SEALIER PRING DATE: 1998-10-09
SEQ ID NOS: 107
SSEQ ID NOS: 107
SSEQ ID NOS: 107
SEQ ID NOS: 107
SEQ ID NOS: 107
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Pred. No. 4e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.0%; Score 31; DB 2; Length 622; 85.7%; Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Endothia parasitica (Cryphonectria ) ORGANISM: parasitica) STRAIN: EP713 US-08-459-065-2
                           US 07/832,117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 86, Application US/09413814
Patent No. 6225064
GENERAL INFORMATION:
                  APPLICATION NUMBER: US 07/832, FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION: NAME: ROSEMAN, CALLETINE R REGISTRATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 65696
TELEFONMUNICATION INFORMATION: TELEFONE: (201) 235-6208
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT CRGANISM: Sorangium cellulosum US-09-413-814-86
                                                                                                                                                                                                                                                                                                                                        LENGTH: 622 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 62.5
---nhes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 VPXGXDYS 11
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RESULT 11 US-09-617-594A-2

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Pred. No. 83;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                          Query Match 60.0%; Score 30; DB 4; Length 120; Best Local Similarity 50.0%; Pred. No. 82; Matches 5; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14

US-09-152-060-68

Sequence 64 Application US/09152060

Sequence 64 Application US/09152060

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REPERRUE: PZ003P1.US
CURRENT APPLICATION NUMBER: US/09/152,060

CURRENT FILING DATE: 1998-09-11

EARLIER APPLICATION NUMBER: PCT/US98/04858

EARLIER APPLICATION NUMBER: 60/040,762

EARLIER PILING DATE: 1997-03-14

EARLIER FILING DATE: 1997-03-14

EARLIER FILING DATE: 1997-03-14

EARLIER APPLICATION NUMBER: 60/040,710

EARLIER APPLICATION NUMBER: 60/040,100

EARLIER APPLICATION NUMBER: 60/048,100

EARLIER APPLICATION NUMBER: 60/048,100

EARLIER APPLICATION NUMBER: 60/048,100

EARLIER APPLICATION NUMBER: 60/048,100

EARLIER PILING DATE: 1997-05-30

EARLIER APPLICATION NUMBER: 60/048,199

EARLIER PILING DATE: 1997-05-30

EARLIER PILING DATE: 1997-06-60

EARLIER PILING DATE: 1997-06-10

EARLIER PILING DATE: 1997-06-60

EARLIER PILING: DATE: 1997-06-60

EARLIER PILING: DATE: 1997-06-60

CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 4604
LENGTH: 120
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                                                               TYPE: PRT CAGANISM: Homo sapiens US-09-621-976-4604
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Sequence 85, Application US/09152060
Patent No. 6448230
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REPERENCE: PZ003P1.US

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RESULT 15 US-09-152-060-85

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LOCATION: (67)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PEATURE:
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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EARLIER FILING DATE: 1998-03-12
ERALIER PILING DATE: 1998-03-12
ERALIER APPLICATION NUMBER: 60/040,762
ERALIER PILING DATE: 1997-03-14
ERALIER PILING DATE: 1997-03-14
ERALIER FILING DATE: 1997-03-14
ERALIER FILING DATE: 1997-03-30
ERALIER FILING DATE: 1997-05-30
ERALIER FILING DATE: 1997-06-05
ERALIER FILING DATE: 1997-06-05
ERALIER FILING DATE: 1997-06-05
ERALIER APPLICATION NUMBER: 60/048,970
ERALIER FILING DATE: 1997-06-05
ERALIER FILING DATE: 1997-06-05
ERALIER FILING DATE: 1997-06-05
ERALIER FILING DATE: 1997-06-05
ERALIER FILING DATE: 1997-06-05
ERALIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VUMBER: 60/068,368
ERALIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
LENGTH: 121
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 6; Conserv
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LOCATION: (89)
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4 16:16:12 2004

Fri Jun

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                        June 3, 2004, 11:57:42; Search time 33.7333 Seconds
(without alignments)
91.741 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_TBW FUBL.pep:*
3: /cgn2_6/ptodata/1/pubpaa/PCT_TBW FUBL.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO7_NBW FUBL.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO7_NBW PUBL.pep:*
7/cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/1/pubpaa/USO08_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO08_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/USO08_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-909-164-35
US-09-909-164-40
US-09-909-164-41
US-09-909-164-41
US-09-909-164-12
US-09-909-164-13
US-09-909-164-13
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
Sequence:
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Maximum DB
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ALIGNMENTS

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Sequence 31. Application US/09909164
; Sequence 31. Application US/09909164
; Publication No. US20020068702A1
; Publication No. US20020068702A1
; GENERAL INFORMATION:
    APPLICANT: Lim-Wilby, Marguerita
    CURRENT APPLICANT: NOWEL: 100/99/909,164
    CURRENT APPLICANT: NOWER: 60/220,101
    PRIOR FILING DATE: 2000-07-21
    NUMBER OF SEQ ID NOS: 62
    SOFTWARE: Patentin Version 3.1
    SEQ ID NO 31
    LENGTH: 11
    LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
CTHER INFORMATION: norvaline-(CO)
US-09-909-164-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: ACETYLATION PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MOD RES
LOCATION: (11). (11)
OTHER INFORMATION: AMIDATION
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LOCATION: (1). (1)
   US-09-909-164-31
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DB 12; Length 11;

94.0%; Score 47;

Query Match

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US-UN-JUN-184-40
| Sequence 40, Application US/09909164
| Publication No. US20020068702A1
| Publication No. US20020068702A1
| GENERAL INFORMATION:
| APPLICANT: Corvas International, Inc.
| APPLICANT: Levy, Odile E
| APPLICANT: Levy, Odile E
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OTHER INFORMATION: norvaline-(CO)
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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NAME/KEY: MISC FEATURE

LOCATION: (9)...(9)

OTHER INFORMATION: D-amino acid
US-09-909-164-35
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DIHER INFORMATION: ACETYLATION
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                     SOFTWARE: Patentin version 3.1 SEQ ID NO 35 LENGTH: 11
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Best Local Similarity 90.9%;
Matches 10; Conservative
                                                                                                                                                            TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OCHER INFORMATION: AMIDATION
FEATURE:
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THER INFORMATION: AMIDATION
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NUMBER OF SEQ ID NOS: 62
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NAME/KEY: MOD_RES
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                                                                                                                                                                                                                                                                                                                                                  NES-09-164-32
Sequence 32, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim Wilby, Marguerita
APPLICANT: Lim Wilby, Marguerita
APPLICANT: Lim Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Evy, Odile E
APPLICANT: Brunck, Terence K
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
SEQ ID NO 32
SEQ ID NO 32
LINGTH APPLICATION VINDER: LIM SEQ ID NO 32
SEQ ID NO 32
LINGTH APPLICATION VINDER: LIM SEQ ID NO 32
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Sequence 35, Application US/09909164
Publication No. US20020068702A1
Sequence 15, Application No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odlie B
APPLICANT: Levy, Odlie B
APPLICANT: Lim-Wilby, Terence K
TILE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEFATITIS C
FILE REPERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-03
PRIOR FILING DATE: 2000-07-21
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                                              0; Gaps
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Pred. No. 0.0049;
0; Mismatches 1; Indels
    Pred. No. 0.0049;
0; Mismatches 1; Indels
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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LOCATION: (9)...(9)
CTHER INFORMATION: D-amino acid
US-09-909-164-32
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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Best Local Similarity 90.9%;
Matches 10; Conservative
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ORGANISM: artificial sequence
    Best Local Similarity 90.9%;
Matches 10; Conservative
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OTHER INFORMATION: AMIDATION
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FRATURE:
NAME/KEY: MOD RES
LOCATION: (1) \( \tilde{\text{L}}(1) \)
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CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
LENGTH. 11
                                                                                                                                                                                                                                                                                                                          NAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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NAME/KRY: MISC_FEATURE
LOCATION: (9)..(9).
OTHER INFORMATION: D-amino acid
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OTHER INFORMATION: ACETYLATION
FEATURE:
                                                                                                                                                      TYPE: PRT
ORGANISM: artificial sequence
PEATURE:
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.5
Matches 10; Conservative
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Sequence 41, Application US/09903164

Publication No. US2002068702A1

Publication No. US2002068702A1

GENERAL INFORMATION:

APPLICANT: Lim-Wibby, Marguerita

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PatentIn version 3.1

LENGTH: 11

LENGTH: 11
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APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
APPLICANT: DEVINGNEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
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                                                              Score 47; DB 12; Length 11;
Pred. No. 0.0049;
                                                                                                      1; Indels
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OTHER INFORMATION: norvaline-(CO)
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LOCATION: (1)...(1)
COTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11)...(11)
OTHER INFORMATION: PEATURE:
          ; OTHER INFORMATION: D-amino acid JS-09-909-164-40
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                                                                Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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Matches 10; Conservative
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us-09-909-164-45.rapb

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Sequence 18 Application US/09909164
; Sequence 18 Application US/09909164
; Publication No. US20202068702A1
; GENERAL INFORMATION:
    APPLICANT: Corvas International, Inc.
    APPLICANT: Lim-Wilby, Marguerita
    APPLICANT: Levy, Odile E
    APPLICANT: Levy, Odile E
    APPLICANT: Levy, Odile E
    APPLICANT: Levy, Odile E
    APPLICANT: Lovy, Odile E
    APPLICANT: NOUNEER: US 2003-03-25
    PRIOR PRILING DATE: 2003-03-25
    PRIOR APPLICATION NUMBER: 60/220,101
    PRIOR APPLICATION NUMBER: 60/220,101
    PRIOR PRILING DATE: 2000-07-21
    NUMBER OF SEQ ID NOS: 62
    SOFTWARE: Patentin version 3.1
    SEQ ID NO 18
    INVERSIOR PRILING DATE: Lovy CONTAINS APPLICANT NUMBER: DATE TYPE: PRI
    TYPE: PRI
    TYPE: PRI
    TYPE: PRI
    TYPE: PRI
    TYPE: PRI
    TYPE: PRI
    TYPE: PRI
    DEGARISM: artificial sequence
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEBATITIS C
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 17
LENGTH: 11
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92.0%; Score 46; DB 12
Best Local Similarity 90.9%; Pred. No. 0.008;
Matches 10; Conservative 0; Mismatches
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; OTHER INFORMATION: norvaline-(CO)
US-09-909-164-17
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NAME/KRE:
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KRY: MOD_RES
LOCATION: (11)... (11)
OTHER INFORMATION: AMIDATION
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THER INFORMATION: D-amino acid
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LOCATION: (1)...(1)
OTHER INPORMATION: ACETYLATION
PEATURE:
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NAME/KEY: MISC_FEATURE
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NAME/KEY: MOD_RES
LOCATION: (11)..(11)
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US-09-909-164-13
Sequence 13, Application US/09909164
Publication No. US20020068702A1
Publication No. US20020068702A1
APPLICANT: Corvas International, Inc.
APPLICANT: Lim Wilby, Marquerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
ITILE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR PELING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEQ ID NO 13
TENGTH: 11
TENGTH: 11
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Pred. No. 0.008
0; Mismatches
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Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
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) LOCATION: (8)..(9)
) OTHER INFORMATION: D-amino acids
US-09-909-164-13
             OTHER INFORMATION: norvaline-(CO)
                                   FEATURE:
NAME/RET:
NAME/RET:
LOCATION: (8). 7(8)
CTHER INFORMATION: D-amino acid
US-09-909-164-12
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
PEATURE:
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.9
Matches 10; Conservative
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Best Local Similarity 90.9
Matches 10; Conservative
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US-09-909-164-17
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APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERENCE: INOLUBER: US/09/909,164
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR PLILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTION NUMBER: 2000-07-21
NUMBER OF SEQ ID NOS: 62
LENGTH: 11
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Pred. No. 0.008;
0; Mismatches 1; Indels
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OTHER INFORMATION: norvaline-(CO)
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NAME/KEY: MOD RES
LOCATION: (1) - (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11) - (11)
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NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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Best Local Similarity 90.9%;
Matches 10; Conservative
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OTHER INFORMATION: AMIDATION
FEATURE:
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Levy, 'Odile E
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NAME/KEY: MISC FEATURE
LOCATION: (8). (8)
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NAME/KEY: MOD_RES
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Sublication No. US20020068702A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Levy, Odile B
APPLICANT: Levy, Odile B
APPLICANT: Levy, Odile B
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL BEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: INDIJ92-US
CURRENT FILING DATE: 2003-03-25
RICK APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
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                                                                                                                                  DB 12; Length 11;
                                                                                                                                                                   1; Indels
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                                                                                                                                Query Match 92.0%; Score 46; DB 12
Best Local Similarity 90.9%; Pred. No. 0.008;
Matches 10; Conservative 0; Mismatches
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Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc
APPLICANT: Lim-Wilby, Marguerita
                               NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
CTHER INFORMATION: norvaline-(CO)
US-09-909-164-18
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OTHER INFORMATION: norvaline-(CO)
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OTHER INFORMATION: D-amino acid
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NAME/KEX: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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   OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.9
Matches 10; Conservative
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LENGTH: 11
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US-09-909-164-46

Sequence 46, Application US/09909164

Sequence 46, Application US/09909164

Sequence 46, Application US/09909164

Sequence 46, Application No. US20020068702A1

SEQUENCE 1 Lim-Willby, Marguerita

APPLICANT: Lim-Willby, Marguerita

APPLICANT: Lim-Willby, Marguerita

APPLICANT: Lim-Willby, Marguerita

APPLICANT: Lim-Willby, Marguerita

APPLICANT: Lim-Willby, Marguerita

APPLICANT: NO.192-US

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT FILING DATE: 2000-07-21

PRIOR PILING DATE: 2000-07-21

NUMBER OF EEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQUENCE 1.1
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ORGANISM: artificial sequence
PEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
PEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(11)
OTHER INFORMATION: AMIDATION
OTHER INFORMATION: AMIDATION
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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OTHER INFORMATION: D-amino acids
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COTHER INFORMATION: Met(0)
US-09-909-164-46
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NAME/KEY: MISC_FEATURE
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US-09-909-164-45
US-09-909-164-45
Sequence 45, Application US/09909164
Sequence 45, Application US/09909164
Sequence 45, Application No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TILLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINB PROTEASE INHIBITORS OF HEPATITIS C
TILLE REPRENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2000-07-21
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 45
LENGTH: 11
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OTHER INFORMATION: 11-mer synthesized according to example 1
PEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
PEATURE:
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                                  FALUACE:

NAME/KEY: MISC FEATURE

LOCATION: (8)..(8)

FOTHER INFORMATION: D-amino acid

FEATURE:

NAME/KEY: MISC_FEATURE

COCATION: (8)..(8)

COCATION: (8)..(8)

US-09-909-164-45
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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Best Local Similarity 90.9%;
Matches 10; Conservative
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ORGANISM: artificial sequence
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LOCATION: (11). (11)
OTHER INFORMATION: AMIDATION
OTHER INFORMATION: AMIDATION
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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protein search, using sw model M protein June 3, 2004, 11:35:47; Search time 9 Seconds (without alignments) 117.567 Million cell updates/sec tun on:

US-09-909-164-45 1 EEVVPXGXDYS 11 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 scoring table: equence:

283366 segs, 96191526 residues searched: Fotal number of hits satisfying chosen parameters:

dinimum DB seq length: 0
Aaximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: Dirl:*
2: Dirl:*
3: Dird:*
4: Dird:* Jatabase

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	conserved hypothet	-1	O6-methylguanine-D	succinate dehydrog				hypothetical prote	d hyp	unknown protein [i	ferrisiderophore r	peptidoglycan-bind	fat facets (faf) s		thiol peroxidases	per	conserved hypothet	hypothetical prote	ical	acyl-CoA dehydroge	probable alkaline	ATP-dependent DNA	probable chitinase	hypothetical prote	plastocyanin b - L	plastocyanin precu	plastocyanin b pre	o t	hypothetical prote
QI	D69551	AG3104	D98182	m	T48898	T48899	A42452	S54619	A96001	A96546	F82491	H87660	B49132	VKLJSI	AG1272	AH1635	AD0454	857810	840753	DERTCM	H72784	AF3286	8224	2017	800210	3825	5820	AI0931	995
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Score	36	35	35	35	35	35	34	34	34	34	34	34	34		33		33	33	33	33	33	33	33	33	32	32	32	32	32
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hypothetical prote	hypothetical prote	probable hexosyltr	L-lactate dehydrog	hypothetical prote	tolB protein - Hae	ABC transporter AT	oligopeptidase [im	protein B0212.3 [i	probable membrane	hypothetical 367K	projectin - fruit	response regulator	S-adenosylmethioni	conserved hypothet	hypothetical prote	
F84330	AH1912	G69290	G69350	T24111	F64064	E86665	H84350	G88651	F69009	T31308	T13931	A69487	H97247	E72330	F72745	
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307	314	357	366	425	427	565	632	672	1474	3472	6658	117	202	233	296	
64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0	62.0	62.0	62.0	62.0	
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30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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3	551	

conserved hypothetical protein AF2411 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: D69551
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodsor
R;Klenk, H.P.; Clayton, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness; E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Wosse, C.R.; Venter, J.C.
A;Tile: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D65551
A;Accession: D65551
A;Residues; 1-363 <KLE>
A;Residues: 1-363 <KLE>
A;Residues: 1-363 <KLE>
A;Residues: 1-363 <KLE>
A;Cross-references: GB:AE001109; GB:AE000782; NID:g2689432; PIDN:AAB91255.1; PID:g265068

ö Gaps Score 36; DB 2; Length 363; Pred. No. 9.1; 2; Mismatches 3; Indels 72.0%; Query Match 72.0 Best Local Similarity 54.5 Matches 6; Conservative

1 EEVVPXGXDYS 11 ઠે

120 ENIVPYGIDFS 130 g

G-O-methylguanine-DNA methyltransferase [imported] - Agrobacterium tumefaciens (strain C C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Date: 11-Uan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C; Accession AG3104.
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L R; Wood, D.W.; Setubal, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2332, 2001
A; Atthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

Bter, E.W.
A;Tile: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Tile: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Refatus: preliminary
A;Status: preliminary
A;Rolente type: DNA
A;Readdues: 1-290 <XXIR>
A;Readdues: 1-290 <XXIR>
A;Readdues: GB:AE008689; PIDN:AAL45253.1; PID:G17742937; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)

A;Gene: ada A;Map position: linear chromosome

|:: | | || 9 EDITPIGSDY 18

1 EEVVPXGXDY 10

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RESULT 7

42455

V1 protein - tobacco yellow dwarf virus (strain Australia)

C;Species: tobacco yellow dwarf virus
C;Species: tobacco yellow dwarf virus
C;Species: 15-dan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Accession: A42452
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
A;Triole: The nucleotide sequence of the infectious cloned DNA component of tobacco yellow A;Reference number: A42452
A;Accession: A42452
A;Accession: A42452
A;Molecule type: DNA
A;Residues: 1-102 <MOR>
disease resistance protein rpp8 [similarity] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cross)
C;Species: O2-Unr-2000 #sequence_revision 02-Unr-2000 #text_change 21-Jul-2000
C;Accession: Unr-88899
R;McDowell, U.M.; Dhandaydham, M.; Long, T.A.; Aarts, M.G.; Goff, S.; Holub, E.B.; Dang Plant Call 10, 1861-1874, 1998
A;Title: Intragenic recombination and diversifying selection contribute to the evolution A;Reference number: 224999; MUID:99030193; PMID:9811794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A/Gene: rpp8
A/Introns: 293/1; 342/1
C.Function: Susceptible allele of a gene that promotes resistance to Peronospora par
A/Description: susceptible allele of a gene that promotes resistance to Peronospora par
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-908 «MCD-
A;Coss-references: EMBL:AF089711; NID:G3901293; PIDN:AAC78631.1; PID:G3901294
A;Experimental source: Columbia
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Local Similarity 60.0%; Pred. No. 40;
local Similarity 60.0%; Pred. No. 40;
los 6; Conservative 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Description: promotes resistance to Peronospora parasitica
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883 EKLVPGGEDY 892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         C)Genetics:
A,Gene: RPP8
A,Introns: 293/1; 342/1
C,Function:
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                                                                                                                                                                                                                                                                                                                                                                                         06-methylguanine-DNA methyltransferase PA2118 [imported] - Agrobacterium tumefaciens (st
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Accession: D98182
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Scince 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C,Accession: P81138
R,Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.; Hickey, B. K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A,Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, B.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Accession: F81138
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A;Molecule type: DNA
A;Residues: 1-587 <TET>
A;Crost-references: GB:AE002446; GB:AE002098; NID:g7226185; PIDN:AAF41356.1; PID:g722618
A;Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           succinate dehydrogenase, flavoprotein chain NMB0950 [imported] - Neisseria meningitidis
C,Species: Neisseria meningitidis
C,Date: 31-Mar_2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: NMB0950
C;Superfamily: fumarate reductase flavoprotein; 3-oxosteroid 1-dehydrogenase homology;
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                                                     Query Match 70.0%; Score 35; DB 2; Length 290; Best Local Similarity 50.0%; Pred. No. 12; Matches 5; Conservative 2; Mismatches 3; Indels
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A,Gene: AGR L_818
A,Map position: linear chromosome
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Best Local Similarity 70.0%;
Matches 7; Conservative
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1 EEVVPXGXDY 10 EDITPIGSDY 18

A,Status: preliminary A,Molecule type: DNA A,Residues: 1-290 <KUR> A, Accession: D98182

RESULT 5 T48898

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unknown protein [imported] - Arabidopsis thaliana
Cispecies Arabidopsis thaliana (mouse-ear cress)
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**Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
**Akture 406, 477-483, 2000
**Akture 406, 477-483, 2000
**Afficie: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
**Afficie: DNA Sequence of both chromosomes of the Cholera pathogen Vibrio cholerae.
**Afficie: DNA Sequence of both chromosomes of the Cholera pathogen Vibrio cholerae.
**Afficie: DNA Sequence of both chromosomes of the Cholera pathogen Vibrio cholerae.
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A;Molecule type: DNA
A;Residues: 1-394 GELI>
A;Cross-references: GB:AE004358; GB:AE003853; NID:g9657566; PIDN:AAF96096.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ferrisiderophore reductase VCA0183 [imported] - Vibrio cholerae (strain N16961 serogroup C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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C;Superfamily: flavohemoglobin; cytochrome-b5 reductase homology; globin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB; AE005173; NID: g11094688; PIDN: AAG29624.1; GSPDB: GN00141
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                                                                                                                     Length 247;
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73
                                                                                                                 Score 34; DB
Pred. No. 16;
1; Mismatches
                                                                                                                 68.0%;
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-257 <STO>
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A;Gene: SMb21444
A;Genome: plasmid
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Gene: F8A12.12
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A,Status: preliminary
A,Status: preliminary
A,Status: preliminary
A,Rotoss-references: GB:AL591985, PIDN:CAC49673.1; PID:g15141160; GSPDB:GN00167
A,Rosidues: 1-247 <KURS
A,Experimental source: strain 1021, megaplaemid pSymb
A,Experimental source: strain 1021, megaplaemid pSymb
B,Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
B,Galibert, F.; Finan, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A,Authors: Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.A; Reference number: A96039; MUID:21368234; PMID:11474104
A,Contents: annotation
C;Genetics:
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1, Residues: 1-156 < DEW>
1, Cross-references: EMBL: 274920; NID: g1420109; PIDN: CAA99201.1; PID: g1420111; MIPS: YOR01
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R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb psymB megaplasmid from the N2-fixing endc A;Reference number: A95842; WUID:21396508; PMID:11481431
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C,Species: Sinorhizobium meliloti
C,Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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1,Alternate names: hypothetical protein 02612; hypothetical protein YOL303.3

1,Species: Saccharomyces cerevisiae

1,Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002

2,Accession: S54619; S66879

3,Ade Haan, M.; Maarse, A.C.; Grivell, L.A.

1,Reference number: S84617

1,Reference number: S84617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yeast (Saccharomyces cerevisiae)
protein O2612; hypothetical protein YOL303.3
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A;Residues: 1-156 <DEH>
A;Cross-references: EMBL:X87331; NID:g1041652; PIDN:CAA60762.1; PID:g829123
A;Cross-references: EMBL:X87331; NID:g1041652; PIDN:CAA60762.1; PID:g829123
A;GE Haan, M.; Grivell, L.A.; Maarse, A.C.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66877
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    4, Cross-references: GB: M81103; NID: 9335283; PIDN: AAA47947.1; PID: 9335284
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                                                                              68.0%; Score 34; DB 2; Length 102; 60.0%; Pred. No. 6.1;
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Pred. No. 9.6;
1; Mismatches
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C;Superfamily: hypothetical protein YOR013w
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                          Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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7 QVVPSGINYS 16
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50 EVMPLGMDY 58
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NiAlternate names: anti-repression trans-activator; art protein; rev protein; trs prote C, Species: simian immunodeficiency virus SIVCpz
A;Note: host Pan troglodytes (chimpanzee)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: S0988 #squence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: S0988 #squence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: S0988 #squence_revision of a chimpanzee lentivirus related to HIV-1.
A;Reference number: S09983; MUD:90259077; PMID:2188136
A;Accession: S09988
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Giacer, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke Staffalser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, F. D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001

A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M., C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thiol peroxidases homolog lmol583 [imported] - Listeria monocytogenes (strain EGD-e) C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #text_change 17-May-2002 C;Date: 27-Nov-2001 #text_change 17-May-2002
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A, Residues: 1-165 <GLA>
A, Cross references: GB:NC_003210; PIDN:CAC99661.1; PID:g16411012; GSPDB:GN00177
A, Experimental source: strain BGD-e
C, Genetics:
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66.7%; Pred. No. 17;
7ative 1; Mismatches
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nes 6; Conservative
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C; Accession: H87660
R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.B.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, N. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A.Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
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C;Species: Drosophila melanogaster
C;Date: 19-Dec-1933 #sequence_revision 25-Apr-1997 #text_change 01-Dec-2000
C;Accession: B49132; A49132
R;Fischer-Vize, J.A.; Rubin, G.M.; Lehmann, R.
Development 116, 985-1000, 1992
A;Aitle: The fat facets gene is required for Drosophila eye and embryo development.
A;Reference number: A49132; MUID:93202020; PMID:1295747
A;Accession: B49132
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A;Molecule type: nucleic acid
A;Residuss: 1-2704, VT., 2707, ANNV' <PI2>
A;Crose references: GB:L04958; NID:g157410; PIDN:AAF01346.1; PID:g6013475
A;Crose: sequence extracted from NCBI backbone (NCBIN:127836, NCBIN:129008, NCBIP:129029)
C;Keywords: alternative splicing
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A;Nolecule type: DNA
A;Residues: 1-433 <STO>
A;Cross-references: GB:AE005673; NID:g13425020; PIDN:AAK25284.1; GSPDB:GN00148
C;Genetics:
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Pred. No. 2.2e+02;
2; Mismatches 3; Indels
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Pred. No. 30;
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54.5%;
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54.5%;
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Best Local Similarity 54.5
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Best Local Similarity 54.5
Matches 6; Conservative
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                                                                                         2 EVVPXGXDY 10
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8 셤 trans-regulatory aplicing protein - simian immunodeficiency virus SIVcpz

RESULT 14 VKLJSI

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STRAIN-CV. Columbia;
Saki M., Iida K., Satuu M., Sakurai T., Akiyama K., Ishida J.,
Saki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
Nakashizaki Y., Shinozaki K.;
Hayashizaki Y., Shinozaki K.;
Shabatica (NOV-2002) to the BMBL/GenBank/DDBJ databases.

I. Submitted (NOV-2002) to the BMBL/GenBank/DDBJ databases.

I. FUNCTION: Potential disease resistance protein.

I. FUNCTION: Potential disease resistance NB-LRR family.

PRESPIRE Subfamily.

I. SIMILARITY: Contains 3 leucine-rich (LRR) repeats.

I. SIMILARITY: Contains 1 NB-ARC domain.

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                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-99087489; PubMed-9872454;
Nakamura Y., Sato S., Asamizu B., Kaneko T., Kotani H., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                              "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned PI and TAC clones.";
DNA Res. 5:297-308(1998).
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EMBL; AK171763; BAG41841.1; -.
INTERPRO; IPRO00767; Disease_resist.
Interpro; IPR001611; LRR.
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SEQUENCE FROM N.A.
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arabidopsis
fusobacteri
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homo sapien
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sus scrofa
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Q8w4j9 arabidopsis
P59584 arabidopsis
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                                                                 June 3, 2004, 11:32:06; Search time 4.86667 Seconds (without alignments) 117.693 Million cell updàtes/sec
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P10941
P11310
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                141681 segs, 52070155 residues
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HMPA V1BCH
FAF DISCME
REV SIVCZ
TPX LISIN
TPX LISIN
YX14 CABEL
ACDM RAT
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TR2M_PANAY
PLAS_DAUCA
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TOLB HAEIN
A10A HUMAN
CHAC HUMAN
HIS9 THEMA
YHAI CRYPA
ACDM HUMAN
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YJ49 ARCFU
HES3 RAT
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                                             - protein search, using sw model
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SYR_STRP3
SYR_STRP8
SYR_STRPY
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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1 EEVVPXGXDYS 11
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Match Length DB
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Perfect score:
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203 1 CTC BACSU P14194 231 1 ARAD ECOLI P08203	231 1	232 1 SCOA HELPY P56006	259 1 OVUH_LYMST P06308	421 1 AMP2_YEAST P38174	421 1 ECB2_HALEL O52250 halomonas	423 1 ECB1_HALEL Q9zeu7 halomonas	430 1 FOLC BACSU Q05865	457 1 Z185 HUMAN 015Z31	469	ALIGNMENTS		STANDARD; PRT; 908 AA.		42, Creat	42, Last	updare)	Probable disease resistance kred-like procein 4.	KPFSLG OK AISCHAGEO OK AISTONIA.9.	Arabidopsis charrana (Mouse-ear cress): Enkarvota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;	ra; eudicotyle	eurosids II; Brassicales; Brassicaceae; Arabidopsis.				STRAIN=CV. COLUMDIA:
												ANDARD;		42	42,	42, Last	resistance	A OK ALSI	ana (Mouse Dlantae: 2	gnoliophyt	sicales; I				18; Dubwod-00
60.0	60.0	0.0	60.09	0.09	0.09	0.09	0.09	60.0	0.09			ST			(Rel	(Rel.	Bease	1156486	Viridi	ta; Ma	; Bras	3702;		N WO	COLUME
30											7 1 APATH	RBL4 ARATH	Q9FJK8;	10-0CT-2003	10-OCT-2003	0-0CT-2003	robable di	FFBL4 OK A	rabidopsis ukarvota:	permatophy	urosids II	NCBI_TaxID=3702;	[]	SEQUENCE FROM N.A.	STRAIN-CV. COLUMDIA;
9. S.	36	37	9 6	40	41	42	43	44	4.5		RESULT 1	· · ·	-						200						350

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STRAIN-CV. Columbia, and cv. Landsberg erecta;
MEDLINE-99030193; PubMed-9811794;
MCDOWell J.M., Dhandsydham M., Long T.A., Aarts M.G.M., Goff S.,
Holub E.B., Dangl J.L.;
"Intragenic recombination and diversifying selection contribute to the evolution of downy mildew resistance at the RPP8 locus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cooley M.B., Pathirana S., Wu H.J., Kachroo P., Klessig D.F., "Members of the Arabidopsis HRT/KPP8 family of resistance genes confer resistance to both viral and comycete pathogens."; plant Cell 12:663-676 (2200)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tabata S.,;
"Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
features of the regions of 3,076,755 bp covered by sixty P1 and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                  ALCENTAIN STANDARD, 1092SY3; Q92SY4; 10-OCT-2003 (Rel. 42, Created) 10-OCT-2003 (Rel. 42, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) 15-MAR-2004 (Rel. 43, Last annotation update) protein 8).
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STRAIN=cv. Columbia;
MEDLINE=22954850; PubMed=14593172;
Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=cv. Columbia;
MEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
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0
                                                                                                                                                                                                                      70.0%; Score 35; DB 1; Length 908; 60.0%; Pred. No. 18; 2; Mismatches 2; Indels
InterPro; IPRULLER; 2.
Pfam; PP00560; LRR; 2.
Pfam; PP00931; NB-ARC; 1.
PRINTS; PR00364; DISRASERSIST.
Plant defense; ATP-bidding; Repeat; Leucine-rich repeat.
Plant defense ATP-bid NB-ARC.
NB-ARC.
                                                                                   10 45 LEUCINE-ZIPPER.
146 459 NB-ARC.
575 599 LRR 1.
600 623 LRR 2.
842 867 LRR 2.
192 199 ATP (POTENTIAL).
908 AA; 104448 MW; 3111991B17239693 CRC64;
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SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS.
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MEDLINE=20271766; PubMed=10810142;
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                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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DNA Res. 7:31-63(2000).
                                                                                                                                                                                                                                                                                        1 EEVVPXGXDY 10
                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702;
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REPEAT
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NP BIND
SEQUENCE
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RPP8_ARATH
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Characha M., Quand H.L. Tripp M., Cangen C.H., Lee J.M., Tothina M.J.

A chan M.M., Tang C.C., Conders C.S., Deng J.M., Actyman S., Antanti Y.,

A chan M.M., Tang C.C., Conders C.S., Deng J.M., Actyman S., Antanati Y.,

A chas O., Chor N., Edit, A., Goldenth A.D., Gurjal M., Hamsen N.F.,

A chan O. M., Tang C.C., Mandiam M. Mannath M., Hamsen N.F.,

A chan J.M., Tang C.C., Mandiam M. Mannath M., Mannen N.F.,

Randya M., Tang W., Walthoon C., Isanu Y.W., Link A.K., Mathiam J.,

Randya M., Tang W., Walthoon C., Isanu W. W., Link A.K., Mathiam J.,

Randya M., Tang W., Walthoon C., Isanu W. W., Link A.K., Mathiam J.,

Randya M., Tang W., Walthoon M., Mallander E.K., Wong C., Yamamura Y.,

Randya M., Tang W., Walthoon M., Mallander E.K., Wong C., Yamamura Y.,

Randya M., Tang W., Walthoon M., Mallander E.K., Wong C., Yamamura Y.,

Randya M., Tang W., Walthoon M., Mallander E.K., Wong C., Yamamura Y.,

Randya M., Malla M., Malland M., Lang M., Malland M., Tang M., Malland M., Tang M.,

Randya M., Malland M., Tang W., Sakurai T., Attyama K., Tahida J.,

Randya M., Malla M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Tang M.,

Randya M., Malland M., Tang M., Sakurai T., Attyama K., Tahida J.,

Randya M., Malland M., Tang M., Sakurai T., Attyama K., Tahida J.,

Randya M., Malland M., Tang M., Sakurai T., Attyama K., Tahida J.,

Randya M., Malland M., Tang M., Sakurai T., Attyama K., Tahida J.,

Randya M., Malland M., Tang M., Sakurai T., Attyama K., Tahida J.,

Randya M., Malland M., Malla M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Malland M., Mal
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RP8H_ARATH
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IDGQL -> VDEQI (in cv. landsberg erecta).

G -> E (in cv. bi-17).

SGK -> RGE (in cv. bi-17).

GKGV -> EKGE (in cv. bi-17).

GKGV -> EKGE (in cv. bi-17).

GKGV -> EKGE (in cv. landsberg erecta).

GKGV -> EKGI (in cv. landsberg erecta).

E -> D (in cv. landsberg erecta).

E -> D (in cv. bi-17).

G -> Q (in cv. bi-17).

G -> Q (in cv. bi-17).

G -> Q (in cv. bi-17).

K -> T (in cv. bi-17).

G -> C (in cv. bi-17).

G -> C (in cv. bi-17).

K -> F (in cv. bi-17).

M -> F (in cv. bi-17).

N -> S (in cv. bi-17).

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C -> S (in cv. Di-17 and cv. Landsberg erecta).

T -> I (in cv. Di-17).

S -> R (in cv. Di-17).

S -> R (in cv. Di-17).

H -> Q (in cv. Di-17).

I -> L (in cv. Landsberg erecta).

K -> N (in cv. Landsberg erecta).

K -> N (in cv. Landsberg erecta).

R -> N (in cv. Landsberg erecta).
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I -> K (in cv. Di-17 and cv. Landsberg
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E197YS -> KITYOE (in cv. Di-17).

A -> V (in cv. Landsberg erecta).

E -> Q (in cv. Landsberg erecta).

DNYLSWQ -> NYKIRWH (in cv. Di-17).

NY IN cv. Landsberg erecta).

WQ -> SH (in cv. Landsberg erecta).
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DSEISTYSLFY -> YSKISAYDLFN (in cv.
                                                                                                              PERMIY PROUSES, LERY, 2.
Pfam; PF00560; LERY, 2.
Pfam; PF00561; NB-ARC; 1.
Plant Gefense, ATP-binding; Repeat; Leucine-rich repeat;
Alternative splicing; Polymorphism.
DOMAIN 10 45 LEUCINE-ZIPPER.
DOMAIN 16 459 LERGINE-ZIPPER.
REPEAT 600 623 LER 1.
REPEAT 842 867 LER 1.
REPEAT 842 867 LER 1.
VARSPLIC 294 308 WEMLLTSRNEGVGIH -> ELLWYIHEALFL
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EMBL; AF234174; AAF36987.1; -.
EMBL; AB025638; BA497426.1; -.
EMBL; AX06314; AAL33592.1; -.
EMBL; AX18862; BAC4349.1; -.
InterPro; IPR001671; Disease_resist.
InterPro; IPR001611; LRR.
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Liplant Cell 10:1874(1998).
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STRANGEV. Landsberge erecta;
MEDLINE-99030193; PubMed=9811794;
MCDOwell J.M., Dhandaydham M., Long T.A., Aarts M.G.M., Goff S.,
Hollub E.B., Dangl J.L.;
"Intragenic recombination and diversifying selection contribute to the evolution of downy mildew resistance at the RPP8 locus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                              Gaps
PRF -> SRFK (in cv. Di-17).
Y -> F (in cv. Di-17).
Y -> F (in cv. indebberg erecta).
C -> S (in cv. Di-17 and cv. Landsberg
                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homologs;

mww=http://niblrrs.ucdavis.edu".

InterPro; IPR000767; Disease_resist.

InterPro; IPR000767; Disease_resist.

InterPro; IPR000161; LRR.

R pfam; PR00560; LRR; 2.

R PFINTS; PR00364; DISEASERSIST.

R PRINTS; PR00364; ATP-binding; Repeat; Leucine-rich repeat.

I DOMAIN 146 459 LRR 1.

I REPEAT 602 625 LRR 1.

T REPEAT 648 669 LRR 2.

T NP_BIND 192 199 ATP (POTENTIAL).

T NP_BIND 192 199 ATP (SBIE9F6SA19A12EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.0%; Score 35; DB 1; Length 910; 60.0%; Pred. No. 18;
                                                                                                                                                                                                                                                    Score 35; DB 1; Length 908;
Pred. No. 18;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Disease resistance protein RPH8A (RPP8 homolog A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 910 AA.
                                                                                                                                                                                    erecta).
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |::|| | ||
883 EKLVPGGEDY 892
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EEVVPXGXDY 10
                  0 9 8 8 0 0 0 4 4 8 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                  558
564
595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RP8H ARATH
P59584;
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ALLOSTERIC DOMAIN

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16-OCT-2001
16-OCT-2001
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HMPA VIBCH
Q9KMY3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y11K TYDVA
P31619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                          Query Match
                                                                        NP_BIND
NP_BIND
METAL
METAL
METAL
                                                                                                                                                                                                                                                                   SEQUENCE
DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
HMPA_VIBCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPATALLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C STRAIN—ATCC 2556.

SX KADAL—ATCC 2556.

XA PARTN=ATCC 2556.

XA PARTN=ATCC 2556.

XA BALTACLATYA A., BATUMAN A., Gardhar G., Los T., Lykidis A., Bhattachartya A., Batuman A., Gardhar W., Grechkin G., Zhu L., A Battaman A., Gardhar W., Grechkin G., Zhu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walumas T., Pusch G., Haselkorn R., Gronne sequence and analysis of the oral bacterium Fusobacterium arcleatum strain ATCC 25586.";

T. Dacteriol. 184.2005-2018(2002)

J. Batteriol. 184.2005-2018(2002)

J. Batteriol. 184.2005-2018(2002)

J. CARALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + CORALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + CORALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + CORALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + CORALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + CORALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + CORALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + CORALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + CORALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + CORALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + CORALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + CORALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + CORALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + CORALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + CORALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + CORALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + CORALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + CORALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + CO(2) + H(2)O = 2 ADP + CO(2) + H(2)O = 2 ADP + CO(2) + H(2)O = 2 ADP + CO(2) + H(2)O = 2 ADP + CO(2) + H(2)O = 2 ADP + CO(2) + H(2)O = 2 ADP + CO(2) + H(2)O = 2 ADP + CO(2) + H(2)O = 2 ADP + CO(2) + H(2)O = 2 ADP + CO(2) + H(2)O = 2 ADP + CO(2) + H(2)O = 2 ADP + CO(2) + H(2)O = 2 ADP + CO(2
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  Gaps
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PERMY PRO2142; MGS; 1.
PERMY PRO2142; PRO0169; CPSASE.
TIGREAMS; TIGRO1169; CPSASE.1; 2.
PROSITE; PSO0866; CPSASE.1; 2.
PROSITE; PSO0867; CPSASE.2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
Arginine biosynthesis; Complete proteome.
Argining; Manganese; Mangane
                                                                                                                                                                                                                                                                                             ZB-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamcyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamcyl-phosphate synthetase ammonia chain).
CARB OR FN0422.
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fusobacterium nucleatum (subsp. nucleatum).
Bacteria, Fusobacteria, Fusobacterales, Fusobacteriaceae;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -! - SIMILARITY: Belongs to the carB family.
                                                                                                                                                                                                                                              PRT; 1058 AA
  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE010554; AAL94625.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAP, MF 01210, -1.
InterPro; IPR006275; CarA L glu.
InterPro; IPR00649; CP86E. L.
InterPro; IPR00549; CP86E. L.
InterPro; IPR005480; CP86E. L. D2.
InterPro; IPR005481; CP86E. L. D3.
InterPro; IPR005481; CP86E. L. D3.
InterPro; IPR005480; CP86E. L. D3.
InterPro; IPR005480; CP88E. L. D3.
Pfam; PF00289; CP888E. L. D3; 1.
Pfam; PF02786; CP888E. L. D3; 1.
Pfam; PF02187; CP888E. L. D3; 1.
     6; Conservative
                                                                                                                                                                                                                                              STANDARD;
                                                                                                        885 EKLVPGGEDY 894
                                                       1 EEVVPXGXDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fusobacterium
                                                                                                                                                                                                                                           CARB FUSNN
QBRG86;
                                                                                                                                                                                             RESULT 4
CARE FUSNN
     Matches
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                                                                                                                                                                                                                                                                                           Gaps
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ATP (POTENTIAL).

ATP (POTENTIAL).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 1 AND 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E., "The nucleotide sequence of the infectious cloned DNA component tobacco yallow dwarf virus reveals features of geminiviruses infecting monocotylednous plants."; virology 187:633-642(1992).
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                                                                                                                                                                                                                              Score 35; DB 1; Length 1058;
Pred. No. 22;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.0%; Score 34; DB 1; Length 102; 60.0%; Pred. No. 3.1; 2; Indels ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 AA; 11178 MW; A40ECF1E0AF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tobacco yellow dwarf virus (strain Australia) (TYDV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; seDNA viruses; Geminiviridae; Mastrevirus
NCBI_TaxID=31599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=92188538; Pubmed=1546458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A42452; A42452.
InterPro; IRR00261; Gemini mov.
Pfan; PP01708; Gemini mov; I.
Hypothetical protein:
SEQUENCE 102 AA; 11178 MW; A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                            70.0%;
                                                                                                                                                                                       117451
                                                                                                                                                                                                                                                                     60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                            190 EIVPNGLNYS 199
                                                                                                                                                                                                                                                                                                                                             2 EVVPXGXDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EVVPXGXDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OVVPSGINYS 16
                                                                                                                                                                                          1058 AA;
                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=E1 TOY N16651 / Serotype O1;
MEDLINE=20460833; PubMed=10952301;
Heidelberg J.E., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Melson K.E., Read T.D., Tettelin H., Richardson D.,
SErmolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T.v. Pleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATUTE 406:477-483 (2000).

-i- DOMAIN: CONSISTS OF TWO DISTINCT DOMAINS; ONE IS A HEME-CONTAINING OXYGEN BINDING DOMAIN IN THE N-TERMINAL REGION AND THE OTHER IS AN FAD-CONTAINING REDUCTASE DOMAIN FOUND IN THE C-TERMINAL REGION.

-i- SIMILARITY: BELONGS TO THE GLOBIN FAMILY. TWO-DOMAIN FLAVOHEMORPOTEINS SUBFAMILY.

-i- SIMILARITY: TO A NUMBER OF FAD/NAD(P) FLAVOPROTEIN OXIDOREDUCTASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).
IRON (HEME PROXIMAL LIGAND)
(BY SIMILARITY).
(BY SIMILARITY).
NADP (RIBOSE PRRT) (BY SIMILARITY)
DDA3490PAE28823A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR00833; FAD_binding_6.
InterPro; IPR00831; FAD_binding_6.
InterPro; IPR00091; FPN cyt_redctse.
InterPro; IPR00091; Globin.
InterPro; IPR001221; Phe_hdroxylase.
Pfam; PR00970; RAD_binding_6; 1.
Pfam; PR00175; NAD_binding_1; 1.
Pfam; PR00175; NAD_binding_1; 1.
PRINTS; PR00311; PFNCR.
PRINTS; PR00311; PFNCR.
PROSTITS; PS01033; GLOBIN; 1.
Oxidoreductase; NADP; Heme; Flavoprotein; FAD; Iron transport;
   Flavohemoprotein (Hemoglobin-like protein) (Flavohemoglobin).
                                                                                   Bacteria; Protechateria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio. Vibrionaceae; Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio. Vibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRON (HEME DISTAL LIGAND)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oxygen transport; Transport; Complete proteome.
DOMAIN 1 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE004358; AAF96096.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394 AA; 44191 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P39662; 1CQX.
FIGR; VCA0183; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
                               HMP OR VCA0183.
Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23
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RX GTRATH=Bergateley;

RX Adams M.D., Celnikaeley;

RX Adams M.D., Celnikaeley;

RAGENTH=Bergaeley;

RAGENTH=Bergaeley;

RAGENTH EACH COLLINGENERS E. Hold R.A., Hoskins R.A., Galle R.F.,

Adamstides D.G., Scheraer S.E., Ili P.W., Hoskins R.A., Galle R.F.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RAGENT R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RAGENT R.A., Lewis S.E., Richards S., Ashburner M., Feiffer B.D.,

RAGENT R.A., Bernos P.V., Barael R.G., Nalson C.R., Miklos G.L.G.,

RAGENT R.M., Bernos P.V., Bernam B.P., Bandari D., Belahakov S.,

RAGENT R.M., Bernos P.V., Bernam B.P., Bandari D., Bolahakov S.,

RAGENT R.M., Cawley D.A., Buller H., Cadleu E., Center A., Chandra I.,

RAGENTS R.A., Cownes M., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RAGENT R.J., Evangalista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RAGIOGEN R., Gornell J.H., Garyles P., Houck J.,

RAGIOGEN R., Gornell J.H., Garyles P., Houck J.,

RAGIOGEN R., Gornell J.H., Garyles P., Houck J.,

RAGIOGEN R., Gornell J.H., Garyles S., Plaischmann W.,

RAGIOGEN R., Gornell J.H., Garyles S., Plaischmann W.,

RAGIOGEN R., Gornell J.H., Garyles S., Mulp D., Lais S.,

RAGIOGEN R., Mouston K.A., Howland T.U., Merim D.A., Kerlin R.A.,

RAGIOGEN R., Matchin R., Kalush R., Miron J.H., In S., Milp D., Lai Z.,

Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Lidang Y., Lin X.,

RAGIOGEN R., Mount S.M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,

RAGEN R., Mount S.M., Nalson R., Naring S., Pollard J., Weatseeler F., Shen H.,

RAGEN R., Raden R., S., Pan S., Pollard J., Weatseeler F., Shen H.,

RAGEN R., Mount S.M., Wooder R., Wang A.H., Wang X., Yells S., Rang R., Shen R.,

RAGEN R., Rader R., Rodira R., Wang R., Sun S.,

RAGEN R., Rader R., Rodira R., Wang R., Sun S.,

RAGEN R., Rader R., Rodira R., Wang R., Sun S.,

RAGEN R., Rader R., Rodira R., Salpeton M., Strong R., Santh H.,

RAGEN R., Rader R., Rodira R., Rodira R., Rodira R., Salue B.C., Siden-Kiamos I., Simpson M., Strong R., Salue S., Salue R., Salue R.
MEDLINE-22426069; PubMed-1237572;
Mister S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Mister S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
Lewis S.E.;
 TISSUE-Eye imaginal disk;
MEDLINE-93202020; PubMed-1295747;
Fischer-Vize J.A., Rubin G.M., Lehmann R.;
"The fat facets gene is required for Drosophila eye and embryo
 SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), AND TISSUE SPECIFICITY
 development.";
Development 116:985-1000(1992)
 SEQUENCE FROM N.A.
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Gaps

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3; Indels

Conservative

2 EVVPXGXDY 10

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194 EVTPEGSDY

2778 AA.

STANDARD;

FAF DROME

RESULT 7

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092BC5;
28-FEB-2003
28-FEB-2003
28-FEB-2003
 TPX LISIN
 SIVCZ
 CONFLICT
CONFLICT
SEQUENCE
 VARSPLIC
 Query Match
 P17280;
 Best Loca
Matches
 RESULT 9
TPX LISIN
 REV
 RESULT 8
 SPTTTTT
 g
 44444
 A GO; GO: DUALL

R INTERPRO; IPRO01.5-.,

R PROSTIE; PS00973; UCH 2 1; 1.

DR PROSTIE; PS00973; UCH 2 2; 1.

DR PROSTIE; PS00973; UCH 2 3; 1.

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 IsoId=P55824-3; Sequence=VSP_005269; TISSUE SPECITCITY: Eye disks and ovarites. DEVELOPMENTAL STACE: Expressed both maternally and zygotically. SIMILARITY: Belongs to peptidase family C19.
Annotation of the Drosophila melanogaster euchromatic genome: a
 CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)0
 ubiquitin + a thiol.

LATERNATIVE PRODUCTS

BVent=Alternative splicing; Named isoforms=3;
Comment=Experimental confirmation may be lacking for some
 GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0007349; P:cellularization; IMP.
GO; GO:0007455; P:embryonic morphogenesis; IMP.
GO; GO:0007455; P:eye morphogenesis; IMP.
GO; GO:0007455; P:mystery cell fate differentiation (sensu Dr.
GO; GO:00016579; P:mystery cell fate differentiation (sensu Dr.
GO; GO:00016579; P:mystery delbiquitination; IDA.
GO; GO:0016579; P:pysterin deubiquitination; IDA.
InterPro; IPR001394; Peptidase_C19.
 systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
 1089-2778 FROM N.A. (ISOFORM 1)
 IsoId=P55824-2; Sequence=VSP_005270;
 IsoId=P55824-1; Sequence=Displayed;
 EMBL, L04959; AAF01345.1; -.
EMBL, L04958; AAF01346.1; -.
EMBL, L04960; AAF01347.1; -.
EMBL, AE003779; AAF57198.1; -.
EMBL, AR003779; AAF57198.1; -.
EMBL, AF19577; AAF3657.1; -.
EMBL, AF19577; AAD38552.1; -.
MEROPS; C19.007; -.
 FBgn0005632; faf.
 soforms;
 FlyBase;
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 Nature 345:358-359/LD9U).

-!- FUNCTION: REV APPEARS TO ACT POST-TRANSCRIPTIONALLY TO RELIEVE
NEGATIVE REPRESSION OF GAG AND ENV PRODUCTION.
-!- SUBCELLIUAR LOGATION: Nuclear; accumulates in the nucleoli.
-!- PTM: Phosphoprotein whose state of phosphorylation is mediated by
a specific serine kinase activity present in the nucleus.
 ASQUENCE FROM N.A.
MEDLINE=90259077; PubMed=2188136;
Huet T., Cheynter R., Meyerhans A., Roelants G., Wain-Hobson S.;
"Genetic organization of a chimpanzee lentivirus related to HIV-1.";
Nature 345:356-359(1990).
 Gaps
 Gaps
 IATAATLEPAGMSELTTMVEKNLIISQENPQAKSSLQ
 EMBL; X52154; CAA36405.1; -.
PIR; S09988; VKLJSI.
HIV; X52154; REV$CPZ.
InterPro; IPR000625; REV_protein.
Pfam; PF00424; REV; 1.
Transcription regulation; AIDS; Phosphorylation; Nuclear protein.
SEQUENCE 124 AA; 13701 MW; FS877DIBDF65A7B2 CRC64;
 01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FBB-2003 (Rel. 41, Last amnotation update)
REV protein (Anti-repression transactivator protein) (ART/TRS).
 ;
0
 ..
0
 Score 34; DB 1; Length 2778;
Pred. No. 97;
2; Mismatches 3; Indel8
 Score 33; DB 1; Length 124;
Pred. No. 6.2;
1; Mismatches 3; Indels
 234 234 E -> D (IÑ REF. 1).
2725 2725 T -> S (IN REF. 1; AAF01345)
2778 AA; 311139 MW; FFB90438BA53A02B CRC64;
 Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11723,
 SQRQQL (in isoform 2)
/FTId=VSP 005270.
E -> D (IN REF. 1).
T -> S (IN REF. 1; AA.
005269
 (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
 124 AA.
 66.0%;
60.0%;
 / Match 68.0%;
Local Similarity 54.5%;
Les 6; Conservative 2
 Query Match
Best Local Similarity bure
6; Conservative
 1394 EVIVPDGODFS 1404
 STANDARD;
 STANDARD;
 1 EEVVPXGXDYS 11
 107 ETVPAGGNYS 116
 2 EVVPXGXDYS 11
 2742
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EMBL; AL591979; CAC99661.1; -.
PIR; AG1272; AG1272.
Listilist; LMO01583; -.
HAMAP; MF 00269; -; 1.
InterPro; IPR000866; AbpC-TSA.
Plan; PF00578; AbpC-TSA.
PROSITE; PS001265; TPX.
 STANDARD;
 Nature 368:32-38(1994).
 144 EVVPEGSDH 152
 2 EVVPXGXDY 10
 Local Similarity
 SEQUENCE FROM N.A.
 Wohldman P.;
 YK14 CAEEL
P34338;
 Query Match
 elegans.
 Best Loc
Matches
 YK14_CAEEL
 RESULT 11
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 U. SEQUENCE FROM N.A.

C. STRAIN=CLIP 11262 / Serovar 6a;

C. STRAIN=CLIP 11262 / Serovar 7.

C. STRAIN=CLIP 11262 / Serovar 6a;

C. STRAIN=CLIP 11262 / Serovar 7.

C. STRAIN=CLIP 11262 / Serovar 6a;

C. STRAIN=CLI
 Gapa
 ;
0
 STRAIN=EGD-e / Serovar 1/2a;
MEDLINE=21537279; PubMed=11679669;
Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Glaser P., Pernde P., Blocker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
 Antioxidant, Oxidoreductase, Peroxidase, Complete proteome.
SEQUENCE 165 AA; 18162 MW; 77705B7CD8BC8F4D CRC64;
 66.0%; Score 33; DB 1; Length 165; 66.7%; Pred. No. 8.4;
 Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
NCBI_TaxID=1642;
 Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
NCBI_TaxID=1639;
 2; Indels
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable thiol peroxidase (EC 1.11.1.-).
 165 AA
 1; Mismatches
Probable thiol peroxidase (EC 1.11.1.-).
 EMBL; AL596169; CAC96856.1; -.
PIR; AH1635; AH1635.
Listilist; LIN01625; -.
HAMAP; MF 00269; -; 1.
InterPro; IPR000866; AhpC-TSA.
InterPro; IPR0008785; TPX.
Pfam: PP00578; AhpC-TSA; 1.
PROSITE; PS01265; TPX.
 66.78;
 6; Conservative
 STANDARD;
 Listeria monocytogenes.
 144 EVVPEGSDH 152
 2 EVVPXGXDY 10
 Best Local Similarity
Matches 6; Conserv
 SEQUENCE FROM N.A.
 Listeria innocua.
 TPX LISMO
 Query Match
 TPX_LISMO
 RESULT 10
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 Gaps
 Coulson A.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O., Entian K.-D., Fabin H., Garcia-del Portillo F., Garrido P., Gantido P., Jackson D., Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G., Madueno E., Matlournam A., Mata Vicente J., Ny E., Nedjari H., Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A., Vazguez-Boland J.-A., Voss H., Wehland J., Cossart P., Comparative genomics of Listeria species."; Science 294:849-852(2001).

-I-FUNCTION: Has antioxidant activity. Could remove peroxides or H(2)0(2) (By similarity).
 Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
 STRAIN=Bristol N2;

WIEDLINE=94150718; PubMed=7906398;

WIEDLINE=94150718; PubMed=7906398;

WIEDLINE=94150718; PubMed=7906398;

WIEDLINE=94150718; PubMed Toops To
 ပ
 "2.2 Mb of contiguous nucleotide sequence from chromosome III of
 ..
0
 Antioxidant, Oxidoreductase, Peroxidase, Complete proteome.
SEQUENCE 165 AA; 18133 MW; 77705B7CC46D424D CRC64;
 h similarity 66.7%; Score 33; DB 1; Length 165; Similarity 66.7%; Pred. No. 8.4; 6; Conservative 1; Mismatches 2; Indels
 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein C15H7.4 in chromosome III.
Caenorhabditis elegans.
 327 AA
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 01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acyl-CoA dehydrogense, medium-chain specific, mitochondrial precursor (EC 1.3.99.3) (MCAD).
 CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
 SUBUNIT: Homotetramer.
SUBCELLULAR LOCATION: Mitochondrial matrix.
MISCELLANEOUS: A number of straight-chain acyl-CoA dehydrogenases of different substrate specificities are present in mammalian
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
 101. Chem. 262:10104-10108(1987).
FUNCTION: This enzyme is specific for acyl chain lengths of 4 to
 PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
 MEDISTRE-87280028; PubMed=3611054; Maceubara Y., Kraus J.P., Ozasa H., Glassberg R., Finocchiaro G., Ikeda Y., Mole U., Rosenberg L.E., Tanaka K.; Molecular cloning and nucleotide sequence of cDNA encoding the entire precursor of rat liver medium chain acyl coenzyme A.
 ö
 SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
 Score 33; DB 1; Length 327;
Pred. No. 17;
1; Mismatches 3; Indels
 PIR; S40753; S40753.
Wormbep; C15H7.4; CE00082.
Hypothetical protein.
SEQUENCE 327 AA; 35566 WW; 716BC2BDD2E9607E CRC64;
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 Chem. 262:10104-10108(1987)
 PRT;
 EMBL; Z22173; CAA80126.1; -.
 EMBL; J02791; AAA40670.1; -.
PIR; A28436; DERTCM.
 Query Match 66.0%;
Best Local Similarity 63.6%;
Matches 7; Conservative
 175 KEVVPNGGDKS 185
 STANDARD;
 Rattus norvegicus (Rat).
 1 EEVVPXGXDYS 11
 HSSP, P11310; 1EGD
 COFACTOR: FAD
 dehydrogenase.";
 Biol.
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 STRAIN=SSI-1 / Serctype M3;
MEDLINE=22683278; PubMed=12799345;
Nakagawa I., Kurokawa K., Yamashiita A., Nakata M., Tomiyasu Y.,
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
Hayashi H., Hattori M., Hamada S.;
"Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
large-scale genomic rearrangement in invasive strains and new insights
 ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN
SPECIFIC.
FORMS A HYDROGEN-BOND WITH THE FLAVIN
NGS OF THE FAD COFACTOR (BY SIMILARITY)
NASE (BY SIMILARITY).
2CF076F8C919BDE8 CRC64;
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS)
ARGS OR SPYM3_1809 OR SPS1807.
 STRAIN=MGAS315 / Serotype M3;
MEDIINE=22133808; PubMed=12122206;
Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Barnes J.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlitevert P.M., Musser J.M.,
"Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
 Gaps
 into phage evolution.";

Genome Res. 13:1042-1055(2003).

Genome Res. 13:1042-1055(2003).

-1- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +

diphosphate + L-arginyl-tRNA(Arg).

-1- SUBUNIT: Monomer (By similarity).

-1- SUBCELULIAR LOCATION: Cytoplassmic.

-1- SUBCELULIAR LOCATION: Cytoplassmic.

-1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
 .
0
DR InterPro; IPR006099; Acyl-CoA_dh.

DR InterPro; IPR006090; Acyl-CoA_dh.C.

DR InterPro; IPR006092; Acyl-CoA_dh.M.

DR Ffam; PP02770; Acyl-CoA_dh.N.

DR Pfam; PP02770; Acyl-CoA_dh.N.

DR Pfam; PF02771; Acyl-CoA_dh.N.

DR Pfam; PF02771; Acyl-CoA_dh.N.

DR Pfam; PF02771; Acyl-CoA_dh.N.

NR PROSITE; PS00072; Acyl-CoA_dh.N.

NR PROSITE; PS00073; Acyl-CoA_DH.2; 1.

NR PROSITE; PS00073; Acyl-CoA_DH.2; 1.

NR PROSITE; PS00071; Acyl-CoA_DH.2; 1.

NR Prochondrion; Transit peptide.

NR Cochondrion; Transit peptide.

NR CCHAIN
 Score 33; DB 1; Length 421;
Pred. No. 22;
2; Mismatches 3; Indels
 Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002)
 563 AA.
 46555 MW;
 66.08;
 50.08;
 Local Similarity 50.0
 193
 1 EEVVPXGXDY 10
 58 EEIIPVAPDY 67
 401
 421 AA;
 NCBI_TaxID=198466;
 SEQUENCE FROM N.A.
 SECUENCE FROM N.A.
 193
 401
 STRP3
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 Query Match
 RESULT 13
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us-09-909-164-45.rsp

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 EMBL; AE014171; AAM80416.1; -.

R EMBL; AP001514; BAC64902.1; -.

R HAMAPP, MF 00123; -; 1.

R InterPro; IPR001278; Arg_tRNA-synt_1d.

R InterPro; IPR001518; N.

R InterPro; IPR001519; TRNA-synt_1d.

R InterPro; IPR001519; TRNA-synt_1d.

R Pfam; PF00750; TRNA-synt_1d; 1.

R Pfam; PF00770; TRNA-synt_1d; 1.

R Pf00770; TRNA-synt_1d; 1.

R Pf00770; TRNA-synt_1d; 1.

R Pf0770; TRNA-synt_1d; 1.

R Pf00770; TRNA-synt_1d; 1.

R Pf00770; TR
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Arginyl--FNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
ARGS OR SPYM18_2183.
 0; Gaps
 Query Match 66.0%; Score 33; DB 1; Length 563; Best Local Similarity 45.5%; Pred. No. 30; Matches 5; Conservative 3; Mismatches 3; Indels
 Streptococcus pyogenes (serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 SITE 121 131 "HIGH" REGION.
SEQUENCE 563 AA; 63134 MW; B0B7DEC31A9DCF63 CRC64;
 PRT; 563 AA.
 EMBL; AE010119; AAL98627.1; -.
HAMAP; MF_00123; -; 1.
 STANDARD;
 |:|: | ||:
94 EQVITAGSDYA 104
 1 EEVVPXGXDYS 11
 Complete proteome.
SITE 121
 Streptococcus.
NCBI_TaxID=186103;
 STRPB
 RESULT 14
SYR STRRB
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REALMESTRIO / ATCC 700294 / Serotype M1;

REALMESTRIO / ATCC 700294 / Serotype M1;

REALMESTRIO / ATCC 700294 / Serotype M1;

REALMESTRIO / ATCC 700294 / Serotype M1;

RETERETE J1926484; PubMed=112956296;

REALMESTRIO / ATCC 700294 / Serotype M1;

RETERETE J1026484; PubMed=11296296;

REALMESTRIO / Serate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,

RA YAN X., Clifton S.W., Roe B.A., McLaughlin R.,

RA YAN X., Clifton S.W., Roe B.A., McLaughlin R.,

RI "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";

RE Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

C. - CATALYTC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +

C. - CATALYTC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +

C. - SUBCELLULAR LOCATION: Cytoplasmic.

C. - SUBCELLULAR LOCATI
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InterPro; IPR001278; Arg_tRNA-synt_lc.
InterPro; IPR005148; N.
InterPro; IPR00590; tRNA-synt_ld_C.
InterPro; IPR001412; tRNA-synt_ld_C.
InterPro; IPR001412; tRNA-synt_ld_C.
Pfam; PR00750; tRNA-synt_ld; 1.
Pfam; PR00756; tRNA-synt_ld; 1.
PRINTS; PR01038; TRNASYNTHARG.
TIGRRAMS; ITTR000456; args, 1.
PR0571E; P800178; AA TRNA, LIGARE I; FALSE NEG.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 SYR STRPY STANDARD; PRT; 563 AA.

Q957E5;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Arginyl-RNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS)
ARGS OR SPY21S1.
 Score 33; DB 1; Length 563;
Pred. No. 30;
3; Mismatches 3; Indels
 Streptococcus pyogenes.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
 SITE 121 131 "HIGH" REGION.
SEQUENCE 563 AA; 63134 MW; FECAF176A68D8B5B CRC64;
 ENBL; AE006633; AAK34788.1; -.
HSSP; Q05506; 1BS2.
ILAEPPO: IPRO01278; -; 1.
ILLEPPO: IPRO01278; Arg_tRNA-synt_1C.
ILLEPPO: IPRO03909; LRNA-synt 1d.C.
ILLEPPO: IPRO03909; LRNA-synt 1d.C.
ILLEPPO: IPRO01412; LRNA-synt_I.
Pfam; PP03485; N-Arg; 1.
Pfam; PP03485; N-Arg; 1.
Pfam; PP05746; TRNA-synt_1d; 1.
Pfam; PR05746; TRNA-synt_1dc; 1.
PRINTS; PR01038; TRNA-SYNT_1dG; 1.
PRINTS; PR01038; TRNASYNTIAGC; 1.
 Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative 3
 |:|:
94 EQVITAGSDYA 104
 1 EEVVPXGXDYS 11
 Complete proteome.
 NCBI_TaxID=1314;
 RESULT 15
SYR STRPY
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PROSITE; PS00178; AA TRNA LIGASE I; FALSE NEG.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
Complete proteome.
31.78
12.1
SEQUENCE 563 AA; 63120 MW; ROF2CAC28D03B613 CRC64;
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0; Gaps Query Match 66.0%; Score 33; DB 1; Length 563; Best Local Similarity 45.5%; Pred. No. 30; Matches 5; Conservative 3; Mismatches 3; Indels

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1 EEVVPXGXDYS 11 |:|:| | ||: 94 EQVITAGSDYA 104

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Search completed: June 3, 2004, 11:49:56 Job time: 5.86667 secs

Q89788 arabidopsis Q8936 bacteriopha Q8936 bacteriopha Q92066 thisolum m Q9c6j0 arabidopsis gar16 correbacte Q82dt streptcomyce Q9495 sulfolows Q8tx62 methanopyru Q82ag9 yersinia pe Q8519 streptcococc Q40129 lycopersico Q8xpa clostridium e Q8tpy corrynebacte Q8xpa clostridium e Q8tpy corrynebacte Q8xpa clostridium e Q8xpa musuulu Q8bts mus musculu Q8bts muscul

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Deline 20550857; PubMed=12663827; PubMed=12663827; Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R., Paulsen I.T., Banerjei L., Myers G.S.A., Haidelberg J.F., Read T.D., Fours D.E., Eisen J.A., Gill S.R., Haidelberg J.F., Daugherty S., DeBoy R.J., Umayam L., Brinkac L., Beanan M., Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W., Vamathavan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H., Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.; Role of mobile DNA in the evolution of vancomycin-resistant Enterococcus faccalis ";
Science 299:2071-2074(2003).
EMBL, AB016956; AA082828.1; -.
 Enterococcus faccalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI TaxID=1351;
 16127 MW; 555799BF1E47D34E CRC64;
 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
10-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Large conductance mechanosensitive channel protein.
MSCL OR BF3152.
 DB 16;
 GO; GO:0016020; C:membrane; IEA.
GO; GO:0006216; F:ion channel activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR001185; MS channel.
Pfam; PF01741; MsCL; 1.
Propon; PD007253; MS Channel;
IIGRPAMS; TIGR00220; mscL; 1.
 149 AA
 ALIGNMENTS
 74.0%; Score 37;
 Q92U66
Q9C6J0
Q8NR16
Q82DT4
Q9A382
Q96YH5
Q8TX62
Q8ZAQ9
 083NN9
083G59
 Q40129
Q8XPA8
Q8FPY9
 QBKL43
Q7VGY0
 QBBTX4
QBBK35
 Q8XZL5
Q9DDJ4
 Q8E5L9
 Q8VD18
 [1]
SEQUENCE FROM N.A.
STRAIN=V583 / ATCC 700802;
 PRELIMINARY;
 149 AA;
 Complete proteome. SEQUENCE 149 AA;
Q82ZB4
 RESULT 1
 Q8EEV7 oceanobacil
Q8EEV7 oceanobacil
Q946j7 andrographi
Q86i03 bos taurus
Q81031 bos taurus
Q81031 bos taurus
Q81031 bos taurus
Q81031 bos taurus
Q81031 bos taurus
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Q81031 bos taurus
Q81031 bos taurus
Q81039 bos taurus
Q81030 agrobacteri
Q81030 agrobacteri
Q81030 agrobacteri
Q81030 agrobacteri
Q91208 neisseria m
Q91208 neisseria m
 Q82zb4 enterococcu
O52367 rhizobium t
 June 3, 2004, 11:35:06; Search time 29.8667 Seconds (without alignments) 116.206 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 1017041
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1017041 seqs, 315518202 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - protein search, using sw model
 052367
08ESV7
030260
094637
08DIH0
09XST4
081033
000404
0867A5
0867A5
 Q9UEE9
Q9JZP8
Q9VI90
 sp_organelle:*
sp_organelle:*
sp_phage:*
sp_rodent:*
sp_rodent:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
 Q82ZB4
 Gapop 10.0 , Gapext 0.5
 sp_archea:*
sp_bacteria:*
sp_fungl:*
sp_fungl:*
sp_invertebrate:*
sp_mammal:*
 seq length: 0
seq length: 2000000000
 US-09-909-164-45
50
1 EEVVPXGXDYS 11
 Length DB
 SPIREMBL 25:*
 BLOSUM62
 Query
Match 1
 Score
 Scoring table:
 Title:
Perfect score:
 Minimum DB
Maximum DB
 OM protein
 Database :
 Sequence:
 Searched:
 Run on:
 Result
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Length 149;

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Nucleic Acids Res. 30:3927-3935(2002)
 PRELIMINARY;
 120 ENIVPYGIDFS 130
 PRELIMINARY;
 1 EEVVPXGXDYS 11
 189 ЕДІЎРНСІЎЎ 198
 Archaeoglobus fulgidus.
 1 EEVVPXGXDY 10
 Best Local Similarity
Matches 6, Conserv
 Local Similarity
 SEQUENCE FROM N.A.
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 EMBL, AF036920, AAC04779.1, -.
GO; GO:00046821; C:extrachromosomal DNA; IEA.
GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0008270; F:zinc_ion_binding; IEA.
 SEQUENCE FROM N.A.
STRAINS-HTEBA1 / DSM 14371 / JCM 11309;
STRAINS-HTEBA1 / DSM 14371 / JCM 11309;
MEDLINE-22220767; PubMed=12235576;
Takami H., Takaki Y., Uchiyama 1.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments.";
 Rosenblueth M. Hynes M.F., Martinez-Romero E.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!-COPACTOR: ZINC (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE PAMILY.
 Gaps
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 Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
NCBL_TaxID=182710;
 Plasmid pRtrCFN299a.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Rhizobium/Agrobacterium group, Rhizobium.
NCBI_TaxID=398;
 72.0%; Score 36; DB 2; Length 298; 50.0%; Pred. No. 19;
 2; Indels
 Indels
 298 AA; 31092 MW; 49B2F8117C33AE87 CRC64;
 01-UUN-1998 (TrEMBLrel. 06, Created)
01-UUN-1998 (TrEMBLrel. 06, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Aryl-alfochol dehydrogenase homolog (Fragment).
 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 InterPro; IFRO0238; AbH zinc.
InterPro; IPRO0238; AbH zinc.
InterPro; IPRO02085; AbH zinc.
InterPro; IPRO02085; AbH zinc.
InterPro; IPRO02085; NaD BS.
PROSITE; PS00059; ĀDH ZINC; 1.
PROSITE; PS00059; ĀDH ZINC; 1.
MORTAL-binding; Oxidotedtase; Zinc; Plasmid.
SQŪCENCE 298 AA; 31092 MW; 4982F8117C33AB
 319 AA
 298 AA
 Pred. No. 5.2;
); Mismatches
 3; Mismatches
 01-MAR-2003 (TrEMBLrel. 23, Created)
 PRT;
 PRT;
 Hypothetical conserved protein.
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 Best Local Similarity 70.0%;
Matches 7; Conservative
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Best Local Similarity 50...
5, Conservative
 PRELIMINARY;
 PRELIMINARY;
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250 EIIPEGADFS 259
 113 EEVVPTSEDY 122
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 2 EVVPXGXDYS 11
 1 BEVVPXGXDY
 SEQUENCE FROM N.A.
 Rhizobium tropici
 OSESV7
 XYLB1.
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QBESV7
 RESULT 2
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 "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
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 01-DEC-2001 (TrEMBLrel. 19, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
3-hydroxy-3-methylglutaryl-coenzyme A reductase (EC 1.1.1.34).
HMGR1.
 ö
 72.0%; Score 36; DB 17; Length 363; 54.5%; Pred. No. 24; 3; Indels iive 2; Mismatches 3; Indels
 16; Length 319;
 Indels
EMBL; AP004594; BAC12465.1; -.
InterPro; IPR001279; Blactmase-like.
Pfan, PF00753; Jactamase B; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 319 AA; 35617 MW; 3BDAE4BF13E79E37 CRC64;
 InterPro, IPRO02103; Bac_luciferase.
Pfam, PR00296; bac_luciferase; I.
Hypothetical protein; Complete proteome.
BEQUENCE 363 AA; 41736 MW; 0E976EAE788F4803 CRC64;
 Archaea; Euryarchãeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein AF2411.
 ..
N
 h Score 36; DB Similarity 60.0%; Pred. No. 20; 6; Conservative 2; Mismatches
 PRT;
 Nature 390.364-370(1997).
EMBL; AE001109; AAE91255.1; -.
PIR; D69551; D69551.
 6; Conservative
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Complete proteome.
SEQUENCE 1044 AA; 113205 WW; 00E9C13F0F636D2F CRC64;
 Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
 Local Similarity 63.6%;
tes 7; Conservative
 PRELIMINARY;
 PRELIMINARY;
 843 EEVLPNGIGYS 853
 1 EEVVPXGXDYS 11
 1 EEVVPXGXDYS 11
 |: || | :||
EDYVPSGGEYS 26
 Canis familiaris (Dog)
 Bovidae, Bovinae, Bos.
 NCBI_TaxID=9615;
 NCBI_TaxID=9913;
 16
 Query Match
 Q9XST4
Q9XST4;
 Q8I033
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Matches
 RESULT 7
 RESULT 8
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 Exequence From No. 1.

A Krishnan S., Banderjee N.S.;

I "3-hydroxy-3-methylglutaryl coenzyme A reductase gene from "3-hydroxy-3-methylglutaryl coenzyme A reductase gene from Andrographis panicultata.";

Examitted (NoV-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; A2389879; AAL28015.2; -

R GO; GO:0004420; F:hydroxymethylglutaryl-CoA reductase (NADPH). . ; IEA.

R GO; GO:00016491; F:cxidoreductase activity; IEA.

R GO; GO:00016491; F:cxidoreductase activity; IEA.

R GO; GO:0005629; P:hipid metabolism; IEA.

R GO; GO:0005629; P:hipid metabolism; IEA.

InterPro; IPR0092029; HMG_CoA_NAD_bind.

InterPro; IPR0092029; HMG_CoA_NAD_bind.

InterPro; IPR0092029; HMG_CoA_NAD_bind.

InterPro; IPR0092029; HMG_CoA_NAD_bind.
 ö
Andrographis paniculata.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Lamiales; Acanthaceae; Acanthoideae; Ruellieae;
Andrographinae; Andrographis.
NCBI_TaxID=175694;
 Gaps
 STRAIN=BP-1;

MEDLINE-2225144; PubMed=12240834;

MEDLINE-2225144; PubMed=12240834;

Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,

Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,

Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N.,

Kiyokawa C., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

"Complete genome structure of the thermophilic cyanobacterium

Thermosynechococcus elongatus BP-1.";
 ô
 72.0%; Score 36; DB 10; Length 595; 70.0%; Pred. No. 42; tive 0; Mismatches 3; Indels
 Syne-chococcus elongatus (Thermosynechococcus elongatus).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
 595 AA; 63268 MW; 19A3EA572F67AB2E CRC64;
 OSDIHO;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Multidrug efflux transporter.
 InterPro; IPR000554; HWG_COA_R NADP.
InterPro; IPR009029; HWG_COA_Rub_bind.
Pfam, PF00368; HWG-COA_Rub_bind.
PRINTS; PR0071; HWGCOARDTASE.
TIGRFAMS; TIGR00533; HWG COA_REDUCTASE_1;
PR051TE; PS00185; HWG COA_REDUCTASE_2;
PR051TE; PS0192; HWG_COA_REDUCTASE_3; 1.
PR051TE; PS0065; HWG_COA_REDUCTASE_3; 1.
PR051TE; PS0065; HWG_COA_REDUCTASE_4; 1.
Oxidoreductase.
SEQUENCE 595 AA; 63268 WW; 19A3EA572F67A
 DNA Res. 9:123-130(2002).

EMBL, APROS14; BACC9170.1; -

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0005215; F:transporter activity; IEA.

GO; GO:0005215; F:transport; IEA.

InterPro; IPR001036; Acfflvin_res.

InterPro; IPR004764; HAEI.
 PRT; 1044 AA.
 Pfam; PF00873; ACR tran; 1.
PRINTS; PR00702; ACRIFLAVINRP.
TIGRFAMs; TIGR00915; 2A0602; 1.
 Query Match 72.0
Best Local Similarity 70.0
Matches 7; Conservative
 PRELIMINARY;
 2 EVVPXGXDYS 11
 15 EVAPPGHĎÝS 24
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 QBDIHO
 RESULT 6
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 TISSUB=Thyroid;
MEDLINE=20422104; PubMed=10964405;
MEDLINE=20422104; PubMed=10964405;
MEDLINE=20422104; PubMed=10964405;
Christophe D., Pouillon V., Christophe-Hobertus C.,
Christophe D.;
Method for the large-scale cloning of nuclear proteins and nuclear targeting sequences on a functional basis.";
Anal. Biochem. 284:231-239(2000).
EMBL; AJ388531; CAB46833.1; -.

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SEQÜENCE 78 AA, 8895 MW, B62486313555FBAI CRC64;
 Gaps
 Gaps
 Gaps
 Q81033;
01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Human-type bcnt protein.
Base taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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72.0%; Score 36; DB 16; Length 1044; 63.6%; Pred. No. 79; 3; Indels C
 Query Match 70.0%; Score 35; DB 6; Length 175; Best Local Similarity 54.5%; Pred. No. 17; Matches 6; Conservative 2; Mismatches 3; Indels
 Score 35; DB 6; Length 78; Pred. No. 6.8; 3; Indels 2; Mismatches 3; Indels
 SEQUENCE FROM N.A.
STRAIN=Jersey;
Iwashita S., Itch T.,
"A LINE-mediated gene diversity.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB081003; BAC11552.1;
SEQUENCE 175 AA; 19529 WW; CE7283CB98393BE
 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 78 AA
 175 AA
 PRT;
 PRT;
 P97 homologous protein (Fragment)
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MEDITNE=21608550; PubMed=11743193; Monks D.E., Kitajima J.P., Nood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okuta V.K., Zhou Y., Chen L., Wood G.E., Almeda N.F. Jr., Woo L., Chen Y., Paulsen I.T., Essen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Rutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Mester E.W.;
 SEQUENCE FROM N.A.
TISSUELLY.
TISSUELLY.
Ubono S., Kimura J., Kurohmaru M., Fukuta K., Iwashita S.;
"Gene organization of the chevrotain bont whose paralogue in
ruminantia includes an endonuclease domain of RTE-1 in the protein.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB103377; BACS7061.1; -.
 MEDINE-SIGNOSTI, PubMed=11743194; Miller N., Blanchard M., MEDINE-2160551; PubMed=11743194; Miller N., Blanchard M., Mullin L., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmtel K., Gordon J., Yaudin M., Iartchouk O., Epp A., Liu F., Houmtel K., Allinger M., Dought P., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Ciel C., Sater S.; Cielo C., Slater S.; Alter S.; Agres S., Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";
 01-0TN-2003 (TrEMBLrel. 24, Created)
01-0TN-2003 (TrEMBLrel. 24, Last sequence update)
01-0TN-2003 (TrEMBLrel. 24, Last annotation update)
Human-type Bont (Fragment).
Human-type Bont (Fragment).
Engallus javanicus (Lesser Malay chevrotain).
Eukaryota; Metazoa; Chordata; Carniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Tragullana;
 01-JTN-2002 (TrEMBLrel. 21, Created)
01-JTN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
6-O-methylguanine-DNA methylransferase.
ADA OR ATU4459 OR AGR L 818, (strain CS8 / ATCC 33970).
Bacteria, Protoobacteria, Alphaproteobacteria, Rhizobiales;
Rhizobiacees, Rhizobium/Agrobacterium group; Agrobacterium.
 / Match 70.0%; Score 35; DB 6; Length 281; Local Similarity 54.5%; Pred. No. 29; lndels is 6; Conservative 2; Mismatches 3; Indels
 NON TER 1 1
NON TER 281 281
SEQUENCE 281 AA; 31557 MW; 8133A9BAFF7509A6 CRC64;
 290 AA.
 281 AA.
 Science 294:2317-2323(2001).
 PRELIMINARY;
 PRELIMINARY;
 1 EEVVEXGXDYS 11
 B EDYVPSGGEYS 18
 Tragulidae; Tragulus.
 SEQUENCE FROM N.A.
 NCBI_TaxID=9849;
 Query Match
Q867A5

D Q867A5,

DT Q1-JUN-:

DT Q1-JUN-:

DT Q1-JUN-:

DE Human-ri-

DE Human-ri-

OC Traguliu

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ID 0807J0
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 TISSUE=Placenta;
MEDLINE=97160586; PubMed=9006920;
MEDLINE=97160586; PubMed=9006920;
MeDLINE=97160586; PubMed=9006920;
Takahashi I., Kobayashi M., Oomori A., Ichinose S., Iwanaga T.,
Takahashi I., Hashimoto K., Hattori S., Kaibuchi K., Miyata Y.;
Takahashi I., Hashimoto K., Hattori S., Kaibuchi K., Miyata Y.;
Takahashi I., Hashimoto K., Hattori S., Kaibuchi K., Miyata Y.;
Takahashi I., Hashimoto K., Hattori S., Kaibuchi K., Miyata Y.;
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Takahashi I., Hashimoto K., Hattori S., Kaibuchi K., Miyata Y.,
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Takahashi I., Hashimoto K., Hattori S., Kaibuchi K., Miyata Y.,
Takahashi I., Hashimoto K., Hattori J., Hattori J., Hashimoto K., Hattori J., Hashimoto K., Hattori J., Hashimoto K., Hattori J., Hattori
 Gaps
 Bos taurus (Bovine).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
 Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 70.0%; Score 35; DB 4; Length 217; 54.5%; Pred. No. 22; ive 2; Mismatches 3; Indels
 70.0%; Score 35; DB 6; Length 215; 54.5%; Pred. No. 22; 3; Indels rative 2; Mismatches 3; Indels
 STRAIN=RZPD #750;
Iwashita S., Itoh T., Sezaki M., Oshima K., Hashimoto E. Ritagawawa Y., Takahashi T., Masui T., Hashimoto K.;
"A LINE-mediated gene diversity.";
Submitted (MRAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB081095; BAC15593.1;
NON TER 215
 217 AA; 24061 MW; E404BA2E35497828 CRC64;
 215 215 218 23822 MW; 7287C8B98E9D05C8 CRC64;
 (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
 Last sequence update)
Last annotation update)
 215 AA
 217 AA
 Created)
 PRT;
 O81031 PRELIMINARY; PR
O81031, O1-MAR-2003 (TrEMBLrel. 23, Crea
01-MAR-2003 (TrEMBLrel. 23, Last
H-type bont protein (Fragment)
H-TYPE BONT
 01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-OCT-2002 (TrEMBLrel. 22, P97) homologous protein. Homo sapiens (Human).
 Query Match
Best Local Similarity 54..
6; Conservative
 Query Match
Best Local Similarity 54.5
Matches 6; Conservative
 PRELIMINARY;
 1 REVVPXGXDYS 11
 16 EDYVPSGGEYS 26
 EDYVPSGGEYS 26
 16 EDYVPSGGEYS 26
 1 EEVVPXGXDYS 11
 EEVVPXGXDYS 11
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
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RESULT 10 000404

SEQUENCE

RESULT 11

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Gaps

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NA PROPERTY OF A 
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SEQUENCE FROM N.A.
STRAIN=MCS8 / Serogroup B;
STRAIN=MCS8 / Serogroup B;
STRAIN=MCS8 / Serogroup B;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
Nelson W.C., Gawinn M.L., DeBoy K., Peterson J.D., Hickey E.K.,
Haft D.H., Salaberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Son L.,
Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,
"Complete genome sequence of Neisseria meningitidis serogroup B strain
 MEDLINE-98267221; PubMed-9602175;
Takahashi I., Nobukuni I., Chmori H., Kobayashi M., Tanaka S.,
Chshima K., Okada N., Masui T., Hashimoto K., Iwashita S.;
"Existence of a bovine LINE repetitive insert that appears in the cDNA
of bovine protein BCNT in ruminant, but not in human, genomes.";
Gene 211:387-394(1998).
 Kalnine N. Chen X., Rolfs A., Halleck A., Hines L., Bisenstein S., Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin X., Phelan M., Rarmer A.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AB00928; BAA31867.1; -.

EMBL; BC00991; AAH00991.1; -.

EMBL; BT009819; AAH00991.1; -.

Genew, HGNC:1873; CFDP1.

SEQUENCE 299 AA; 33593 WW; F4A9E928B669451A CRC64;
 Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales, Nelsseriaceae; Nelsseria. NCSI_TaxID=491;
 Score 35; DB 4; Length 299; Pred. No. 32; Mismatches 3; Indels
Eutheria; Primates; Catarrhini; Hominidae; Homo.
 HSSP; P00363; IKF6.
TIGR; NMB0950; -
GO; GO:0015036; Tidisulfide oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR003953; FAD bind2.
InterPro; IPR001327; FAD_Dyr_redox.
 Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Succinate dehydrogenase, flavoprotein subunit.
 587 AA
 â
 Neisseria meningitidis (serogroup
 Sciencé 287:1809-1815(2000).
-1- COFACTOR: FAD (BY SIMILARITY).
EMBL; AEO02446; AAF41356.1; -.
PIR; F81138; F81138.
 70.0%;
 Query Match
Best Local Similarity 54.5
Matches 6; Conservative
 PRELIMINARY;
 1 EEVVPXGXDYS 11
 16 EDYVPSGGEYS 26
 FROM N.A.
 SEQUENCE FROM N.A.
TISSUE=Placenta;
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 SEQUENCE
 NMB0950
 Q9JZP8
 RESULT 15
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 DRAR REPARANTE DE LA CONTRE ö
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 First, Destact; Cintracellular; IEA.

GO; GO:0003908; F:methylated-DNA-[protein]-cysteine S-methylt. . .; IEA.

GO; GO:0003908; F:methylated-DNA-[protein]-cysteine S-methylt. . .; IEA.

GO; GO:0003100; F:transferase activity; IEA.

GO; GO:0005740; F:transferase activity; IEA.

GO; GO:0005281; P:DNA repair; IEA.

GO; GO:000551; P:GO:0055; P:FRAnco.

InterPro; IPR001497; Methyltransf_1.

Pfam; PF00155; HTH AraC; 2.

Pfam; PF00155; Methyltransf_1; 1.
 Gaps
 Gaps
 Human-type Bcnt.
Bos taurus (Bovine).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
BCNT protein (CRANIOFACIAL development protein 1).
BCNT protein (Human)
HOmo saplens (Human)
BLONT CARAINOFACIAL Gevelopment protein 1).
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 70.0%; Score 35; DB 16; Length 290; 50.0%; Pred. No. 31;
 70.0%; Score 35; DB 6; Length 297; 54.5%; Pred. No. 31;
 3; Indels
 SEQUENCE FROM N.A.
TISSUE=Kidney;
INSCRESKidney;
INSCRESKID T.;
A LINE-mediated gene diversity.";
ALINE-mediated Gene diversity.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO81004; BAC11953.1;
SEQUENCE 297 AA; 33354 WW; D4A944BC8740373C CRC64;
 3; Indels
 SMART; SM00342; HTH ARAC; I...
TIGREAMS; TIGR00589; OGU; 1...
PROSITE; PS01124; HTH ARAC FAMILY 2; 1.
MCHYLtransferase; Transferase; Complete proteome.
SEQUENCE 290 AA; 31587 MW; B626592EF519977F CRC64;
 01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
 297 AA
 2; Mismatches
 2; Mismatches
 PRT;
 EMBL, AE009374; AAL45253.1; --
EMBL, AE008340; AAX88982.1; --
PIR, AG3104; AG3104
PIR, D98182; D98182.
 Local Similarity 50.0
les 5; Conservative
 Best Local Similarity 54.5
Matches 6; Conservative
 PRELIMINARY;
 PRELIMINARY;
 1 EEVVPXGXDYS 11
 16 EDYVPSGGEYS 26
 1 EEVVPXGXDY 10
 18
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9 EDITPIGSDY
 Query Match
 Query Match
 Q9UEE9;
 Q8HXY9
 Best Loc
Matches
 RESULT 13
 RESULT 14
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Q8HXY9

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Gaps

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DR InterPro; IPR0013952; FRD/SDH.FAD_BS.

DR InterPro; IPR001120; Pyr.redox.

DR InterPro; IPR004112; Succ DH flav.C.

DR Pfam; PF002910; Succ DH flav.C; 1.

DR PRINTS; PR00411; PRNDFABEL

DR PRINTS; PR00411; PRNDFABEL

DR PROSTER; PS0564; FRD SDH FAD BINDING; 1.

KW FAD; Flavoprotein; Oxidoreductase; Complete protecome.

SQ SEQUENCE 587 AA; 64502 MW; 9581701B08069003 CRC64;

Query Match

Guery Match

Atches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 1 ERVYPXGXDY 10
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Search completed: June 3, 2004, 11:57:34 Job time: 29.8667 secs

366 EvvvPodeby 375

gg

| 26 40 80.0 11 5 ABB80546 Abb80546 Hepatitis Abb80563 Hepatitis Abb80563 Hepatitis Abb80563 Hepatitis S                                                                                                                                                                                                                                                                                                         | ALIGNWENTS RESULT 1 ABB00548 ID ABB80548 standard; peptide; 11 AA.                                                                         | ABB80548, 08-OCT-2002 (fi) Hepatitis C viru Virucide. Synthetic. Key Modified-site Modified-site | "C-termi 023169. 20101P. Brunck having h eating di p; Englie s a pepti ) proteas                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| GenCore version 5.1.6  Copyright (c) 1993 - 2004 Compugen Ltd.  DM protein - protein search, using sw model  Run on: June 3, 2004, 11:31:01; Search time 45.9333 Seconds  (without alignments) 67.664 Million cell updates/sec  Perfect score: 50  Sequence: 1 EEVVPXGXDYS 11  Scoring table: BLOSUM62  Searched: 1586107 seqs, 282547505 residues  Fotal number of hits satisfying chosen parameters: 1586107 | finimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries | 4 2943<br>eqp199<br>eqp199<br>eqp200<br>eqp200<br>eqp200<br>eqp200<br>eqp200<br>eqp200<br>eqp200 | ## 47 94.0   11 5 ABB80548   Abb80548   Hepatitis   2 47 94.0   11 5 ABB80554   Abb80547   Hepatitis   3 47 94.0   11 5 ABB80556   Abb80557   Hepatitis   4 47 94.0   11 5 ABB80551   Abb80557   Hepatitis   5 46 92.0   11 5 ABB80551   Abb80551   Hepatitis   10 46 92.0   11 5 ABB80543   Abb80561   Hepatitis   11 46 92.0   11 5 ABB80543   Abb80561   Hepatitis   12 46 92.0   11 5 ABB80543   Abb80554   Hepatitis   13 46 92.0   11 5 ABB80543   Abb80554   Hepatitis   14 46 92.0   11 5 ABB80549   Abb80554   Hepatitis   15 46 92.0   11 5 ABB80549   Abb80554   Hepatitis   16 41 82.0   11 5 ABB80549   Abb80554   Hepatitis   16 41 82.0   11 5 ABB80549   Abb80554   Hepatitis   18 41 82.0   11 5 ABB80540   Abb80554   Hepatitis   19 41 82.0   11 5 ABB80540   Abb80554   Hepatitis   19 41 82.0   11 5 ABB80540   Abb80554   Hepatitis   19 41 82.0   11 5 ABB80540   Abb80554   Hepatitis   19 41 82.0   11 5 ABB80540   Abb80554   Hepatitis   19 41 82.0   11 5 ABB80540   Abb80554   Hepatitis   22 40 80.0   11 5 ABB80540   Abb80554   Hepatitis   24 40 80.0   11 5 ABB80554   Abb80554   Hepatitis   25 40 80.0   11 5 ABB80555   Abb80555   Hepatitis   26 41 82.0   11 5 ABB80555   Abb80555   Hepatitis   27 40 80.0   11 5 ABB80554   Abb80555   Hepatitis   28 40 80.0   11 5 ABB80554   Abb80556   Hepatitis   29 40 80.0   11 5 ABB80554   Abb80556   Hepatitis   20 41 82.0   11 5 ABB80555   Abb80556   Hepatitis   20 41 82.0   11 5 ABB80555   Abb80556   Hepatitis   21 40 80.0   11 5 ABB80556   Abb80556   Hepatitis   22 40 80.0   11 5 ABB80556   Abb80556   Hepatitis   23 40 80.0   11 5 ABB80556   Abb80556   Hepatitis   24 40 80.0   11 5 ABB80556   Abb80556   Hepatitis   25 40 80.0   11 5 ABB80566   Hepatitis   26 41 82.0   11 5 ABB80566   Hepatitis   27 40 80.0   11 5 ABB80556   Abb80556   Hepatitis   28 40 80.0   11 5 ABB80556   Abb80556   Hepatitis   29 40 80.0   11 5 ABB80566   Abb80566   Hepatitis   20 41 82.0   11 5 ABB80566   Abb80566   Hepatitis   20 41 82.0   11 5 ABB80566   Abb80566   Hepatitis   21 40 80.0   11 5 ABB80566   Abb80566   Abb8 |

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Gaps

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Indels

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Mismatches

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Matches
 RESULT 3
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 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "Norvaly1 carbony1 forming keto-amide linkage with
 ingredient
invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C ^{\circ}
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #27.
 ö
 Length 11;
 1; Indels
 Length 11;
 Score 47; DB 5;
Pred. No. 0.012;
0; Mismatches
 Score 47; DB 5;
Pred. No. 0.012;
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 Location/Qualifiers
 ŦŸ.
 ABB80547 standard; peptide; 11 AA.
 Claim 17; Page 65; 69pp; English.
 0
 Brunck
 94.0%;
90.9%;
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 94.0%;
 (first entry)
 residue 7"
 10; Conservative
 1 EEVVPXGXDYS 11
 EEVVPXGTDYS 11
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39
 Query Match
Best Local Similarity
 Query Match
Best Local Similarity
 Sequence 11 AA;
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002
 Synthetic
 ABB80547;
 virucide
 protease
 Best Loc
Matches
 RESULT 2
ABB80547
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 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 virus
 Gaps
 Hepatitis C virus, HCV, serine protease, inhibitor, alpha-ketoamide,
 Jhepatitis C virus protease inhibitory disorders associated with hepatitis C
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #36.
 ö
 94.0%; Score 47; DB 5; Length 11; 90.9%; Pred. No. 0.012; ive 0; Mismatches 1; Indels
 /note= "N-terminal acetyl"
 /note= "C-terminal amide"
 'note= "D-form residue"
 Location/Qualifiers
 Brunck TK;
 ABB80556 standard; peptide; 11 AA
 Claim 17; Page 65; 69pp; English.
 compound having
 useful for treating
 19-JUL-2001; 2001WO-US023169.
 21-JUL-2000; 2000US-0220101P
 08-OCT-2002 (first entry)
 10; Conservative
H
 1 REVVPXGXDYS 11
 ;
 REVVPXGTDYS 11
 Levy OE,
EEVVPXGXDYS
 EEWPXGSDYS
 WPI; 2002-361643/39
 (CORV-) CORVAS INT
 Similarity
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Novel peptide
activity usefu
 Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 31-JAN-2002
 Synthetic.
 ABB80556;
 Query Match
 virucide
 protease
 Local
 Best Loca
Matches
```

RESULT

ABB80557

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "Norvaly1 carbonyl forming keto-amide linkage with
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C '
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #31.
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #14.
 94.0%; Score 47; DB 5; Length 11; 90.9%; Pred. No. 0.012; ive 0; Mismatches 1; Indels
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 /note= "D-form residue"
 Location/Qualifiers
 ŢĶ;
 Ė
 Claim 17; Page 65; 69pp; English.
 11
 Brunck
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169
 ABB80534 standard; peptide;
 residue 7"
 (first entry)
 Conservative
 1 EEVVPXGXDYS 11
 EEVVPXGSDYS 11
 (CORV-) CORVAS INT INC
 Lim-Wilby M, Levy OE,
 WPI; 2002-361643/39.
 Similarity
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Modified-site
 Modified-site
 Modified-site
 10;
 31-JAN-2002
 08-OCT-2002
 Synthetic
 Synthetic
 ABB80534;
 virucide
 protease
 Query Match
 Local
 Best Loca
Matches
 ABB80534
 RESULT
원
 X S X & E X E X E X S X S X
 à
 ;
0
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 'note= "Norvaly1 carbony1 forming keto-amide linkage with
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #37.
 ;
 Score 47; DB 5; Length 11;
Pred. No. 0.012;
0; Mismatches 1; Indels
 'note= "N-terminal acetyl"
 'note= "C-terminal amide"
 note= "D-form residue"
 'note= "D-form residue"
 Location/Qualifiers
 ABB80551
ID ABB80551 standard; peptide; 11 AA.
 Brunck TK;
 ABB80557 standard; peptide; 11 AA
 Claim 17; Page 65; 69pp; English.
 94.0%;
 19-JUL-2001; 2001WO-US023169.
 21-JUL-2000; 2000US-0220101P.
 residue 7"
 (first entry)
 10; Conservative
 1 EEVVPXGXDYS 11
 EEVVPXGSDYS 11
 Levy OE,
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39.
 Local Similarity
 Misc-difference
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 08-OCT-2002
 31-JAN-2002
 Synthetic
 ABB80551;
 ABB80557
 virucide
 protease
 Query Match
 Best Loca
Matches
```

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Gabs

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RESULT 5

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```
'note= "D-form residue"
Misc-difference 8
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 WO200208251-A2
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 31-JAN-2002.
 31-JAN-2002
 Synthetic
 protease.
 ABB80542;
 ABB80541
 ઠે
 셤
 ö
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7^{\rm n}
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 The sequence represents a peptide compound of the invention having the peptides of the invention are alpha *ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HRCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
 ö
 Score 46; DB 5; Length 11; Pred. No. 0.02;
 1; Indels
 0; Mismatches
 'note= "N-terminal acetyl"
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 note= "D-form residue"
 /note= "Oxymethionine"
 Location/Qualifiers
 Location/Qualifiers
 ABB80561 standard; peptide; 11 AA.
 Claim 17; Page 64; 69pp; English
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169
 (first entry)
 Conservative
 11
 1 EEVVPXGXDYS 11
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 1 EEVVPXGGDYS
 WPI; 2002-361643/39
 Similarity
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Key
Modified-site
 Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002
 10;
 Synthetic
 virucide.
 protease.
 Query Match
Best Local &
 Matches
 ABB80561
```

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ô
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #22
 ;
0
 92.0%; Score 46; DB 5; Length 11; 90.9%; Pred. No. 0.02; ive 0; Mismatches 1; Indels
 'note= "N-terminal acetyl"
/note= "C-terminal amide"
 /note= "C-terminal amide"
 /note= "D-form residue"
 Location/Qualifiers
 Brunck TK;
 ABB80542 standard; peptide; 11 AA.
 Claim 17; Page 65; 69pp; English.
 19-JUL-2001; 2001WO-US023169.
 21-JUL-2000; 2000US-0220101P.
 08-OCT-2002 (first entry)
 Query Match
Best Local Similarity 90.9
Matches 10; Conservative
 1 EEVVPXGXDYS 11
 Levy OE,
 (CORV-) CORVAS INT INC
 1 EEVVPXGMDYS
 WPI; 2002-361643/39.
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Lim-Wilby M,
 Synthetic.
 ABB80524;
 protease
 Query Match
 Best Loca
Matches
 RESULT 10
 ઠે
 윱
 ö
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #23
 ö
 Score 46; DB 5; Length 11;
Pred. No. 0.02;
); Mismatches 1; Indels
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 'note= "D-form residue"
 'note= "D-form residue"
 Location/Qualifiers
 ŦŔ;
 ABB80543 standard; peptide; 11 AA.
 Claim 17; Page 65; 69pp; English.
 ö
 Brunck
 92.0%;
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 (first entry
 10; Conservative
 1 EEVVPXGXDYS 11
 디
 Levy OE,
 (CORV-) CORVAS INT INC
 (CORV-) CORVAS INT INC
 EEVVPXGODYS
 WPI; 2002-361643/39
 Query Match
Best Local Similarity
Matches 10; Conser
 Misc-difference
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Novel peptide
activity usefu
 Key
Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-CCT-2002
 31-JAN-2002
 Synthetic
 ABB80543;
 protease
 RESULT 9
 ABB80543
 8
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ö
 The sequence represents a peptide compound of the invention having the peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 "Norvaly1 carbony1 forming keto-amide linkage with
 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
 ;
0
 Score 46; DB 5; Length 11;
Pred. No. 0.02;
 Indels
 /note= "C-terminal amide"
 'note= "D-form residue"
 Location/Qualifiers
 'note= "N-terminal
Brunck TK;
 ABB80524 standard; peptide; 11 AA.
 Brunck TK;
 English
 6
 92.0%;
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 /note= "No)
residue 7"
 (first entry)
 Local Similarity 90.5 es 10; Conservative
 Claim 17; Page 65; 69pp;
 1 EEVVPXGXDYS 11
 11
 Œ,
 Levy OE,
 (CORV-) CORVAS INT INC
 EEVVPXGQDYS
 WPI; 2002-361643/39.
 WPI; 2002-361643/39
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Novel peptide
activity usefu
 Key
Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
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Length 11;

5,

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Sequence 11 AA;
 WO200208251-A2
 Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 31-JAN-2002
 Synthetic
 ABB80529;
 virucide
 protease
 RESULT 12
 ABB80529
 ХS
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 g
 ö
 The sequence represents a peptide compound of the invention having the peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 note= "Norvaly1 carbony1 forming keto-amide linkage with
 virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #13
 ô
 92.0%; Score 46; DB 5; Length 11; 90.9%; Pred. No. 0.02; 1; Indels 1:ive 0; Mismatches 1; Indels
 'note= "N-terminal acetyl"
 'note= "C-terminal amide"
 Location/Qualifiers
 Brunck TK;
 Ā
 Claim 17; Page 64; 69pp; English.
 Claim 17; Page 64; 69pp; English.
 ABB80533 standard; peptide; 11
 19-JUL-2001, 2001WO-US023169.
 2000US-0220101P.
 (first entry)
 residue 7'
 Conservative
 1 EEVVPXGXDYS 11
 1
 (CORV-) CORVAS INT INC
 Lim-Wilby M, Levy OE,
 EEVVPXGMDYS
 WPI; 2002-361643/39.
 Similarity
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 21-JUL-2000;
 08-OCT-2002
 10;
 31-JAN-2002.
 Synthetic
 ABB80533;
 virucide,
 Query Match
Best Local S
 proteasê
 Best Loc
Matches
 RESULT 11
 ABB80533
```

```
ö
 ô
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9
 ö
 ..
0
 Length 11;
 1; Indels
 IndelE
 Score 46; DB 5;
Pred. No. 0.02;
0; Mismatches
 0.02;
 Mismatches
 /note= "N-terminal acetyl"
 /note= "C-terminal amide"
 'note= "D-form residue"
 Score 46;
Pred. No.
 'note= "D-form residue"
 Location/Qualifiers
 ż
 Brunck TK;
 Claim 17; Page 64; 69pp; English.
 .
0
 ABB80529 standard; peptide; 11
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative C
 19-JUL-2001; 2001WO-US023169.
 21-JUL-2000; 2000US-0220101P.
92.0%;
 08-OCT-2002 (first entry)
 92.0
Best Local Similarity 90.9
Matches 10; Conservative
 residue
 11
 11
 Levy OE,
 (CORV-) CORVAS INT INC
 1 EEVVPXGXDYS
 EEVVPXGGDYS
 WPI; 2002-361643/39.
 Misc-difference
 Misc-difference
 Sequence 11 AA;
```

ġ.

(first entry)

```
Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #18.
ABB80538 standard; peptide; 11
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169
 (CORV-) CORVAS INT INC
 Lim-Wilby M, Levy OE,
 WPI; 2002-361643/39
 Misc-difference
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002
 Synthetic.
 protease.
 셤
 ઠ
 The sequence represents a peptide compound of the invention having the peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comperising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 note= "Norvalyl carbonyl forming keto-amide linkage with
 virus
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8.
 Length 11
 Score 46; DB 5;
Pred. No. 0.02;
0; Mismatches 1
 note= "N-terminal acetyl"
 /note= "C-terminal amide"
 'note= "D-form residue"
 Location/Qualifiers
 Brunck TK;
 ABB80528 standard; peptide; 11 AA
 Claim 17, Page 64; 69pp, English.
 92.0%;
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 residue 7"
 (first entry
 Query Match
Best Local Similarity 90.9
Matches 10; Conservative
 1 EEVVPXGXDYS 11
 Levy OE,
 (CORV-) CORVAS INT INC
 EEVVPXGMDYS
 WPI; 2002-361643/39
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Novel peptide
activity usefu
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 Synthetic
 ABB80528;
 virucide.
 protease
 RESULT 13
 ABB80528
 ઠે
 셤
```

/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"

/note= "C-terminal amide" 'note= "D-form residue"

Brunck TK;

'note= "N-terminal acetyl"

Location/Qualifiers

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ö
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Gaps
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #42
 ö
 DB 5; Length 11; 0.02;
 1; Indels
 Score 46; DB E
Pred. No. 0.02;
0; Mismatches
 AA.
Claim 17; Page 64; 69pp; English.
 11
 ABB80562
ID ABB80562 standard; peptide; 11
XX
AC ABB80562;
XX
DT 08-OCT-2002 (first entry)
XX
XX
XX
XX
XX
XX
XX
XX
XX
XX
XX
XX
 92.0%;
90.9%;
 Query Match
Sest Local Similarity
Local 10, Conservative
The Total 10, Conservative
 1 EEVVPXGXDYS 11
 11
 1 EEVVPXGQDYS
 Sequence 11 AA;
 RESULT 15
```

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Gaps

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Indels

:

1 REVVPXGXDYS 11

à g RESULT 14 ABB80538

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The sequence represents a peptide compound of the invention having the peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
 Query Match
92.0%; Score 46; DB 5; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 1; Indels
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 'note= "D-form residue"
 'note= "D-form residue"
 note= "Oxymethionine"
 Location/Qualifiers
 Brunck TK;
 Claim 17; Page 65; 69pp; English.
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001, 2001WO-US023169
 (CORV-) CORVAS INT INC.
 Lim-Wilby M, Levy OE,
 WPI; 2002-361643/39.
 Misc-difference
 Misc-difference
 Key
Modified-site
 Sequence 11 AA;
 WO200208251-A2
 Modified-site
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 Modified-site
 31-JAN-2002.
 Synthetic
 proteasë.
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Gaps

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Search completed: June 3, 2004, 11:48:25 Job time : 46.9333 secs

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STREET: One Liberty Place - 46th Floor CITY: Philadelphia STAIE: PA COUNTY: U.S.A. ZIP: 19103 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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 June 3, 2004, 11:36:47; Search time 11.7333 Seconds (without alignments) 48.399 Million cell updates/sec
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Sequence
Sequence
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 US-09-134-000C-4848

US-08-569-147-76

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US-09-408-020-4318

US-09-418-000C-4318

US-08-146-2

US-08-146-2

US-08-146-2

US-08-146-2

US-09-13-146-2

US-09-13-146-4

US-09-13-176-460-4

US-09-152-060-85

US-09-152-060-85

US-09-152-060-85

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US-09-153-0818-5172

US-09-153-0818-5172

US-08-248-8428-21

US-08-23-3488-5
 US-09-813-555-4
US-09-523-263B-18
 Total number of hits satisfying chosen parameters:
 389414 seqs, 51625971 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1 EEVVPXGXDYS 11
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Perfect score:
Sequence:
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 Database :
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 Result
No.
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|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 4 US-09-252-991A-25088<br>2 US-09-0040-799-3<br>3 US-09-0033-448-1<br>3 US-09-0033-448-3<br>4 US-09-0033-448-3<br>4 US-09-0033-448-3<br>4 US-09-0033-448-3<br>4 US-09-0033-448-3<br>4 US-09-0033-455-3<br>4 US-09-0033-255-3<br>4 US-09-523-263B-4<br>4 US-09-523-263B-17<br>4 US-09-533-263B-17<br>4 US-09-134-272-10<br>2 US-08-11-268-3<br>US-09-11-341-7<br>3 US-09-314-272-8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ALIGNMENTS  4000C  al and AMINO ACID  FAECALIS FOR  /134,000C  55,778                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 0%; Score 37; DB 4; Len<br>0%; Pred. No. 5.1;<br>e 0; Mismatches 3;                                                   | . US/08569147 HUMANISED ANTIBODIES 95 SIS: K Washburn Kurtz Mackiewicz & (037715, LLF)                                                                                                                                                                               |
| 28 30 60.0 428 30 30 60.0 478 31 30 60.0 478 32 30 60.0 478 32 30 60.0 478 32 30 60.0 478 30 60.0 478 30 60.0 478 42 30 60.0 478 42 30 60.0 1068 44 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 1068 45 30 60.0 10 | RESULT 1 US-09-134-000C-4848   Sequence 4848, Application US/0913, Patent No. 6617156   GENERAL INFORMATION:   APPLICANT Lynn Doucette-Stamm et TITLE OF INVENTION: NUCLEIC ACID   TITLE OF INVENTION: NUCLEIC ACID   TITLE OF INVENTION: NUCLEIC ACID   TITLE OF INVENTION: NUCLEIC ACID   TITLE OF INVENTION: NUCLEIC ACID   TITLE OF INVENTION: NUCLEIC ACID   TITLE OF INVENTION: NUMBER: US/09, CURRENT FILING DATE: 1998-08-13   PRIOR FILING DATE: 1997-08-15   NUMBER OF SEQ ID NOS: 6612   SEQ ID NO 4848   LENGTH: 181   TYPE: RRT   TYPE: RRT   CRGANISM: Entercoccus faecalis   US-09-134-000C-4848 | Query Match Best Local Similarity 70 Matches 7; Conservative Qy 1 BEVVPXGXDY 10                 Db 145 BEVVPTSEDY 154 | RESULT 2 US-08-569-147-76 Sequence 76, Application US/085691- Patent No. 6180377 GENERAL INFORMATION: APPLICANT: TITLE OF INVENTION: HUMANISED AND ADDRESSEE: Woodcock Washburn ADDRESSEE: Woodcock Washburn STREET: One Liberty Place - STREET: One Liberty Place - |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                                                                       |                                                                                                                                                                                                                                                                      |

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 64.0%; Score 32; DB 4; Length 139; 55.6%; Pred. No. 38; tive 2; Mismatches 2; Indels
 Score 32; DB 4; Length 301;
Pred. No. 92;
2; Mismatches 2; Indels
 ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5124
 US-09-830-217-14; Sequence 14, Application US/09830217; Patent No. 6521441
 ; Sequence 4, Application US/09408020; Patent No. 6632937
 ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-830-217-14
 64.0%;
55.6%;
 Query Match
Best Local Similarity 55.6
Matches 5; Conservative
 Query Match
Best Local Similarity 55.6
Matches 5; Conservative
 :|| | ||:
195 IVPFGRDYN 203
 3 VVPXGXDYS 11
 32 IVPEGHDYN 40
 3 WPXGXDYS 11
 122 VVPTGFDY 129
 3 VVPXGXDY 10
 RESULT 6
US-09-408-020-4
 SEQ ID NO 14
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 COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM FC Compatible
OMPRATING FOR COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/59,147
FILING DATE: ZS-MARCH-1996
ATTORNEY/AGENT INFORMATION:
NAME: TRUJILO, DORGEN YATKO
REGISTRATION NUMBER: 35,719
REFERENCE/POCKET NUMBER: 35,719
REFERENCE/POCKET NUMBER: CARP-0047
TELECHONE: (215) 568-3100
ITELEPHONE: (215) 568-3100
ITELEPHONE: (215) 568-3100
ITELEPHONE: CARACTERISTICS:
LENGTH: 140 amino acids
TWVPR: amino acids
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,147
FILING DATE: 25-March-1996
ATTORNEY/ABORT INFORMATION:
ATTORNEY/ABORT INFORMATION:
NAME: Trujilo, Doren Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0047
TELEPHONE: (215) 568-3100
INFORMATION POR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
 Ouery Match
66.0%; Score 33; DB 3; Length 140;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 2; Indels
 Score 33; DB 3; Length 140;
Pred. No. 24;
 2; Indels
 TITLE OF INVENTION: HUMANISED ANTIBODIES
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Woo 6180377xis, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
 0; Mismatches
 Sequence 82, Application US/08569147
Patent No. 6180377
GENERAL INFORMATION:
APPLICANT:
 66.0%;
75.0%;
 LENGTH: 140 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-147-76
 Query Match
Best Local Similarity 75.0
Matches 6; Conservative
 MOLECULE TYPE: protein US-08-569-147-82
 122 WPTGFDY 129
 3 VVPXGXDY 10
 RESULT 3
US-08-569-147-82
```

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RESULT 4

US-09-134-001C-5124

US-09-114-001C-5124

Sequence 5124, Application US/09134001C

Retent No. 6380370

GENERAL INFORMATION:

ADPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERABEUTICS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERABEUTICS

TITLE OF INVENTION: US/09/134,001C

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

ERNOR 139

LENGTH: 139
 ö
 Gaps
 FALCEL NO. 0.5.1.114.

APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
FILE REPERBUCE: PB461PCT
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: ECT/US99/06199
PRIOR APPLICATION NUMBER: 60/080,296
PRIOR PILING DATE: 1998-03-03
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1098-05-07
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340 Kingsland Street

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STREET:
 Best Loca
Matches
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 Sequence 4318, Application US/09134000C
; Sequence 4318, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
 TITLE OF INVENTION: WICLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 TITLE OF INVENTION: BYTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
 TITLE OF INVENTION: UNMBER: US/09/134,000C
 CURRENT APPLICATION NUMBER: US/09/134,000C
 CURRENT FILING DATE: 1998-08-13
 FRIOR APPLICATION NUMBER: US 60/055,778
 FRIOR APPLICATION NUMBER: US 60/055,778
 FRIOR PELLING DATE: 1997-08-15
 NUMBER OF SEQ ID NOS: 6812
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 4318
 LENGTH: 303
 ö
 APPLICANT: Swanson, Ronald V.
APPLICANT: Swanson, Ronald V.
APPLICANT: Schleber Christa A
APPLICANT: Schleber Christa A
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REPERBNCE: DCORP, 002A
CURRENT APPLICATION NUMBER: US/09/408,020
CURRENT FILING DATE: 1999-09-29
PRIOR PEDITORION NUMBER: 60/102,294
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE FREESE FREESEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 3472
 Gaps
 NAME/KEY: MISC_FEATURE
INCATION: (2)..(2)
CTHER INFORMATION: Amino acid 2 is Xaa wherein Xaa = any amino acid.
US-09-134-000C-4318
 Sequence 2, Application US/08459146
Patent No. 586405
GENERAL INFORMATION:
APPLICANT: Choi, Gil Ho
APPLICANT: Nuss, Donald Lee
APPLICANT: Nuss, Donald Lee
TITLE OF INVENTION: Genetically Engineered Transmissible
TITLE OF INVENTION: Hypovirulence
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: George M. Gould, Esq., Hoffmann-La Roche Inc.
 64.0%; Score 32; DB 4; Length 3472; 45.5%; Pred. No. 1.5e+03;
 62.0%; Score 31; DB 4; Length 303; 40.0%; Pred. No. 1.5e+02; tive 3; Mismatches 3; Indels
 3; Indels
 3; Mismatches
 ; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum US-09-408-020-4
 TYPE: PRT ORGANISM: Enterococcus faecalis
 |:|:| :|
2294 EDVIPRGISFS 2304
 Best Local Similarity 45.5
Matches 5; Conservative
 4; Conservative
 1 EEVVPXGXDYS 11
 222 EQITPIGIEY 231
 1 EEVVPXGXDY 10
 Ouery Match
Best Local Similarity
Matches 4; Conservat
GENERAL INFORMATION:
 US-09-134-000C-4318
 RESULT 8
US-08-459-146-2
 Query Match
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 셤
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Gaps
 GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Choi, Gil Ho
APPLICANT: Nuss, Donald Lee
TITLE OF INVENTION: Genetically Engineered Transmissible
TITLE OF INV
 Length 622;
 COUNTY: U.S. COUNTY: U.S. COUNTY: U.S. COUNTY: U.S. COUNTY: U.S. COUNTY: U.S. COUNTY: U.S. COUNTY: U.S. COUNTY: U.S. COUNTY: U.S. COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: DATE: PC-DOS/MS-DOS SOFTWARE: PATCHION DATA: PSPLICATION NUMBER: US/08/459,146
FILING DATE: 0.2-JUN-1995
CLASSIFICATION DATA: PRILICATION NUMBER: US 07/832,117
FILING DATE: 0.6-FEB-1992
ATTORNEY/AGENT INFORMATION:
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,065
FILING DATE: US-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
) ORGANISM: Endothia parasitica (Cryphonectria) ORGANISM: parasitica) ; STRAIN: EP713 US-08-459-146-2
 62.0%; Score 31; DB 2;
85.7%; Pred. No. 3.3e+02;
iive 0; Mismatches 1.
 NAME: Roseman, Catherine R
REGISTRATION NUMBER: 34,240
REFENCE/DOCKET NUMBER: 3589
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6208
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
 US-08-459-065-2
; Sequence 2, Application US/08459065
; Patent No. 5882642
 : 622 amino acids
amino acid
 6; Conservative
 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
 New Jersey
: U.S.A.
 Query Match
Best Local Similarity
 31 EEVVPAG 37
 1 EEVVPXG 7
Nutley
 TOPOLOGY:
```

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APPLICANT: Audonnet, et al.

TITLE OF INVENTION: FELINE CALICIVIRUS GENES AND VACCINES IN PARTICULAR RECOMBINANT
FILE REPRENCE: 454313-3151.1

CURRENT APPLICATION WINGER: US/09/617,594A

CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION WINGER: France 00 01761
PRIOR PILING DATE: 2000-03-30
PRIOR PILING DATE: 2000-02-11
PRIOR PILING DATE: 2000-02-11
PRIOR PILING DATE: 1999-07-16
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 2
LENGTHALE: PATENTIN VERSION 3.0
SEQ ID NO 2
LENGTH: 669
 Score 30.5; DB 4; Length 669;
Pred. No. 4.5e+02;
1; Mismatches 2: Indela
 Score 30; DB 4; Length 59;
Pred. No. 37;
3; Mismatches 3; Indels
 Sequence 14, Application US/08963851
Patent No. 6300116
GENERAL INFORMATION:
APPLICANT: NADER OSTEN, CLAUS
APPLICANT: HALKIER, TORDEN
APPLICANT: HALKIER, TORDEN
APPLICANT: HANSEN, PETER KAMP
TITLE OF INVENTION: PROTERSE VARIANTS AND COMPOSITIONS
FILE REFERENCE: 4946,200-US
CURRENT APPLICATION NUMBER: US/08/963,851
CURRENT FILING DATE: 1997-11-04
NUMBER OF SEQ ID NOS: 357-11-04
SOFTWARE: FASLERQ for Windows Version 3.0
SEQ ID NO 14
 Sequence 4604, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTE and Encoded Human Proteins.
FILE REPERRENCE: GENSET.054FR2
CURRENT APPLICATION NUMBER: US/09/621,976
Sequence 2, Application US/09617594A Patent No. 6541458 GENERAL INFORMATION:
 ORGANISM: Enterococcus faecalis
US-08-963-851-14
 Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
 Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
 , ORGANISM: Feline calicivirus
US-09-617-594A-2
 428 EELTPAG-DYS 437
 1 EEVVPXGXDYS 11
 1 EEVVPXGXDYS 11
 38 EXHIPGGLEYS 48
 RESULT 13
US-09-621-976-4604
 TYPE: PRT
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 ਨੇ
 US-99-413-814-86

US-99-413-814-86

US-99-413-814-86

US-99-413-814-86

EARL INFORMATION:

APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH

APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH

APPLICANT: Blecker, Helmut

APPLICANT: Brandt, Petra

APPLICANT: Brandt, Petra

APPLICANT: Dougherty, Brian A

APPLICANT: Cino, Paul M

APPLICANT: Cino, Paul M

APPLICANT: Goldberg, Steven L

APPLICANT: Moldberg, Steven L

APPLICANT: Reichenbach, Hans

TITLE OF INVENTION: Dackim

APPLICANT: Reichenbach, Hans

TITLE OF INVENTION: Dackim

APPLICANT: PLING DATE: 1999-10-07

EARLIER FILING DATE: 1999-10-07

EARLIER FILING DATE: 1998-10-09

NUMBER OF SEQ ID NOS: 107

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 86

LENGTH. 759

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 62.0%; Score 31; DB 2; Length 622; 85.7%; Pred. No. 3.3e+02; tive 0; Mismatches 1; Indels
 Query Match 62.0%; Score 31; DB 3; Length 739; Best Local Similarity 62.5%; Pred. No. 4e+02; Matches 5; Conservative 1; Mismatches 2; Indels
 NAME: ROSEMEN, Catherine R
REGISTRATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 36,240
REFERENCE/DOCKET NUMBER: 8589
TELECOMMUNICATION INPORMATION:
TELEFAX: (201) 235-6208
TELEFAX: (201) 235-6208
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
TYPE: amino acid
TOPPLOGY: 11near
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORGANISM: Endothia parasitica (Cryphonectria STRANISM: BP713
OB-459-065-2
 TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-413-814-86
 Query Match
Best Local Similarity 85.7
Matches 6; Conservative
 663 IPLĠGĎÝS 670
 4 VPXGXDYS 11
 31 EEVVPAG 37
 RESULT 11
US-09-617-594A-2
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 Score 30; DB 4; Length 121;
Pred. No. 83;
0; Mismatches 1; Indels
 60.0%; Score 30; DB 4; Length 120; 50.0%; Pred. No. 82;
 3; Indels
 APPLICATION:
APPLICATION:
APPLICATION:
APPLICATION:
TITLE OF INVENTION: 28 Human Secreted Proteins
TITLE REFERENCE: P5003P1, 29
CURRENT APPLICATION NUMBER: US/09/152,060
CURRENT FILING DATE: 1998-09-11
EARLIER FILING DATE: 1998-03-12
EARLIER FILING DATE: 1997-03-14
EARLIER RILING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/040,710
EARLIER APPLICATION NUMBER: 60/040,710
EARLIER FILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,100
EARLIER APPLICATION NUMBER: 60/048,109
EARLIER APPLICATION NUMBER: 60/048,109
EARLIER APPLICATION NUMBER: 60/048,109
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-06
EARLIER FILING DATE: 1997-05-06
EARLIER FILING DATE: 1997-05-06
EARLIER FILING DATE: 1997-05-06
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EARLIER FILING DATE: 1997-05-06
EARLIER FILING DATE: 1997-05-06
EARLIER APPLICATION NUMBER: 60/048,169
EARLIER FILING DATE: 1997-05-06
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EARLIER FILING DATE: 1997-05-06
EARLIER FILING DATE: 1997-05-06
EARLIER FILING DATE: 1997-05-06
EARLIER PILING DATE: 1997-05-06
EAR
 Sequence 85, Application US/09152060
Patent No. 6448230
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: P2003P1.US
 2; Mismatches
 Sequence 68, Application US/09152060
Patent No. 6448230
GENERAL INFORMATION:
CURRENT FILING DATE: 2000-(NUMBER OF SEQ ID NOS: 19335 SOFTWARE: Patent.pm SEQ ID NO 4604 LENGTH: 120
 Query Match
Best Local Similarity 50.03
Matches 5; Conservative
 37 EILPSGSDRS 46
 2 EVVPXGXDYS 11
 TYPE: PRT
CORGANISM: Homo sapiens
US-09-621-976-4604
 ; ORGANISM: Homo sapiens
US-09-152-060-68
 28 EEVVPGG 34
 1 EEVVPXG 7
 RESULT 15
US-09-152-060-85
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y CURRENT FILING DATE: 1998-90-11

FEALURE AFLICATION NUMBER: DG/040/52

FAALURE FILING DATE: 1998-90-12

FAALURE FILING DATE: 1998-90-31

FAALURE FILING DATE: 1998-03-12

FAALURE FILING DATE: 1997-03-14

FEARLIR FILING DATE: 1997-03-14

FEARLIR FILING DATE: 1997-03-14

FEARLIR FILING DATE: 1997-05-30

FEARLIR FILING DATE: 1997-06-30

FEARLIR FILING DATE: 1997-06-30

FEARLIR FILING DATE: 1997-06-30

FEARLIR FILING DATE: 1997-06-30

FEARLIR PLING DATE: 1997-06-30

FEARLIR FILING DATE: 1997-0
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us-09-909-164-46.rapb

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Query Match
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 June 3, 2004, 11:57:42; Search time 33.7333 Seconds (without alignments) 91.741 Million cell updates/sec
 Sequence 31,
 Sequence
Sequence
Sequence
Sequence
Sequence
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Sequence
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Sequence
Sequence
 Sequence
 Description
 Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 US-09-909-164-31
US-09-909-164-32
US-09-909-164-43
US-09-909-164-41
US-09-909-164-12
US-09-909-164-12
US-09-909-164-12
US-09-909-164-13
US-09-909-164-13
US-09-909-164-13
US-09-909-164-13
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US-09-909-164-13
US-09-909-164-13
US-09-909-164-13
US-09-909-164-13
US-09-909-164-27
US-09-909-164-45
 Total number of hits satisfying chosen parameters:
 1155919 seqs, 281338677 residues
 SUMMARIES
 OM protein - protein search, using sw model
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 US-09-909-164-46
50
 1 EEVVPXGXDYS 11
 Query
Match Length DB
 Title:
Perfect score:
 Scoring table:
 Score
 Database :
 Sequence:
 Searched:
 Run on:
 Š.
 Result
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| Appl        | Appl       | Appl        | Appl        | Appl        | Appli    | Appli      | Appli      | Appl       | , Appl      | Appl     | Appl        | Appl        | Appl        | Appl        | Appl        | Appl        | Appl        | Appl     | App1        | Appl     | Appl       | Appl       | Appl     | Appl        | Appli      | Appl        | Appl     | Appl   | Appl       |            |  |
|-------------|------------|-------------|-------------|-------------|----------|------------|------------|------------|-------------|----------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|----------|-------------|----------|------------|------------|----------|-------------|------------|-------------|----------|--------|------------|------------|--|
| m           | S.         | m           | S           | ~           |          |            | σ          | 10,        | 14,         | 19,      | 20,         | 23          | 24          | 30          | 34          | 38          | 39          | 43       | 47,         | 48,      | 49         | 20         | 51       | 22          | 7,         | 17,         |          | v,     | ٦ì         |            |  |
| Sequence    | Sequence   | Sequence    | Sequence    | Sequence    | Sequence | Sequence   | Sequence   | Sequence   | Sequence    | Sequence | Sequence    | Sequence    | Sequence    | Sequence    | Sequence    | Sequence    | Sequence    | Sequence | Sequence    | Sequence | Sequence   | Sequence   | Sequence | Sequence    | Sequence   | Sequence    | Sequence | Φ      | Sequence   |            |  |
| 9-909-164-2 | 9-909-164- | 9-909-164-3 | 9-909-164-3 | 9-909-164-3 | 9-909-16 | 9-909-164- | 9-909-164- | 9-909-164- | 9-909-164-1 | 9-909-16 | 9-909-164-2 | 9-909-164-2 | 9-909-164-2 | 9-909-164-3 | 9-909-164-3 | 9-909-164-3 | 9-909-164-3 | 6        | 9-909-164-4 | 6        | 9-909-164- | 9-909-164- | 91-606-6 | 9-909-164-5 | 9-909-164- | 9-909-164-1 | 9-909-16 | -164-1 | -909-164-2 | ALIGNMENTS |  |
| us-         | us-        |             |             |             | us-      |            |            |            | US-         |          |             | 2 US-0      |             |             |             |             |             |          | 12 US-0     | US-0     | ns-0       | US-0       | 0-80     | ns-0        | 2 US-0     | ₽           | ns       | US-0   | ns-o       | A          |  |
|             |            |             |             |             |          |            |            |            |             |          |             |             |             |             |             |             |             |          |             |          |            |            |          |             |            |             |          |        |            |            |  |
| 11          | 11         | 11          | 11          | 11          | 11       | 11         | 11         | 11         | 11          | 11       | 11          | 11          | 11          | 11          | 11          | r r         | 11          | H        | 11          | 17       | 11         | 11         | 11       | 11          | 11         | 11          | 11       | 11     | 11         |            |  |
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| 41          | 41         | 41          | 41          | 41          | 40       | 40         | 40         | 40         | 40          | 40       | 40          | 40          | 40          | 40          | 40          | 40          | 40          | 40       | 40          | 40       | 4.0        | 40         | 40       | 40          | 39         | 39          | 39       | 39     | 39         | •          |  |
| 16          | 17         | 18          | 13          | 20          | 21       | 22         | 23         | 24         | 25          | 56       | 27          | 28          | 29          | 30          | 31          | 32          | 33          | 34       | 35          | 36       | 37         | 38         | 39       | 40          | 41         |             |          |        |            |            |  |
|             |            |             |             |             |          |            |            |            |             |          |             |             |             |             |             |             |             |          |             |          |            |            |          |             |            |             |          |        |            |            |  |

```
Sequence 31, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Levy, Odile B

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REPRENCE: INTO 192-02

FILE REPRENCE: 1010 NUMBER: US/09/909,164

CURRENT APPLICATION NUMBER: US/09/909,164

PRIOR APPLICATION NUMBER: 00/220,101

PRIOR PILLING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PALENTH Version 3.1

SEQ ID NO 31

LENGTH: 11

TENGTH: 11
 FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
 LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
 PEATURE:
NAME/KRY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 TYPE: PRT ORGANISM: artificial sequence
 LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 NAME/KEY: MISC_FEATURE
 NAME/KEY: MOD RES
JS-09-909-164-31
 US-09-909-164-31
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400

Length 11;

DB 12;

94.0%; Score 47;

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RESULT 4

US-09-164-40

US-09-909-164-40

Sequence 40, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Lim-Wilby, Marguerita

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FRIENCENTY APPLICATION NUMBER: 105/09/909,164

CURRENT FILING DATE: 2003-03-25

NUMBER OF SEQ ID NOS: 62

SOFTWARE PATENTY

SEQ ID NOS: 62

SEQ ID NO 40

LENGTH: 11

LENGTH: 11
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 o;
 FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
 FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
 Length 11;
 1; Indels
 Query Match 94.0%; Score 47; DB 12; Best Local Similarity 90.9%; Pred. No. 0.0049; Matches 10; Conservative 0; Mismatches 1
 LOCATION: (1) - (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11) - (11)
FEATURE: INFORMATION: AMIDATION
FEATURE: NAME/KEY: MISC_PEATURE
LOCATION: (6) - (6)
OTHER INFORMATION: NOTVALINE - (CO)
 COCATION: (6). (6)

THER INFORMATION: norvaline-(CO)
 LOCATION: (9). (9)

CTHER INFORMATION: D-amino acid

US-09-909-164-35
 NAME/KEY: MOD RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
 TYPE: PRT
ORGANISM: artificial sequence
 TYPE: PRT ORGANISM: artificial sequence
 FEATURE:
NAME/KEY: WOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
FEATURE:
 1 EEVVPXGSDYS 11
 1 EEVVPXGXDYS 11
 PEATURE:
NAME/KEY: MISC FEATURE
 NAME/KEY: MISC FEATURE
 FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (8)...(8)
 ઠે
 US-09-909-164-32
US-09-909-164-32
Sequence 32, Application US/09909164
| Publication No. US20020068702A1
| Sequence 32, Application No. US20020068702A1
| GENERAL INFORMATION:
| APPLICANT: Corvas International, Inc.
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Brunck, Terence K
| TITLE OF INVENTION NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
| TITLE OF INVENTION NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
| TITLE OF INVENTION NUMBER: 60/220, 101
| PRIOR FILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 32
| LENGTH: 11
| TYPE: PRT
| ORGANISM: artificial sequence | PRIORE TITLE OF TAXABLE OF TAXA
 US-09-909-164-35
Sequence 35, Application US/0909164
Publication No. US20020068702A1
Sequence 35, Application US/2020068702A1
SEDDICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT PAPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
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 THER INFORMATION: 11-mer synthesized according to example 1 EATURE:
 Query Match
94.0%; Score 47; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 1; Indels
 Pred. No. 0.0049;
0; Mismatches 1; Indels
 FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
 FEATURE:
NAME/KEY: NISC FEATURE
LOCATION: (9)...(9)
OTHER INFORMATION: D-amino acid
US-09-909-164-32
 NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
Best Local Similarity 90.9%;
Matches 10; Conservative
 NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 1 EEVVPXGXDYS 11
 1 EEVVPXGXDYS 11
 1 EEVVPXGTDYS 11
```

à

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US-09-09-164-12

US-09-09-164-12

Sequence 12, Application US/09909164

Publication No. US2002068902A1

GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Law., Odile B
APPLICANT: Lew., Odile B
APPLICANT: Low. NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT FILING DATE: 2000-03-25

PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SEQ ID NO 12

LENGTH: 11

LENGTH: 11
 ö
 FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
 FRATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
 Score 46; DB 12; Length 11; Pred. No. 0.008; 0; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIA VERSION 3.1
SEQ ID NO 8
LENGTH: 11
 PEATURE:
NAME/KEY:
NOD RES
LOCATION: (1)...(1)
CTHER INFORMATION: ACSTYLATION
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
CTHER INFORMATION: norvaline-(CO)
FEATURE:
 NAME/KEY: MISC FEATURE LOCATION: (9). [9) OTHER INFORMATION: D-amino acid
 NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 TYPE: PRT
ORGANISM: artificial sequence
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
 TYPE: PRT ORGANISM: artificial sequence
 FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 ; NAME/KEY: MOD RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: AMIDATION
US-09-909-164-8
 1 EEVVPXGXDYS 11
 1 REVVPXGMDYS 11
 NAME/KEY: MISC FEATURE LOCATION: (6)..(6)
 ઠે
 Sequence 41. Application US/09909164

| Sequence 41. Application US/09909164
| Septence 41. Application No. US20020068702A1
| GENERAL INFORMATION:
| APPLICANT: Corvas International, Inc.
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Odile E
| APPLICANT: Lim-Wilby, Odile E
| APPLICANT: Lim-Wilby, NoveL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
| TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
| TITLE OF INVENTION: NUMBER: US/09/909,164
| CURRENT APPLICATION NUMBER: 60/220,101
| PRIOR FILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SEQ ID NO 41
| LENGTH: 11
| LENGTH: 11
 RESULT 6

US-09-164-8

Sequence 8, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Levy, Odile E

TAPLICANT: Brunck, Terence K

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: IN01192-US
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0
 PEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)...(1)
CTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
 Query Match

94.0%; Score 47; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 1; Indels
 Score 47; DB 12; Length 11;
Pred. No. 0.0049;
0; Mismatches 1; Indels
 NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
 LOCATION: (8).7(9)
CTHER INFORMATION: D-amino acids
US-09-909-164-41
 i OTHER INFORMATION: D-amino acid US-09-909-164-40
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
 TYPE: PRT
ORGANISM: artificial sequence
 1 EEVVPXGXDYS 11
 1 EEVVPXGSDYS 11
 1 EEVVPXGXDYS 11
 1 EEVVPXGSDYS 11
 NAME/KEY: MISC_FEATURE
 g
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Sequence 18 Application US/09909164

| Sequence 18 Application No. US20020089702A1
| Septicantion No. US20020089702A1
| GENERAL INFORMATION:
| APPLICANT: Corvas International, Inc.
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Levy, Odile E
| APPLICANT: Brunck, Terence K
| TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
| TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
| TILE OF INING APPLICATION NUMBER: 06/220,101
| PRIOR APPLICATION NUMBER: 60/220,101
| PRIOR PRIOR FILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SOFTWARE: PATENTIN OF SEQ ID NOS: 62
| SEQ ID NO 18
| LENTH: 11
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERENCE: INOL192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT PILING DATE: 2003-03-25
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOPTMARE: PATENTION OF: 63
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SOPTMARE: PATENTION OF:
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 FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
 TYPE: PRT
CREANISM: artificial sequence
FRATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
 Length 11;
 92.0%; Score 46; DB 12; 90.9%; Pred, No. 0.008;
 0; Mismatches
 ; LOCATION: (6).7(6)
; OTHER INFORMATION: norvaline-(CO)
US-09-909-164-17
 LOCATION: (9). (9)

THER INFORMATION: D-amino acid
 FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)...(1)
FEATURE:
FRATURE:
 FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 TYPE: PRT
ORGANISM: artificial sequence
 LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
 Query Match
Best Local Similarity 90.9
Matches 10; Conservative
 1 REVVPXGXDYS 11
 1 EEVVPXGGDYS 11
 NAME/KEY: MISC FEATURE
 NAME/KEY: MISC_FEATURE
 FEATURE:
NAME/KEY: MOD RES
 RESULT 10
US-09-909-164-18
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 APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
URRENT APPLICATION NUMBER: US/09/909,164
CURRENT PILING DATE: 2000-03-25
PRIOR PRILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Retentin version 3.1
SEQ ID NO 13
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 Gaps
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 PEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
 92.0%; Score 46; DB 12; Length 11; 90.9%; Pred. No. 0.008; tive 0; Mismatches 1; Indels
 Score 46; DB 12; Length 11;
Pred. No. 0.008;
0; Mismatches 1; Indels
 APPLICANT: Corvas International, Inc. APPLICANT: Lim-Wilby, Marguerita
 Sequence 17, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
 Sequence 13, Application US/09909164
Sequence 13, Application US/09909164
Publication No. US20020068702A1
GENERAL INPORMATION:
 NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
 NAME/KEY: MISC_FEATURE; LOCATION: (8)..(9); OTHER INFORMATION: D-amino acids US-09-909-164-13
 FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER: INFORMATION: ACETYLATION
PEATURE:
LOCATION: (11)...(11)
OTHER: INFORMATION: AMIDATION
 OTHER INFORMATION: norvaline-(CO)
 NAME/KEY: MISC_FRATURE
COCATION: (8)...(8)
COCHER INFORMATION: D-amino acid
US-09-909-164-12
 LENGTH: 11
TYPE: PRT
ORGANISM: artificial sequence
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
 Conservative
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EEVVPXGMDYS 11
 1 EEVVPXGXDYS 11
 1 EEVVPXGMDYS 11
 1 EEVVPXGXDYS 11
 Query Match
Best Local Similarity
Matches 10; Conserva
 RESULT 9
US-09-909-164-17
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LEVY, Odile E

APPLICANT: Brunck, Terence K

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: IN01192-US

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT PILING DATE: 2003-03-25

PRIOR APPLICATION NUMBER: 6/220,101

PRIOR APPLICATION NUMBER: 6/220,101

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQ ID NO 26

LENGTH: 11

TYPE
 APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, calle E
APPLICANT: Levy, calle E
APPLICANT: Levy, calle E
APPLICANT: Levy, calle E
APPLICANT: Levy, calle E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT PLIJUGATION NUMBER: 105/09/09/164
CURRENT FILING DATE: 2000-00-21
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-00-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 27
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 Gaps
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 OTHER INFORMATION: 11-mer synthesized according to example 1
 ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
 Score 46; DB 12; Length 11;
Pred, No. 0.008;
 1; Indels
 0; Mismatches
 Sequence 27, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
 LOCATION: (6).7(6)
OTHER INFORMATION: norvaline-(CO)
 OTHER INFORMATION: D-amino acid US-09-909-164-26
 FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
 NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 92.0%;
 TYPE: PRT ORGANISM: artificial sequence
 NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 Query Match
Best Local Similarity 90.9.
....hes 10; Conservative
 1 EEVVPXGXDYS 11
 EEVVPXGQDYS 11
 NAME/KEY: MISC_FEATURE
 NAME/KEY: MISC FEATURE
 LENGTH:
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 Suggrance 22, Application US/09909164

Suggrance 22, Application US/09909164

Publication No. US20020068702A1

GENERAL INPOWATION:

APPLICANT: Corvae International, Inc.

APPLICANT: Lim-Wilby, Marguerita

CURRENT FILING DATE: 2003-03-25

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1
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 OTHER INFORMATION: 11-mer synthesized according to example 1 FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
 92.0%; Score 46; DB 12; Length 11; 90.9%; Pred. No. 0.008; Live 0; Mismatches 1; Indel8
 Score 46; DB 12; Length 11;
Pred. No. 0.008;
0; Mismatches 1; Indels
 RESULT 12

12-02-09-164-26

Sequence 26, Application US/09909164

Publication No. US20020068702A1

GENERAL INPORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
 NAME/KEY: MISC FEATURE
LOCATION: (6)..(6)
FEATURE INFORMATION: norvaline-(CO)
FEATURE:
 NAME/KEY: MISC_FEATURE
DCCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
US-09-909-164-18
) LOCATION: (9). (9) . OTHER INFORMATION: D-amino acid US-09-909-164-22
 TYPE: PRT ORGANISM: artificial sequence
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
 NAME/KEY: MOD RES LOCATION: (11). (11) OTHER INFORMATION: AMIDATION
 OTHER INFORMATION: AMIDATION FEATURE:
 92.0
Best Local Similarity 90.5
Matches 10; Conservative
 1 EEVVPXGXDYS 11
 1 EEVVPXGXDYS 11
 EEVVPXGQDYS 11
 1 EEVVPXGGDYS 11
 NAME/KEY: MISC_FEATURE
 SEQ ID NO 22
LENGTH: 11
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APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wiby, Marguerita
APPLICANT: Lim-Wiby, Marguerita
APPLICANT: Lim-Wiby, Marguerita
APPLICANT: Lim-Wiby, Marguerita
APPLICANT: Lim-Wiby, Marguerita
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TURRENT APPLICATION WUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION WUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PARENTIN VERSION 3.1
SSEQ ID NO 46
LENGTH: 11
 FEMTURE: OTHER INFORMATION: 11-mer synthesized according to example 1
 Query Match 92.0%; Score 46; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.008; Matches 11; Conservative 0; Mismatches 0; Indels
 Search completed: June 3, 2004, 12:57:17 Job time: 33.7333 secs
 NAME/KEY: MOD RES
LOCATION: (11)...(11)
COTHER INFORMATION: AMIDATION
FEATURE:
NAME/KEY: MISC. EBATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
 Sequence 46, Application US/09909164; Publication No. US20020068702A1; GENERAL INFORMATION:
 NAME/KEY: MISC_FEATURE
LOCATION: (8)...(9)
OTHER INFORMATION: D-amino acids
FRATURE:
 NAME/KBY: MOD RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
 TYPE: PRT
ORGANISM: artificial sequence
 NAME/KRY: MISC FEATURE
LOCATION: (8)...(8)
CTHER INFORMATION: Met(0)
US-09-909-164-46
 1 EEVVPXGXDYS 11
 1 EEVVPXGXDYS 11
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 APPLICANT: COCYAS International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile B
APPLICANT: Levy, Odile B
APPLICANT: Levy, Odile B
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: INO1192-US
CURRENT APPLICATION NUMBER: 05/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.1
SEQ ID NO 45
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 FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
 92.0%; Score 46; DB 12; Length 11; 100.0%; Pred. No. 0.008; tive 0; Mismatches 0; Indels
 Score 46; DB 12; Length 11;
Pred. No. 0.008;
0; Mismatches 1; Indels
 Sequence 45, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
 FEATURE:
NAME/KEY: MISC_FEATURE
COCATION: (8)...(8)
COTHER INFORMATION: D-amino acid
FEATURE:
NAME/KEY: MISC_FEATURE
COCATION: (8)...(8)
COTHER INFORMATION: Met (0)
US-09-909-164-45
 NAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
 FEATURE:
NAME/KEY: MISC FEATURE
NACATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
 NAME/KEY: MISC_FEATURE
) LOCATION: (8)..(9)
) OTHER INFORMATION: D-amino acids
02-09-909-164-27
 NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
 TYPE: PRT ORGANISM: artificial sequence
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
 NAME/KEY: MOD RES
LOCATION: (11)...(11)
CTHER INFORMATION: AMIDATION
FRATURE:
OTHER INFORMATION: AMIDATION
 Query Match
Best Local Similarity 100.
Matches 11; Conservative
 1 EEVVPXGXDYS 11
 1 EEVVPXGXDYS 11
 1 BEVVPXGXDYS 11
 JS-09-909-164-45
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Gaps ö

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GenCore version 5.1.6
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OM protein - protein search, using sw model

(without alignments) 117.567 Million cell updates/sec 3, 2004, 11:35:47 ; Search time 9 Seconds June

US-09-909-164-46 50 1 EEVVPXGXDYS 11 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Re

| SUMMAKIES | ij           | 2 D69551 conserved hypothet | AG3104 6-O-methy | D98182 O6-methylg | F81138 | T48898 disease | 2 T48899 disease resistance | A42452 Vl protein | S54619 hypotheti | A96001 | A96546 u | F82491 | д 09928н | B49132 | VKLJSI trans- | AG1272 thiol | AH1635 | AD0454 conser | S57810 hypothetical | S40753 hypotheti | DERTCM acyl-CoA dehy | H72784 probable | AF3286 | D82246 | T20173 | S00210 plastocyanin | \$38255 | S58208 plastocyanin |   | AIO |
|-----------|--------------|-----------------------------|------------------|-------------------|--------|----------------|-----------------------------|-------------------|------------------|--------|----------|--------|----------|--------|---------------|--------------|--------|---------------|---------------------|------------------|----------------------|-----------------|--------|--------|--------|---------------------|---------|---------------------|---|-----|
|           | DB           | 7                           | 7                | ~                 | ~      | N              | ~                           | ~                 | ~                | ~      | ~        | N      | 0        |        |               |              |        |               |                     |                  |                      |                 |        |        |        |                     |         |                     |   |     |
|           | Length       | 363                         | 290              | 290               | 587    | 906            | 908                         | 102               | 156              | 247    | 257      | 394    | 433      | 2747   | 124           | 165          | 165    | 196           | 225                 | 327              | 421                  | 440             | 1028   | 1088   | 1150   | 66                  | 155     | 168                 |   | 7   |
| a         | ery          | 72.0                        |                  | 70.0              |        |                | 70.0                        |                   |                  |        |          |        | 68.0     | 68.0   | 66.0          |              |        | 0.99          |                     |                  |                      | 0.99            |        |        | ٠      | 64.0                |         | 64.0                |   | 9.  |
|           | Score        | 36                          | 35               | 35                | 35     | 32             | 32                          | 34                | 34               | 34     | 34       | 34     | 34       | 34     | 33            | 33           | 33     | 33            | 33                  | 33               | 33                   | 33              | 33     | 33     | 33     | 32                  | 32      | 32                  | ( | 77  |
|           | ssult<br>No. |                             | 7                | ო                 | 4      | 'n             | 9                           | 7                 | 00               | σ      | 0.1      | 11     | 12       | 13     | 14            | 15           | 16     | 17            | 18                  | 19               | 50                   | 21              | 22     | 23     | 24     | 25                  | 56      | 27                  | Ċ | ON. |

| hypothetical prote<br>hypothetical prote<br>probable hexosyltr | î-lactate dehydrog<br>hypothetical prote<br>tolB protein - Hae | ABC transporter AT oligopeptidase [im protein B0212.3 [i | promate membrane<br>hypothetical 367K<br>projectin - fruit<br>response regulator | s-adenosylmethioni<br>conserved hypothet<br>hypothetical prote |
|----------------------------------------------------------------|----------------------------------------------------------------|----------------------------------------------------------|----------------------------------------------------------------------------------|----------------------------------------------------------------|
| F84330<br>AH1912<br>G69290                                     | G69350<br>T24111<br>F64064                                     | E86665<br>H84350<br>G88651                               | F69009<br>T31308<br>T13931                                                       | H97247<br>B72330<br>F72745                                     |
| 01 01 H                                                        | 0 0 0                                                          | 0000                                                     | 1000                                                                             | 1000                                                           |
| 307                                                            | 366<br>425<br>427                                              | 565<br>632<br>672                                        | 3472 6658                                                                        | 233<br>233<br>233<br>262                                       |
| 000                                                            | 000                                                            | 0000                                                     | 9000                                                                             | 2000                                                           |
| 64.<br>64.                                                     | 64.0<br>64.0                                                   | 644                                                      | 64.0                                                                             | 625                                                            |
| ପ ପ ପ                                                          | 1 2 2 2 2<br>1 2 3 3 4                                         | 2 2 2 2 C                                                | 7 C C C                                                                          | 1 H H H                                                        |
| 30<br>931<br>32                                                | 9 9 9 9 1<br>2 4 9 1                                           | 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8                    | 2, 4, 4, 4<br>2, 0 H C                                                           | 1 4 4 4<br>1 6 4 10                                            |

# AL IGNMENTS

Conserved hypothetical protein AP2411 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #text\_change 22-Oct-1999
C;Gacession: 05-Dec-1997 #text\_change 22-Oct-1999
C;Accession: D69551
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodso.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeA;Accession: D69551
A;Accession: D69551

A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residue type: DNA A; Residue: 1-363 <KLE>A; Residue: 1-363 <KLE>A; Cross-references: GB: AE001109; GB: AE000782; NID: 92689432; PIDN: AAB91255.1; PID: 926506

Gaps ó. DB 2; Length 363; 3; Indels Pred. No. 9.1; 2; Mismatches Score 36; Pred. No. 72.0%; 54.5%; Query Match
Best Local Similarity 54.5These 6; Conservative

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### 1 EEVVPXGXDYS 11 ઠે 셤

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AG3104
6-0-methylguanine-DNA methyltransferase [imported] - Agrobacterium tumefaciens (strain (c) methylguanine-DNA methyltransferase [imported] - Agrobacterium tumefaciens
C) Species Agrobacterium tumefaciens
C) Species Ag3104
C) Accession: AG3104
C) Accession: AG3104
C) Accession: AG3104
C) Accession: AG3104
C) Accession: AG3104
C) Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W. A.Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A.Reference number: AB2577; MUID:21608550; PMID:11743193

A; Accession: AG3104

A; Status: preliminary A; Molecule type: DNA

A;Residues: 1-290 «KUR» A;Cross-references: GB:AE008689; PIDN:AAL45253.1; PID:g17742937; GSPDB:GN00187 A;Experimental source: strain C58 (Dupont)

A; Map position: linear chromosome

Score 35; DB Pred. No. 12; 2; Mismatches

Query Match
Best Local Similarity 50.0%;
Matches 5; Conservative

1 EEVVPXGXDY 10 |:: | | || 9 EDITPIGSDY 18

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A2452
V1 protein - tobacco yellow dwarf virus (strain Australia)
C1 Species: tobacco yellow dwarf virus
C1 Species: tobacco yellow dwarf virus
C1 Species: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C1 Accession: A42452
A7Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yell
A1 Reference number: A42452; MUID:92188538; PMID:1546458
A1 Molecule type: DNA
A1 Residues: 1-102 < MOR>
 RimcDowell, J.M.; Dhandaydham, M.; Long, T.A.; Aarts, M.G.; Goff, S.; Holub, E.B.; Dang Plant Cell 10, 1861-1874, 1998
A;Title: Intragenic recombination and diversifying selection contribute to the evolutic A;Reference number: Z24999; MUID:99030193; PMID:9811794
A;Accession: T48899
A;Accession: T48899
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-908 <MCD>
A;Residues: 1-908 <MCD>
disease resistance protein RPPB (validated) - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T48898
R;McDowell, J.M.; Dhandaydham, M.; Long, T.A.; Aarts, M.G.; Goff, S.; Holub, E.B.; Dang Plant Cell 10, 1861-1874, 1998
A;Title: Intragenic recombination and diversifying selection contribute to the evolutic A;Reference number: Z24999; MUID:99030193; PMID:9811794
A;Accession: T4889
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-906 cWD>
 A, Description: susceptible allele of a gene that promotes resistance to Peronospora pai
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 A;Cross-references: EMBL:AF089710; NID:g3928861; PIDN:AAC83165.1; PID:g3928862 A;Experimental source: Landsberg erecta C;Genetics: A;Genet RPP8
 A;Cross-references: EMBL:AF089711; NID:g3901293; FIDN:AAC78631.1; FID:g3901294 A;Experimental source: Columbia C;Genetics:
 disease resistance protein rpp8 [similarity] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000 C;Accession: T48899
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 .
 Score 35; DB 2; Length 908; Pred. No. 41; 2; Mismatches 2; Indels
 DB 2; Length 906; 40;
 Indels
 A; Description: promotes resistance to Peronospora parasitica
 Score 35; DB 2; Pred. No. 40; 2; Mismatches
 70.0%;
Local Similarity 60.0%;
hes 6; Conservative 2
 70.0%;
 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
 |::|| | ||
881 EKLVPGGEDY 890
 883 ЁКЦ УРССЕВУ 892
 1 EEVVPXGXDY 10
 1 EEVVPXGXDY 10
 A; Introns: 293/1; 342/1
C; Function:
 A; Introns: 293/1; 342/1
C; Function:
 Query Match
 A;Gene: rpp8
 Best Loc
Matches
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 succinate dehydrogenase, flavoprotein chain NMB0950 [imported] - Neisseria meningitidis CiSpecies: Neisseria meningitidis CiSpecies: Neisseria meningitidis CiSpecies: Neisseria meningitidis CiSpecies: Neisseria meningitidis CiSpecies: Neisseria meningitidis CiSpecies: Neisseria meningitidis CiSpecies: Neisseria meningitidis SiStatesia: SiStatesia: N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Elsen, J.A.; Arctelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Elsen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A;Reference number: Aslono; MUID:2017575; PMID:10710307
A;Reference number: Aslono; MUID:2017575; PMID:10710307
A;Reterence number: CiSpecies CiSp
 C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Accession: D98182
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2333-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Accession: D98182
 9
 Superfamily: fumarate reductase flavoprotein, 3-oxosteroid 1-dehydrogenase homology,
 06-methylguanine-DNA methyltransferase PA2118 [imported] - Agrobacterium tumefaciens
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 A.Cross-references: GB:AE007870; PIDN:AAK88982.1; PID:g15158766; GSPDB:GN00170 C;Genetics:
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 'Match 70.0%; Score 35; DB 2, Length 290; Local Similarity 50.0%; Pred. No. 12; Local Si Conservative 2; Mismatches 3; Indels
 Score 35; DB 2; Length 587;
Pred. No. 25;
0; Mismatches 3; Indels
 Length 290;
 3; Indels
 5,
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A;Gene: AGR L 818 A;Map position: linear chromosome

Query Match Best Loc Matches

A Status: preliminary A Molecule type: DNA A, Residues: 1-290 <KUR>

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Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative

Gene: NMB0950

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Cyptes: Nation 18-0.01
Cyptes: Nation: F82491
RyHeidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Abardson, D.; Erminaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F., R.; McKalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
Ayfitle: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
Ayfacession: F82491
 unknown protein [imported] - Arabidopsis thaliana (Species Arabidopsis thaliana (Species Arabidopsis thaliana (mouse-ear cress)
Cipate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
Cipate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
Cipate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
Cipate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
Cipate: 02-Mar-2001 #sequence_revision 02-Mar-2001
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Cipate: 02-Mar-2001
Cipa
 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <HEL>
A;Residues: 1-394 <HEL>
A;Cross-references: GB:AE004358; GB:AE003853; NID:g9657566; PIDN:AAF96096.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
 ferrisiderophore reductase VCA0183 [imported] - Vibrio cholerae (strain N16961 serogrouf
C;Species: Vibrio cholerae
 A;Map position: 2
C;Superfamily: flavohemoglobin; cytochrome-b5 reductase homology; globin homology
 A; Cross-references: GB: AE005173; NID: g11094688; PIDN: AAG29624.1; GSPDB: GN00141
 ö
 Length 247;
 Score 34; DB 2; Length 257;
Pred. No. 17;
2; Mismatches 3; Indels
 Score 34; DB 2; Length 394;
Pred. No. 27;
0; Mismatches 3; Indels
 Indels
 5
 Score 34; DB 2
Pred. No. 16;
1; Mismatches
 68.0%;
 Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
 68.0%;
54.5%;
 Query Match
Best Local Similarity 54.5
Matches 6; Conservative
 Best Local Similarity 60.0
Matches 6; Conservative
 217 EELLKAGADYS 227
 1 EEVVPXGXDYS 11
 1 EEVVPXGXDY 10
 57
 48 EDVEPRGADY
 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-257 <STC
A;Gene: SMb21444
A;Genome: plasmid
 A, Gene: F8A12.12
A, Map position: 1
 A,Gene: VCA0183
 Query Match
 C;Genetics:
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 Cipacesion: A96001
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endchareference number: A95842; MUID:21396508; PMID:11481431
 A; Accession: A36001
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A; Access
 A; Molecule type: DNA
A; Residues: 1-156 < CEBA
Torcosa-references: EMBL: 274920; NID: 91420109; PIDN: CAA99201.1; PID: 91420111; MIPS: YORO1
A; Experimental source: strain S288C
 conserved hypothetical protein, homolog to osmotically inducible sensory protein SMC22-1
C;Species: Sinorhizoblum meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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 nypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein O2612; hypothetical protein YOL303.3
 C;Species: Saccharomyces cerevisiae
C;Date: 08-0ul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
S;Accession: S54619; S66879
R;Ge Haan, M:; Maarse, A.C.; Grivell, L.A.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54617
 Gaps
 A;Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
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 Length 102;
 Length 156,
 2; Indels
 Score 34; DB 2;
Pred. No. 9.6;
1; Mismatches 2
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2; Mismatches 2
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 68.0%;
66.7%;
 Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
 A; Cross-references: SGD:S0005539
 Query Match
Best Local Similarity 66...
6, Conservative
 7 QVVPSGINYS 16
 2 EVVPXGXDYS 11
 2 EVVPXGXDY 10
 58
 EVMPLGMDY
 Accession: S54619; Molecule type: DNA
 A, Map position: 15R
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C.Species: Listeria monocytogenes
C.Species: Listeria monocytogenes
C.Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 17-May-2002
C.Accession: AG1272
B.Gdaser, D.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
R;Gdaser, D.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
C; Jones, L.M.; Karst, U.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, B.; Maitournam, A.; N.
Ook, C.; Schlueter, T.; Simose, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A; Reference number: AB1077; MUD:21537279; PMID:11679669
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C; Gentetics:
A; Experimental source: strain EGD-e
C; Gentetics:
A; Gentetics:
NiAlternate names: anti-repression trans-activator; art protein; rev protein; trs prote Cispecies: simian immundeficiency virus SIVcpz
A;Note: host Pan troglodytes (chimpanzee)
Cipate: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: 809988
R;Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
Nature 345, 356-359, 1990
A;11.tle: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A;Reference number: 809988
A;Scatesion: 809988
A;Scatesion: 809988
A;Scatesion: S09988
A;Residue type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-124 - KUES
 thiol peroxidases homolog 1mo1583 [imported] - Listeria monocytogenes (strain EGD-e)
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 A;Introns: 27/1
C;Superfamily: AIDS trans-regulatory splicing protein
C;Keywords: AIDS; immunodeficiency; splicing protein; transcription regulation
 A;Cross-references: EMBL:X52154; NID:g58866; PIDN:CAA36405.1; PID:g763085
C;Genetics:
 Gaps
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 66.0%; Score 33; DB 1; Length 124; 60.0%; Pred. No. 12; tive 1; Mismatches 3; Indels
 66.0%; Score 33; DB 2; Length 165; 66.7%; Pred. No. 17;
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 1; Mismatches
 3, 2004, 12:00:03
 6; Conservative
 6; Conservative
 ETVPAGGNYS 116
 2 EVVPXGXDYS 11
 EVVPEGSDH 152
 2 EVVPXGXDY 10
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Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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 A, Gene: rev; trs; art
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 fat facets (faf) splice form 1 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Accession: 19-Dec-1993 #sequence_revision 25-Apr-1997 #text_change 01-Dec-2000
C;Accession: B49132: A49132
R;Fischer-Vize, J.A.; Rubin, G.M.; Lehmann, R.
Development 116, 985-1000, 1992
A;Aitle: The fat facets gene is required for Drosophila eye and embryo development.
A;Reference number: A49132; MUID: 93202020; PMID: 1295747
A;Contents: isogenic st
A;Accession: B49132
A;Accession: B49132
A;Accession: B49132
A;Accession: B49132
A;Residues: 1-2747 <FIS>
A;Cross-references: G104959; NID: 9157411; PIDN: AAF01345.1; PID: 96013474
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN: 127836, NCBIN: 129008, NCBIP: 127839)
 peptidoglycan-binding protein, probable [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: H8766
B;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Haft, D.H.; Nolon
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durinh, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
D; J; Ermolaeva, M.; White, O.; Salzborg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
 A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-2704, 'Wr, 2707,'ANNV' <F12>
A;Residues: 1-2704, 'Wr, 2707,'ANNV' <F12>
A;Coss-references: GB:L04958; NID:g157410; PIDN:AAF01346.1; PID:g6013475
A;Note: sequence extracted from NCBI backbone (NCBIN:127836, NCBIN:129008, NCBIP:129029)
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 A;Status: preliminary
A;Moleoule type: DNA
A;Residues: 1-433 <STO>
A;Cross-references: GB:AE005673; NID:g13425020; PIDN:AAK25284.1; GSPDB:GN00148
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Length 433; 3; Indels

7

Score 34; DB Pred. No. 30; 2; Mismatches

Query Match Best Local Similarity 54.5%; Matches 6; Conservative

C;Genetics: A;Gene: CC3322

266 EVILPPGFDYS 276

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1 EEVVPXGXDYS 11

trans-regulatory splicing protein - simian immunodeficiency virus SIVcpz

RESULT 14 VKLJSI

| :|| | |:| EVIVPDGODFS 1404

1 REVVPXGXDYS 11

68.0%; Score 34; DB 2; Length 2747; 54.5%; Pred. No. 2.2e+02; ive 2; Mismatches 3; Indels

C; Keywords: alternative splicing

Local Similarity 54.

Best Loca Matches

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EMBL, ABO15468; BAB10695.1; -.
EMBL, AKIL163; BAC41841.1; -.
ILICEPPO; IPR000767; Disease_resist.
Interpro; IPR001611; LRR.
 Q9ffke arabidopsis 9844j9 arabidopsis 985954 arabidopsis 985954 arabidopsis 985964 fusobacteri 931619 tobacco yel 95824 drosophila 95824 drosophila 95826 listeria mo 934338 caenorhabdi 90850; atteptococc 98652 streptococc 98652 streptococc 98122 streptococc 98452 streptococc 98453 streptococc 99341s streptococc 99418 night 911970 populus night
 streptococc
streptococc
oryza sativ
hordeum vul
populus nig
 homo sapien
homo sapien
thermotoga
cryphonectr
homo sapien
sus scrofa
pantoea agg
 homo sapien
archaeoglob
rattus norv
 daucus caro
 June 3, 2004, 11:32:06 ; Search time 4.86667 Seconds (without alignments) 117.693 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 047861
P20422
Q9uhf0
O28330
 P41367
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 141681 seqs, 52070155 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 US-09-909-164-46
50
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Query
Match Length DB
 1 EEVVPXGXDYS 11
 SwissProt_42:*
 4 4 2 3 1 4 4 2 3 1 4 4 2 3 1 4 4 2 3 3 4 4 2 1 1 2 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 2 1 1 2
 Title:
Perfect score:
 Scoring table:
 Score
 Database :
 Searched:
 Sequence:
 Run on:
 Result
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| P14194 bacillus su<br>P08203 escherichia<br>P08203 escherichia<br>P08208 belicobacte<br>P56006 helicobacte<br>P06308 lymmaea sta<br>P08174 saccharomyc<br>O52250 halomonas e<br>Q92eu7 halomonas e<br>Q92eu7 halomonas e<br>Q15231 homo sapien<br>P53998 kluyveromyc |
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| CTC BACSU ARAD SALTY SCOA_HELPJ SCOA_HELPJ SCOA_HELPJ OVUH_LYMST OVUH_LYMST AMP2_YEAST RECB2_HALEL ECB1_HALEL ECB1_HALEL FOLC_BACSU Z185_HUMAN LIET1_KUULA                                                                                                           |
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# ALIGNMENTS

| ANDAR  42, 42, 42, 42, 42, 42, 42, 42, 42, 42 | PRT; 908 AA.  PRRIA ARATH STANDARD; PRT; 908 AA.  OSTANTA  REL4 ARATH STANDARD; PRT; 908 AA.  OSTANTA  10-OCT-2003 (Rel. 42, Last sequence update)  10-OCT-2003 (Rel. 42, Last sentence RPB-like protein 4.  REPEALA OR ATGG4620 ON KISNB.9  Arabidopsis thaliana (Mouse-ear cress).  BURATYORA, VIIGADARIAS, Streptophyta; Embryophyta; Tracheophyta;  Spermatophyta; Magnilophyta; endicotyledons; core endicots; rosids;  NCBL TARAYORA, VIIGADARIAS, Brassicaceae, Arabidopsis.  (1)  STANING-V. Columbia;  STANING-V. Columbia;  SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N.A.  SEQUENCE ROW N. |
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|                                               | RATH ST.  -2003 (Rel2003 (R                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |

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 STRAIN=CV. Di-17;
MEDLINE=20271766; PubMed=10810142;
Cooley M.B., Pathirana S., Wu H.-J., Kachroo P., Klessig D.F.;
"Members of the Arabidopsis HRT/RPP8 family of resistance genes confer resistance to both viral and comycete pathogens.";
Plant Cell 12:663-676(2000).
 "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty P1 and TAC clones.";
 MEDLINE=99030193; PubMed=9811794; MCDOWell J.M., Dhandaydham M., Long T.A., Aarts M.G.M., Goff S., McDowell J.M., Dhandaydham M., Long T.A., Aarts M.G.M., Goff S., Holub E.B., Dangl J.L.; Thirdenic recombination and diversifying selection contribute to the evolution of downy mildew resistance at the RPP8 locus of
 NEPS ARALI STANDARD; PRIJ 900 FM. OSCH191, OSCH192, OSCH193, OSCH1
 STRAIN=cv. Columbia,
STRAIN=cv. Columbia,
MEDLINE=22954880; PubMed=14593172;
Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
 Gaps
 (ISOFORM 1), FUNCTION, MUTANTS RPP8-1; RPP8-2 AND
 STRAIN=cv. Columbia;
MEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katch T., Asamizu E., Kotani H.,
Tabata S.;
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 Pfam; PF0560; LRR; 2.
Pfam; PF0031; NB-ARC; 1.
Print PF0031; NB-ARC; 1.
Plant defense; ATP-binding; Repeat; Leucine-rich repeat.
DOMAIN 146 459 NB-ARC.
REPEAT 575 599 LRR 1.
REPEAT 642 667 LRR 3.
 2; Indels
 LRR 1.
LRR 2.
LRR 3.
ATP (POTENTIAL).
MW; 3111991B17239693 CRC64;
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RPP8-3, AND VARIANTS.
STRAIN=cv. Columbia, and cv. Landsberg erecta;
 SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS
 908 AA
 2; Mismatches
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 Arabidopsis.";
Plant Cell 10:1861-1874(1998).
 146 459
575 599
600 623
842 867
192 199
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 DNA Res. 7:31-63(2000).
 883 EKLVPGGEDY 892
 1 EEVVPXGXDY 10
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 NP_BIND
SEQUENCE
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 RPP8_ARATH
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Date -> KGE (in Cv. Di-1) and Cv. Landsberg erecta).

GKGV -> EXGI (in cv. Landsberg erecta).

E -> R (in cv. Landsberg erecta).

E -> D (in cv. Landsberg erecta).

P -> L (in cv. Di-17).

Q -> Q (in cv. Di-17).

G -> V (in cv. Di-17).

Y -> S (in cv. Di-17).

Y -> S (in cv. Di-17).

A -> T (in cv. Di-17).

R -> P (in cv. Di-17).

A -> T (in cv. Di-17).

A -> T (in cv. Di-17).

A -> T (in cv. Di-17).

A -> T (in cv. Di-17).

A -> T (in cv. Di-17).

A -> T (in cv. Di-17).

A -> T (in cv. Di-17).

A -> T (in cv. Di-17).

A -> V (in cv. Di-17).
 /FITG=VSP 007172,
IDGQL -> VDBQI (in cv. Landsberg erecta).
G -> E (in cv. Di-17).
SGK -> RGE (in cv. Di-17 and cv.
 erecta).

C -> S (in cv. Di-17 and cv. Landsberg erecta).

T -> I (in cv. Di-17).

S -> R (in cv. Di-17).

S -> R (in cv. Di-17).

H -> Q (in cv. Di-17).

I -> L (in cv. Landsberg erecta).

KNXT -> RNNA (in cv. Di-17).

K -> N (in cv. Landsberg erecta).

K -> N (in cv. Landsberg erecta).
 erecta). F -> S (in cv. Di-17 and cv. Landsberg erecta). W -> C (in cv. Di-17 and cv. Landsberg W -> C
 ATP (POTENTIAL).
WKMLLTSRNEGVGIH -> ELLWYIHEALFLLNS (in
 -> N (in cv. Landsberg erecta).
 erecta).
C -> R (in cv. Di-17 and cv. Landsberg
 -> F (in cv. Di-17 and cv. Landsberg
 Landsberg erecta).

E.197YS -> KITYQE (in cv. Di-17).

A -> V (in cv. Landsberg erecta).

E -> Q (in cv. Landsberg erecta).

DNILSAQ -> NYCIRNH (in cv. Di-17).

WO -> SH (in cv. Landsberg erecta).
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DSEISTYSLFY -> YSKISAYDLFN (in cv.
EMBL; AF089711; AAC78631.1; -.
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EMBL; ABO25638; BAA974261; -.
EMBL; AN062514; AAL32592.1; -.
EMBL; AX18862; BAC49449.1; -.
EMBL; AX18862; BAC9031; BAC.
PÉRN; PF000567; LRR; 2.
PÉRN; PF00931; NB-ARC.
PÉRN; PF00931; NB-ARC.
PÉRN; AND0364; DISFASERSIST.
PLACT défense; ATP-binding; Repeat; Leucine-rich repeat;
Alternative splicing; Polymorphism.
 LEUCINE-ZIPPER
 erecta),
 NB-ARC.
 LRR 1.
LRR 2.
ATP (F
 45
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RP SEQUENCE FROM N.A., AND FUNCTION.

RP SEQUENCE FROM N.A., AND FUNCTION.

REALIN=cv. Landsberg erects;

RX MEDINE=99030193; PubMed=9811794;

RADOWell J.M., Dhandaydham M., Long T.A., Aarts M.G.M., Goff S.,

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RADOWell J.M., Dhandaydham M., Long T.A., Aarts M.G.M., Goff S.,

RADOWell J.M., Dhandaydham M., Long T.A., Aarts M.G.M., Goff S.,

RT "Intragenic recombination and diversifying selection contribute to the plant against pathogens that contain an appropriate avirulence control of the plant against pathogens that crossensitives a defense system including the hypersensitive response, which restricts the pathogen growth, In contrast to response, which restricts the pathogen growth, In contrast to response, which restricts the pathogen growth, In contrast to protein from Percohogona parasities.

CC That triggers a defense system including the hypersensitive correctes a unique RPPB gene.

CC PRESENT Subfamily.

CC MRCELLANGOUS: In cv. Columbia and cv. Di-17, this protein is not present due to an unequal crossing over between the RPPB and RPBHA Genes that creates a unique RPPB gene.

CC SIMILARITY: Contrains 1 NB-ARC domain.

CC --- SIMILARITY: Contrains 1 NB-ARC domain.

CC --- DATABASE: NAWE-NIB-LRRS;

CC --- DATABASE: NAWE-NIB-LRRS;

CC --- DATABASE: NAWE-NIB-LRRS;
 ö
 Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Supermatrophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

Surcosids II; Brassicales; Brassicaceae; Arabidopsis.
 PRF -> SRFK (in cv. Di-17).
Y -> F (in cv. Di-17).
S -> Y (in cv. landaberg erecta).
C -> S (in cv. Landaberg cv. Landaberg
 ô
 Score 35; DB 1; Length 908;
Pred. No. 18;
2; Mismatches 2; Indels
 | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs | homologs
 DB 1; Length 910;
18;
 10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Disease resistance protein RPHSA (RPPS homolog A).
 PRT; 910 AA.
 70.0%; Score 35; 60.0%; Pred. No.
 erecta).
 70.0%;
 Best Local Similarity 60.0
Matches 6, Conservative
 STANDARD;
 883 EKLVPGGEDÝ 892
 1 EEVVPXGXDY 10
 Query Match
Best Local Similarity
 RP8H ARATH
P59584;
VARIANT
VARIANT
VARIANT
 Query Match
 RESULT 3
RP8H ARATH
 SOLUTION SOL
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VIBCH
 METAL
SEQUENCE
 RESULT 6
HMPA VIBCH
ID HMPA VIBC
AC Q9XMY3;
DOMAIN
REPEAT
REPEAT
NP BIND
NP BIND
NBTAL
METAL
METAL
METAL
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 44444
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 Gaps
 Pfam; Froziaz, MGS; 1.
Fram; PRO2142; MGS; 1.
FRAME; PRO10369; CPSASE.
TIGREAME; TIGRO1369; CPSASE.
TIGREAME; TIGRO1369; CPSASE.
FROSITE; PSO0866; CPSASE.1; 2.
PROSITE; PSO0866; CPSASE.2; 2.
PROSITE; PSO0866; Pytimidine biosynthesis; Ligase; Repeat; Arginine biosynthesis; Pytimidine biosynthesis; Dytimidine biosynthesis; Pytimidine biosynthesis; Ligase; Repeat; Arginine biosynthesis; Pytimidine biosynthesis; Ligase; Repeat; Arginine biosynthesis; Pytimidine bowain.

402 646 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (BC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB OR FN0422.
 ö
 Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
 PRT; 1058 AA
 -!- SIMILARITY: Belongs to the carB family.
 2; Mismatches
 EMBL; AE010554; AAL94625.1; ALT_INIT.
HAMAP; MF_01210; -; 1.
 HAMAP; MF 01210; -; 1.
InterPro; IPR006245; CarA L glu.
InterPro; IPR006349; CPase L
InterPro; IPR005409; CPase L D2.
InterPro; IPR005409; CPase L D3.
InterPro; IPR005401; CPase L D3.
InterPro; IPR00480; MS 11ke.
Pfam; PP00209; CPSase L Chain; 2.
Pfam; PP027046; CPSase L D3; 1.
Pfam; PP02704; MS; 1.
 6; Conservative
 STANDARD;
 ввз Екцурссвый в94
 1 EEVVPXGXDY 10
 SEQUENCE FROM N.A.
 NCBI_TaxID=76856;
 Fusobacterium
 RESULT 4
CARB FUSNN
ID CARB FUSNN
AC Q8RGB6;
 Matches
 THE SEA THE SE
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 Gaps
 MEDITNE-92188538; PubMed-1546458; Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.B.; Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.B.; The nucleotide sequence of the infectious cloned DNA component of tobacco yellow dwarf virus reveals features of geminiviruses infecting monococtyledonus plants."; virology 187:633-642(1992).
 ATP (POTENTIAL).

ATP (POTENTIAL).

MANGANESE 1 (SE SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).
 .
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0
 Score 35; DB 1; Length 1058;
Pred. No. 22;
2; Mismatches 2; Indels
 Score 34; DB 1; Length 102;
Pred. No. 3.1;
2; Mismatches 2; Indels
 ll protein. 11178 MW; A40ECF1E0AF55B67 CRC64;
 Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
NCBI_TaxID=31599;
ALLOSTERIC DOMAIN.
 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
 (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
 PIR; A42452; A42452.
InterPro; IPR002621; Gemini mov.
PEdn; PF01708; Gemini mov; I.
Hypothetical protein:
SEQUENCE 102 AA; 11178 MW; A4
 68.0%;
 EMBL; M81103; AAA47947.1; -.
 70.0%;
 1058 AA; 117451
 60.0%;
 Query Match
Guery Match
Best Local Similarity 60.000
 Query Match 70.0
Best Local Similarity 60.0
Matches 6; Conservative
 STANDARD;
 STANDARD;
 190 EIVPNGLNYS 199
 2 EVVPXGXDYS 11
 2 EVVPXGXDYS 11
 SEQUENCE FROM N.A.
 16-OCT-2001
16-OCT-2001
28-FEB-2003
 RESULT 5
Y11K_TYDVA
ID _Y11K_TYDVA
AC P31619;
```

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 SEQUENCE FROM N.A.
STRAIRE 1 TOV NIG661 / Serctype 01;
MEDLINE=21 TOV NIG661 / Dibbed-10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 cholerae.";
Nature 406:477-483(2000).
-!- DOMAIN: CONSISTS OF TWO DISTINCT DOMAINS; ONE IS A HEME-CONTAINING OXYGEN BINDING DOMAIN IN THE N-TERMINAL REGION AND THE OTHER IS AN FAD-CONTAINING REDUCTASE DOMAIN FOUND IN THE C-TERMINAL REGION.
-!- SMILARITY: BELONGS TO THE GLOBIN FAMILY. TWO-DOMAIN FLAVOHEMOPROTEINS SUBFAMILY.
-!- SIMILARITY: 10 A NUMBER OF FAD/NAD(P) FLAVOPROTEIN OXIDOREDUCTASES.
 InterPro; IPR008333; FAD_binding_6.

InterPro; IPR008333; FAD_binding_6.

InterPro; IPR001709; FPN cyt_redctse.

InterPro; IPR001709; FPN cyt_redctse.

InterPro; IPR001431; Oxced FAD/NAD(P).

InterPro; IPR00121; Phe hydroxylase.

Pfam; PF000175; NAD_binding_1; 1.

Pfam; PF00175; NAD binding_1; 1.

PRINTS; PR003410; PHENCR.

PRINTS; PR004410; PHENCRYLASE.

PROSITE; PS01033; GLOBIN; 1.

M OXYGEN transport; Transport; Complete proteome.

I 136

GLOBAIN.
 'DNA sequence of both chromosomes of the cholera pathogen Vibrio
 (BY SIMILARITY).
IRON (HEME PROXIMAL LIGAND)
(BY SIMILARITY).
NADP (RIBOSE PRAT) (BY SIMILARITY).
) DDA3490FAE28823A CRC64;
 Flavohemoprotein (Hemoglobin-like protein) (Flavohemoglobin).
 Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
 68.0%; Score 34; DB 1; Length 394; 66.7%; Pred. No. 13;
 (HEME DISTAL LIGAND)
 268 273 N
394 AA; 44191 MW;
 EMBL; AE004358; AAF96096.1; -.
PIR; F82491; F82491.
 82
 HSSP; P39662; 1CQX.
TIGR; VCA0183; -.
 Query Match
Best Local Similarity
 Vibrio cholerae.
 82
 HMP OR VCA0183.
 NCBI_TaxID=666;
 NP BIND
SEQUENCE
 METAL
 METAL
```

```
MEDINE-2019066; PubMed=10731132;

MEDINE-20190606; PubMed=10731132;

Manatides F.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Baradon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Feelffer B.D., Man K.H., Doyle C., Baxter E.G., Helt G., Nolson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D., Ballews R.W., Basu A., Baxendall J., Baytaktaroglu L., Beasley E.M., Basendan R.C., Berman B.P., Bhandari D., Bolbhakov S., Bortchan M.R., Botchan M.R., Boutler H., Cadieu E., Center A., Chandra I., Abril J.F., Doule D.A., Dahlke C., Davemport L.B., Davies P. M., Abburis K.C., Busam D.A., Dahlke C., Davemport L.B., Davies P., Dann P., Boddon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Boddon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Boddon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Boddon K., Ond J. H., Malan R.J., Hernandez J.R., Houck J., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jaskop M., Malush F., Karpen G.H., Ke Z., Kennigon J.A., Ketchhum K.A., Andlush F., Karpen G.H., Ke Z., Kennigon J.A., Ketchhum K.A., Morintobh T.C., McLeod M.P., Morintobh J.C., Morrite J., Morntobh J., Muzphy D., Holls M., Morntobh J., Muzphy D., Morintobh J.C., Morrite J., Morntobh J., Malan M.-H., Strong P., Shen H., Reser M., Reinert K., Salden-Kamoo I., Singeon M., Stupek M., Shelsen B., Sherding A., Sahadhano J., Pullame S.M., Woodaer E., Wang K., Malan R., Shelsen B.C., Staden J., Walles P.C., Staphedon M., Strong R., Shelsen B., Spradding A., Sanders R., Wallsenbach J., Walles B.C., Staphedon M., Shelsen B., Shelsen B., Zaveri J.S., Zhan M., Zhong Y., Zhong Y., Zhong Y., Walles B.C., Staphedon M., Shelsen B., Shelsen B., Shelsen B., Shelsen B., Shelsen B., Shel
P55824; Q9V9T6; Q9Y0Z7;
01-NOV-1997 (Rel. 35, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MRR-2004 (Rel. 43, Last annotation update)
Probable ubiquitin carboxyl-terminal hydrolase FAF (EC 3,1.2.15)
Probable ubiquitin acrosyl-terminal hydrolase FAF (EC 3,1.2.15)
(Ubiquitin thiolesterase FAF) (Ubiquitin-specific processing protease
FAF) (Ubiquitin mesanogaster (Fruit fly)
Buraryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Buyaryota; Arthropoda; Hexapoda; Insecta; Pterygota;
Byhydroidea; Drosophilidae; Drosophila.
 REVISIONS, AND ALTERNATIVE SPLICING.
MEDLINE=22450669; Pubmed=1257572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whiffield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), AND TISSUE SPECIFICITY. TISSUE=Bye imaginal disk;
MEDLINE=93.0020; PubMed=195747;
Fischer-Vize J.A., Rubin G.M., Lehmann R.;
"The fat facets gene is required for Drosophila eye and embryo
 development.";
Development 116:985-1000(1992).
 Science 287:2185-2195(2000).
 SEQUENCE FROM N.A.
 Lewis S.E.;
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Gaps

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3; Indela

0; Mismatches

6; Conservative

Matches

à

2778 AA.

PRT;

STANDARD;

FAF\_DROME

FAF\_DROME ID FAF D

RESULT 7

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EMBL; L04959; AAF01345.1; -

EMBL; L04959; AAF01345.1; -

BRED; L04960; AAF01347.1; -

BRED; L04960; AAF01347.1; -

BRED; L04960; AAF01348.1; -

BRED; L04960; AAF01348.1; -

BRED; AE003779; AAN14291.1; -

BRED; AE003779; AAN14291.1; -

BRED; AE0000532; fat,

BRED; AE000533; Princlear migration; IMP.

CO; GO:0006513; Princlear migration; IMP.

BRED; AE000533; UCH 2.1; 1.

BRED; BREOSTE; PS00973; UCH 2.1; 1.

BRED; BRED; BREOSTE; BREOSTE; BREOSTE; BREOSTE; BREOSTE; BREOSTE; BRED; BREOSTE; B
 | SEQUENCE OF 1089-2778 FROM N.A. (ISOFORM 1).
| SEQUENCE OF 1089-2778 FROM N.A. (ISOFORM 1).
| STRAIN=Berkeley; | Secure 10.2. | Strain=20196012; | Submed=10731138; | Strain=20196012; | Submed=10731138; | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012. | Strain=20196012.
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 -i- TISSUB SPECIFICITY: Eye disks and ovaries.
-i- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
-i- SIMILARITY: Belongs to peptidase family C19.
 CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)0 = ubiquitin + a thiol.
ALTERNATIVE PRODUCTS:
 Event=Alternative splicing, Named isoforms=3;
Comment=Experimental confirmation may be lacking for some
Annotation of the Drosophila melanogaster euchromatic genome:
 Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 IsoId=P55824-2; Sequence=VSP_005270;
 sold=P55824-3; Sequence=VSP 005269;
 IsoId=P55824-1; Sequence=Displayed;
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 IATAATLEPAGNSELTTMVEKNLIISQENPQAKSSLQ -> SQRQQL (in isoform 2).
/FTIG-VSP 005270.
E > D (IN REF. 1).
T -> S (IN REF. 1), ARF01345).
MW; FFB90438BA53A02B CRC64;
 Nature 345:356-359(1990).

-!- FUNCTION: REV APPEARS TO ACT POST-TRANSCRIPTIONALLY TO RELIEVE

-!- FUNCTION: REV APPEARS TO ACT POST-TRANSCRIPTIONALLY TO RELIEVE

-!- SUBCELLULAR LOCATION: Nuclear; accumulates in the nucleoli.

-!- PTM: Phosphoprotein whose state of phosphorylation is mediated by a specific serine kinase activity present in the nucleus.
 Gaps
 MEDINE=90259077; PubMed=2188136;
Huet T., Cheynier R., Meyerhans A., Roelants G., Wain-Hobson S.;
"Genetic organization of a chimpanzee lentivirus related to HIV-1.";
 Gaps
 EMBL; X52154; CAA36405.1; -.
PIR, S09988; VKLJSI.
HIV, X52154; REV$CD:
InterPro; IPR000625; REV_protein.
Pfam; PF00424; REV; 1.
Prams PF00424; REV; 1.
Pramscription regulation; AIDS; Phosphorylation; Nuclear protein.
SEQUENCE 124 AA; 13701 MW; FS877DIBDF65A7B2 CRC64;
 01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28.FEB-2103 (Rel. 41, Last amnotation update)
REV protein (Anti-repression transactivator protein) (ART/TRS).
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 Score 34; DB 1; Length 2778; Pred. No. 97; 2; Mismatches 3; Indels
 66.0%; Score 33; DB 1; Length 124; 60.0%; Pred. No. 6.2; indels tive 1; Mismatches 3; Indels
 Chimpanzee immunodeficiency virus (SIV(cp2)) (CIV).
Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11723;
/FTId=VSP_005269
 (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
 68.0%;
54.5%;
 234 234
2725 2725
2778 AA; 311139
 1394 ÉVIVPDGQDFS 1404
 6, Conservative
 Conservative
 STANDARD;
 STANDARD;
 1 EEVVPXGXDYS 11
 | || | :||
ETVPAGGNYS 116
 2 EVVPXGXDYS 11
 Query Match
Best Local Similarity
 Local Similarity
 SEQUENCE FROM N.A.
 28-FEB-2003 () 28-FEB-2003 () 28-FEB-2003 ()
 REV SIVCZ
P17280;
 TPX LISIN
Q92BCS;
 107
 CONFLICT
CONFLICT
SEQUENCE
 VARSPLIC
 TPX_LISIN
ID TPX_LI
AC Q92BC
DT 28-FB
DT 28-FB
DT 28-FB
 Best Loca
Matches
 REV_SIVCZ
ALC SETURE SACTOR
ALC SETURE SETUPE SETUPE SETUPE SETUPE SETURE SETURE SETUPE SETURE RESULT 9
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 셤
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Listilist, LM001583; -.
HAMAP; MF_00269; -; 1.
InterPro; IPR00086f; AhpC-TSA.
InterPro; IPR002065; TPX.
Pfam; PF00578; AhpC-TSA; 1.
PROSITE; PS01265; TPX; 1.
 EMBL; AL591979; CAC99661.1; -.
 Query Match
Best Local Similarity bb...
6, Conservative
 Nature 368:32-38(1994)
 144 EVVPEGSDH 152
 2 EVVPXGXDY 10
 SEQUENCE FROM N.A.
 Wohldman P.;
 RESULT 11
YK14_CAEEL
 PTT SERVE SE
ઠે
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the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license gareement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 ..
 STRAIN-CLIP 11262 / Serovar 6a;

MEDLINE=21537279; Pubbed=11679669;

Glaser P., Frangeul L., Buchrieser C., Rueniok C., Amend A.,

Baquero F., Berche D., Buchrieser H., Brandt P., Chakraborty T.,

Charbit A., Chetouani F., Couve B., de Daruvar A., Deboux P.,

Entian K.-D., Fshih H., Garcia-del Portillo F., Garrido P.,

Entian K.-D., Fshih H., Gamca-Lopez N., Hain T., Hauf J., Dussurget O.,

Adutier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Jones L.-M., Kaerst U., Kreft V., Kunst F., Kurapkat G.,

A Madueno E., Maltournam A., Mata Vicente J., Ng E., Nedjari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,

"Comparative genomics of Listeria species.",

Comparative genomics of Listeria species.",

I. Science 294:849-852(2001).

H.(2)(2) (2) (8) similarity).
 Gaps
 ö
 STRAIN=EGD-e / Serovar 1/2a;
MEDLINE=21537279; PubMed=11679669;
Glaeer P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Glaeer P., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
 -!- SIMILARITY: Belongs to the ahpC/tsa family. Tpx subfamily.
 Antioxidant; Oxidoreductase; Peroxidase; Complete proteome.
 66.0%; Score 33; DB 1; Length 165; 66.7%; Pred. No. 8.4; cive 1; Mismatches 2; Indels
 Listeria monocytogenes.
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TaxID=1639;
 Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
 77705B7CD8BC8F4D CRC64;
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FED-2005 (Rel. 41, Last annotation update)
TPX OR LMO1583.
 165 AA.
Probable thiol peroxidase (EC 1.11.1.-)
 PRT;
 EMBL; AL596169; CAC96856.1; -.
PIR; AH1635; AH1635.
LidtList; LIN01625; -.
HAMAP; MF 00269; -; 1.
InterPro; IPR000866; AhpC-TSA.
Pfam; PF00578; AhpC-TSA.
PROSITE; PS01265; TPX.
 165 AA; 18162 MW;
 Ouery Match
Best Local Similarity 66...
6; Conservative
 STANDARD;
 144 EVVPEGSDH 152
 2 EVVPXGXDY 10
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 IPX OR LIN1625. Listeria innocua.
 NCBI_TaxID=1642;
 TPX LISMO
 SECUENCE
 TPX_LISMO
 RESULT 10
```

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 MEDLINE=STISTOIN?;
MEDLINE=STISTOINS;
Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Wilson R., Ainscough R., Comell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Garcher A., Green P., Hawkins T., Hillier L., Jier M.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Rooper A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer B., Staden R.,
Sulston J., Thlery Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Gaps
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 ..
0
 Antioxidant, Oxidoreductase, Peroxidase, Complete proteome.
SEQUENCE 165 AA, 18133 MW, 77705B7CC46D424D CRC64,
 66.0%; Score 33; DB 1; Length 165; 66.7%; Pred. No. 8.4; 1; Mismatches 2; Indels
 TYTA CAREL STANDARD; PRT; 327 AA. P3438; Created) 01-FEB-1994 (Rel. 28, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Hypothetical protein C15H7.4 in chromosome III. Caenorhabditis elegans.
```

```
STRP3
 ACT SITE
SEQUENCE
 ACT_SITE
 Query Match
 Matches
ઠે
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 ö
 01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acyl-CoA dehydrogenase, medium-chain specific, mitochondrial precursor (EC.1.3.99.3) (MCAD).
 -!- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
 -!- SUBUNIT: Homotetramer.
-!- SUBCELLULAR LOCATION: Mitochondrial matrix.
-!- MISCELLANEOUS: A number of straight-chain acyl-CoA dehydrogenases
of different substrate specificities are present in mammalian
 Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
 iiol. Chem. 262:10104-10108(1987).
FUNCTION: This enzyme is specific for acyl chain lengths of 4 to
 Gaps
 -!- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
 TISSUE-Liver;
MEDLINE-67280028; PubMed=3611054;
Matsubara Y., Kraus J.P., Ozasa H., Glassberg R., Finocchiaro G.,
Ikeda Y., Mole J., Rosenberg L.E., Tanaka K.;
"Molecular cloning and nuclectide sequence of cDNA encoding the
entire precursor of rat liver medium chain acyl coenzyme A
 ..
 -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
 66.0%; Score 33; DB 1; Length 327; 63.6%; Pred. No. 17;
 3; Indels
 PIR; S40753; S40753.

Wormbep, C15H7.4; CB00082.

Hypothetical protein.

SEQUENCE 327 AA; 35566 MW; 716BC2BDD2E9607E CRC64;
 1; Mismatches
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 EMBL, J02791, AAA40670.1; -. PIR, A28436; DERTCM. HSSP; P11310; 1EGD.
 EMBL; Z22173; CAA80126.1; -.
 Conservative
 KEVVPNGGDKS 185
 STANDARD;
 1 EEVVPXGXDYS 11
 Local Similarity
Les 7; Conserv
 - 1 - COFACTOR: FAD
 NCBI_TaxID=10116;
 dehydrogenase.";
J. Biol. Chem. 20
 ACDM RAT
P08503;
 175
 Query Match
 ACADM.
 Best Loc
Matches
 0
```

```
CTRAIN=SSI-1 / Serotype M3;

X MEDLINE=22683278; PubMed=12799345;

Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,

Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,

A Nakagawa I., Kurokawa K., Yamashita A., Shiba T., Yasunaga T.,

A Chanachi N., Kawabata S.,

A Hayashi H., Hattori M., Hamada S.;

A Genome sequence of an M3 strain of Streptococcus pyogenes reveals at a nate-scale genomic rearrangement in invasive strains and new insights into phage evolution.";

Targe-scale genomic rearrangement in invasive strains and new insights into phage evolution.";

Genome Res 13:1042-1055(2003)

C CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +

Gliphosphate + L-arginyl-tRNA(Arg).

C -1 SUBUNIT: Monomer (By similarity).

C -1 SUBUNITY: Belongs to class-I aminoacyl-tRNA synthetase family.
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 ö
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43) Last annotation update)
Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
ARGS OR SPYM3_1809 OR SPS1807.
 193 193 FORMS A HYDROGEN-BOND WITH THE FLAVIN N(5) OF THE FAD COFACTOR (BY SIMILARITY) 401 BASE (BY SIMILARITY). 421 AA, 46555 MW; 2CF076F8C919BDE8 CRC64;
 STRAIN=MGAS315 / Serotype M3;
STRAIN=MGAS315 / Serotype M3;
MEDLINE=22133808; PubMed=12122206;
MEDLINE=22133808; PubMed=12122206;
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D., Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.; Strain of group A Streptococcus: migenome sequence of a serotype M3 strain of group A Streptococcus: phage-encoded toxins, the high-virulence phenotype, and clone
 Gaps
 ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC.
 ;
R InterPro; IPR006089; Acyl-CoA dh.
R InterPro; IPR006090; Acyl-CoA_dh_C.
R InterPro; IPR006091; Acyl-CoA_dh_M.
InterPro; IPR006091; Acyl-CoA_dh_M.
R Pfam; PF00441; Acyl-CoA_dh; 1.
R Pfam; PF00770; Acyl-CoA_dh; 1.
R PR0SITE; PS00072; Acyl-CoA_DH 1; 1.
R PROSITE; PS00073; Acyl-CoA_DH 1; 1.
R Acyl-CoA_DH 1; 1.
R Mitochondrion; Transit peptide.
M Mitochondrion; Transit peptide.
T TRANSIT

T CHAIN

T
 66.0%; Score 33; DB 1; Length 421; 50.0%; Pred. No. 22; tive 2; Mismatches 3; Indels
 Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002)
 Local Similarity 50.0
 1 EEVVPXGXDY 10
 ||::|
58 EEIIPVAPDY 67
 SEQUENCE FROM N.A.
 Streptococcus.
NCBI_TaxID=198466;
```

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RESULT 15
SYR STRPY
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 EMBL; AE014171; AAM80416.1; -.

R EMBL; AP005146; BACG4902.1; -.

R HAMAPP, MF 00123; -; 1.

R INTERPRO; IPR001278; ANG TRNA-synt_lc.

R INTERPRO; IPR005148; N.

R INTERPRO; IPR004192; tRNA-synt_ld_C.

R INTERPRO; IPR004192; tRNA-synt_ld_C.

R INTERPRO; IPR005148; N.

R PFGM; PF00750; tRNA-synt_ld_1.

R PFGM; PF00750; tRNA-synt_ld_1.

R PFGM; PF00750; tRNA-synt_ld_2.

R PRINTS; PR01038; TRNA-SYNTHARG.

R RINTS; PR01038; TRNASYNTHARG.

R RROSTIE; PS00178; AA TRNA LIGASE I; FALSE NEG.

R AMINOSCY1-tRNA SYNTHEASE; ProteIn biosynthesis; Ligase; AIP-binding;
 Z8-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Arginyl--ENA syntherase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
ARGS OR SPYMI8_2183.
 Chaussee M.S.,
 Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Museer J.M.; Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever
 outbreake.";

outbreake.";

outbreake.";

outbreake.";

1- CATALYIL Acad. Sci. U.S.A. 99:4668-4673(2002).

1- CATALYIL ACAT ATP + L-arginine + tRNA(Arg) = AMP +

diphosphate + L-arginyl-tRNA(Arg).

diphosphate + L-arginyl-tRNA(Arg).

- SUBGELULAR LOCATION: Cytoplasmic.

- SUBGELULAR LOCATION: Cytoplasmic.

- SUMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
 Gaps
 ..
 66.0%; Score 33; DB 1; Length 563; 45.5%; Pred. No. 30;
 3; Indels
 Streptococcus pyogenes (serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 121 131 "HIGH" REGION.
563 AA; 63134 MW; BOB7DEC31A9DCF63 CRC64;
 PRT; 563 AA.
 3; Mismatches
 STRAIN=MGAS8232 / Serotype M18;
MEDLINE=21927593; PubMed=11917108;
 EMBL; AE010119; AAL98627.1; -.
HAMAP; MF_00123; -; 1.
 Query Match
Best Local Similarity 45.5
Matches 5; Conservative
 |:|: | ||:
94 EQVITAGSDYA 104
 STANDARD;
 1 EEVVPXGXDYS 11
 Complete proteome.
 NCBI_TaxID=186103;
 SEQUENCE FROM N.A.
 STRP8
 SEQUENCE
 SYR STRP8
```

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 ö
 MEDULINE ALIBYCOGY; FURNICALITY AGAIN BAND. Savic D.J., Savic G., Lyon K., Perretti J.J., McShaw W.M., Again D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar P.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., Mchaughlin R., Complete genome sequence of an M1 strain of Streptococcus pyogenes."; Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
-!- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP + diphosphate + L-arginyl-tRNA(Arg).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
InterPro; IPR001278; Arg_tRNA-synt_lc.
InterPro; IPR0050148; NN.
InterPro; IPR005099; ERNA-synt_ld_C.
InterPro; IPR009099; ERNA-synt_ld_C.
Pfam; PF001485; N-Arg; 1.
Pfam; PF00748; ERNA-synt_ld; 1.
Pfam; PF00746; tRNA-synt_ld; 1.
PRINTS; PR01038; TRNASYNTHARG.
TIGRFAMS; TIGR00456; args; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
ARGS OR SPY2151.
 Gaps
 .
 66.0%; Score 33; DB 1; Length 563; 45.5%; Pred. No. 30; ive 3; Mismatches 3; Indels
 Streptococcus pyogenes.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
 563 AA; 63134 MW; FECAF176A68D8B5B CRC64;
 563 AA.
 "HIGH" REGION
 SEQUENCE FROM N.A. SECUTION SECUTION STRAIN-SF370 / ATCC 700294 / Serotype M1;
 HAMAD, MF_00123; -; 1.
InterPro; IPR001278; Arg_tRNA-synt_lc.
InterPro; IPR005148; N.
InterPro; IPR006959; tRNA-synt_ld_C.
InterPro; IPR001412; tRNA-synt_l.
 STRAIN=SF370 / ATCC 700294 / Serot)
MEDLINE=21192684; PubMed=11296296;
 Pfam, PP03465, N.Arg, 1.
Pfam, PP03465, N.Arg, 1.
Pfam, PP05746, FRNA-Synt_ld, 1.
Pfam, PP05746, FRNA-Synt_ld, 2.
Prints, PR0303, TRNA-SyntHarg.
 ÈMBL; AE006633; AAK34788.1; -.
HSSP; Q05506; 1BS2.
 Query Match 66.0
Best Local Similarity 45.5
Matches 5; Conservative
 STANDARD;
 94 EQVITAGSDYA 104
 1 EEVVPXGXDYS 11
 Complete proteome.
SITE
 NCBI_TaxID=1314;
 SYR STRPY
Q99XL5;
 SEQUENCE
 PHHHBBOOOCOREAREE REAREE ROOCOCOCOCORE REAREE ``

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DR PROSITE; PS00178; AA TRNA LIGASE I; FALSE NEG.

KW Aminoacyl-tRNA synthetase; Protein blosynthesis; Ligase; ATP-binding;

KW Complete proteome.

FT SITE

SQ SEQUENCE 563 AA; 63120 MW; B0F2CAC28D03B613 CRC64;

Query Match

Best Local Similarity 45.5%; Pred. No. 30;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

Search completed: June 3, 2004, 11:49:56 Job time : 4.86667 secs

1 EEVVPXGXDYS 11 |:|: | ||: 94 EQVITAGSDYA 104

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June 3, 2004, 11:35:06; Search time 29.8667 Seconds (without alignments) 116.206 Million cell updates/sec tun on:

US-09-909-164-46

1 EEVVPXGXDYS 11 fitle:
Perfect score: 3equence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1017041 seqs, 315518202 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL 25:* Database :

sp_archea:*
sp_bacteria:*
sp_fungl::*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mter
sp_organelle:*
sp_organelle:*
sp_phage:* unclassified:* sp_vertebrate:* sp_plant:* rvirus:* sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

bacteriap: *

sp_archeap:

SUMMARIES

Q82zb4 enterococcu O52367 rhizoblum t Q8esv7 oceanobacil Q30260 archaecoglob Q946j7 andrographi Q8dihO synechococc Q5xet4 canis famil Q81033 bos taurus Q81031 bos taurus Description Q9xst4 Q8i033 Q8i031 Q000404 Q822B4 O52367 Q8ESV7 O30260 Q94647 Q8DIHO Q9XST4 Q8I033 Q9I031 Query Match Length DB Score Result g

ω Δ	Q40129 lycoperai.co Q8xpa8 clostridium Q8fpy9 corynebacte Q83m9 tropheryma Q88t43 rhizobium e Q8k143 rhizobium e Q9yfi3 aeropyrum p Q87126 mus musculu Q8btx4 mus musculu Q8btx5 mus musculu Q8btx5 mus musculu Q8btx5 mus musculu Q8btx5 mus musculu Q8btx5 raistonia s
Q84V54 Q012479 Q012479 Q012478 Q01266 Q020066 Q01066 Q0174 Q0174 Q01745 Q0174 Q01745 Q01745 Q01745 Q01745 Q01745 Q01745 Q01745 Q01745 Q01745 Q	040129 040129 087878 088789 088743 077030 077030 087126 087126 0887126 0887126 0887126
100 000 000 000 000 000 000 000 000 000	36111116 136111116
9006 117766 1284 1283 14433 114433 1196 1196 1196 1222	22222222222222222222222222222222222222
๚๚๚๚๚๚๚๚๚๚๚๚๛๛๛๛๛	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	W U U U U U U U U U U U U U U U U U U U

ALIGNMENTS

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TEXTURE FROM N.A.

(1)

SEQUENCE FROM N.A.

STRAIN=V583 / ATC. 700802;

STRAIN=V583 / ATC. 700802;

MEDLINE=22550857; PubMed=12663927;

MEDLINE=22550857; PubMed=12663927;

A Read T.D., Fourte D.E., Bleen J.A., Gill S.R., Heidelberg J.F.,

A Read T.D., Fourte D.E., Juyan L., Barinkac L., Beanan M.,

A Tettelin H., Dodson R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,

A Wanthevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,

A Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;

T "Role of mobile DNA in the evolution of vancomycin-resistant

E Entercoccus facelis.";

Science 299:201-2074(2003).

REMBL: AROL6956; AA082828:1;

TIGR: EF152; --
                                                                                                                                                                                                                                                                                                                                    Enterococcus faecalis (Streptococcus faecalis).
Bacteria, Firmicutes, Lactobacillales, Enterococcaceae, Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO1264; MECHGNNEL.
PRODOM; PD007253; MS_channel; 1.
TIGRFAMS; TIGR00220; mscL; 1.
CCMplete Proteome.
SEQUENCE 149 AA, 16127 MW; 555799BF1E47D34E CRC64;
                                                                              0.1070-2003 (TrEMBLrel. 24, Created)
0.1070-2003 (TrEMBLrel. 25, Last sequence update)
0.1070-2003 (TrEMBLrel. 25, Last annotation update)
Large conductance mechanosensitive channel protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR; EF5152; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005216; F:ion channel activity; IEA.
GO; GO:0006810; F:transport; IEA.
InterPro; IPR01185; MS_channel.
Pfam; PF01741; MSGL; 1.
PRT; 149 AA.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                          MSCL OR EF3152
Q82ZB4
                                               ACCOS OCT DE LA CONTRA ```

74.0%; Score 37; DB 16; Length 149;

086745 tragulus ja 080740 agrobacteri 080xy9 bos taurus 090ee9 homo sapien 091708 neisseria m

homo sapien

Q867A5 Q8U7J0

O8HXY9

Q9UEE9 Q9JZP8 Q9VI90

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Nucleic Acids Res. 30:3927-3935(2002).

EMBL, AP004594; BAC12465.1; -
InterPro; IPR001279; Blactmase-like.

Pfam; PF00753; lactmase-B; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 319 AA; 35617 MW; 3BDAE4BF13E79E37 CRC64;
 PRT;
 EMBL, AE01109, AAB91255.1; -. PIR, D69551; D69551.
 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
 6; Conservative
 ENIVPYGIDFS 130
 PRELIMINARY;
 PRELIMINARY;
 1 EEVVPXGXDYS 11
 189 EQLVPHGIDY 198
 1 BEVVPXGXDY 10
 Query Match
Best Local Similarity
 120
 030260
 094637
 RESULT 5
Q946J7
 RESULT 4
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 EMBL, AF036920, AAC04779.1; -.

GO, GO:0046821; C:extrachronosomal DNA; IEA.

GO; GO:004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

InterPro: IPR002298; ADH zinc.

InterPro: IPR0022985; ADH zinc.

InterPro: IPR002085; ADH zinc.

PROSTIR: PS00059; ADH zinc.

PROSTIR: PS00059; ADH Zinc.

Metal-binding; Oxidoreductase; Zinc; Plasmid.
 Gaps
 STRAIN=CFN299;
Rosenblueth M., Hynes M.F., Martinez-Romero E.;
Submitted (BCC-1997) to the EMBL/GenBank/DDBJ databases.
-i- COFACTOR: ZINC (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE FAMILY.
 SECUENCE FROM N.A.
STRAINSHIEBBAI / DSM 14371 / JCM 11309;
STRAINSHIEBBAI / DSM 14371 / JCM 11309;
MEDLINE-22220767;
PLUMPGE 12220767;
PLUMPGE 12220767;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme
 ..
 ;
0
 Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus
 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
 Length 298;
 2; Indels
 3; Indels
 298 AA; 31092 MW; 49B2F8117C33AE87 CRC64;
 OBBENT; PRT; 319 AA.
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-VUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical conserved protein.
 01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TREMBLrel. 06, Last sequence update)
01-CGT-2003 (TrEMBLrel. 25, Last annotation update)
Aryl-alcohol dehydrogenase homolog (Fragment).
 72.0%; Score 36; DB 2; 50.0%; Pred. No. 19;
 Pred. No. 5.2;
0; Mismatches
 298 AA
 3; Mismatches
 70.0%;
 Best Local Similarity 70.0
Matches 7; Conservative
 Local Similarity 50.0
 PRELIMINARY;
 113 EEVVPTSEDY 122
 250 ÉIIPEGADFS 259
 2 EVVPXGXDYS 11
 1 EEVVPXGXDY 10
 Plasmid pRtrCFN299a.
 NCBI_TaxID=182710;
 SEQUENCE FROM N.A.
 Rhizobium tropici
 298
 NCBI_TaxID=398;
 Query Match
Best Local S
Matches 5
 NON TER
SEQUENCE
 052367
 RESULT 2
052367
 RESULT 3
 O8ESV7
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STRAINSTOLING AND ATCC 49558; White O., Nelson K.E., Klenk H.-P., Clayton R.A. Tomb J.-F., White O., Nelson K.E., Klenk H.-P., Clayton R.A. Tomb J.-F., White O., Nelson K.E., Klenk H.-P., Clayton R.A., Gwinn M., Hickey E.K., Peterson J.D., Kerlardeg A.R., Graham D.E., Krypides N.C., Flichadson D.L., Kerlardeg A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Corton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R., Wenter J.C.,
 Gaps
 Gaps
 "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
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 Q946J7;
01-DEC-2001 (TrEMBirel. 19, Created)
01-DRA-2003 (TrEMBirel. 23, Last sequence update)
01-OCT-2003 (TrEMBirel. 25, Last annotation update)
3-hydroxy-3-methylglutaryl-coenzyme A reductase (EC 1.1.1.34).
HMGR1.
 72.0%; Score 36; DB 17; Length 363; 54.5%; Pred. No. 24; tive 2; Mismatches 3; Indels
Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCbl_TaxID=2234;
 Interprof. IPR002103; Bac_luciferase.
Pfam; PR00296; bac_luciferase; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 363 AA; 41736 MW; 0E976EAE788F4803 CRC64;
 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein AF2411.
 595 AA.
 363 AA
 SEQUENCE FROM N.A.
STRAIN=VC-16 / DSM 4304 / ATCC 49558;
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Complete proteome.
SEQUENCE 1044 AA; 113205 MW; 00B9C13F0F636D2F CRC64;
 70.0%;
 72.0%;
 Query Match
Best Local Similarity 54.5
Best Local 6; Conservative
 Query Match
Best Local Similarity 63...
7; Conservative
 PRELIMINARY;
 843 EEVLPNGIGYS 853
 PRELIMINARY;
 |: || | :||
16 EDYVPSGGEYS 26
 1 EEVVPXGXDYS 11
 1 EEVVPXGXDYS 11
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Q9XST4
 Q81033
 RESULT 8
 RESULT 7
 Q8I033
 Q9XST4
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 8
 Andrographis paniculata...;

Andrographis paniculata...;

Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AFS98979, AALS8015.2;

BMBL, AFS989797, AALS8015.2;

GO; GO:0016071; C:integral to membrane; IEA.

GO; GO:0016071; C:integral to membrane; IEA.

GO; GO:0004420; F:hydroxymethylglutaryl-CoA reductase (NADPH)...; IEA.

GO; GO:0006629; P:hipid metabolism; IEA.

GO; GO:0006629; P:hipid metabolism; IEA.

GO; GO:0006629; P:hipid metabolism; IEA.

MILERPRO; IPR00202; HMG_CoA_red.

INTERPRO; IPR00202; HMG_CoA_red.

INTERPRO; IPR009029; HMG_CoA_Rub.

INTERPRO; IPR009029; HMG_COA_Rub.

INTERPRO; IPR009029; HMG_COA_Rub.

INTERPRO; IPR009029; HMG_COA_Rub.

INTERPRO; IPR009039; HMG_COA_RubUCTASE_1; I.

INTERPRO; IPR009039; HMG_COA_RubUCTASE_1; I.

INTERPRO; IPR009039; HMG_COA_RubUCTASE_3; I.
 ö
 C STRAIN=BP-1;

W MEDLINE=2225144; PubMed=12240834;

W MEDLINE=2225144; PubMed=12240834;

W Adamura Y., Kaneko T., Sato S., Itiguchi M., Katoh H., Sasamoto S.,

W Adamabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,

W Atlanabe A., Iriguchi M., Matsumoto M., Matsumo A., Nakazaki N.,

Kiyokawa C., Kohara M., Takeuchi C., Yamada M., Tabata S.,

Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.,

Thermosynachococus elongatus BP-1.";

RL DNA Res 9:123-130(2002).

DR RDS 9: 9:123-130(2002).

DR GO; GO:0005215; Firransporter activity; IEA.

DR InterPro; IPRO0136; Acrflvin_res.

DR Firm; PF00873; ACR Eran; I.

DR PRIWES; PR00702; ACRIFLAVINRP.
 Andrographis paniculata.
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; asterids;
lamiids; Lamiales; Acanthaceae; Acanthoideae; Ruellieae;
 Gaps
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 72.0%; Score 36; DB 10; Length 595; 70.0%; Pred. No. 42; 3; Indels tive 0; Mismatches 3; Indels
 Krishnan S., Banerjee N.S.;
"3-hydroxy-3-methylglutaryl coenzyme A reductase gene from
 Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
 595 AA; 63268 MW; 19A3EA572F67AB2E CRC64;
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Multidrug efflux transporter.
TLLIGIS
 PRT; 1044 AA.
 Andrographinae, Andrographis
 Conservative
 PRELIMINARY;
 2 EVVPXGXDYS 11
 15 EVAPPGHDYS 24
 Query Match
Best Local Similarity
Matches 7; Conserv
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Oxidoreductase
 SEQUENCE
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 RESULT 6
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 Ol-WAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Human-type bont protein.
Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
 Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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Score 36; DB 16; Length 1044;
Pred. No. 79;
 Query Match
70.0%; Score 35; DB 6; Length 175;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 3; Indels
 Score 35; DB 6; Length 78;
Pred. No. 6.8;
2; Mismatches 3; Indels
 STRAIN=Jersey,
Iwashita S., Itoh T.,
Iwashita S., Itoh T.,
A Lins-mediated gene diversity.";
Submitted (MRR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AB081003, BAC11952.1; --
SEQUENCE 175 AA, 19529 MW, CB7283CB98393BE6 CRC64;
 SEQUENCE 78 AA; 8895 MW; B62486313555FBA1 CRC64;
 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 175 AA.
 78 AA
 1; Mismatches
 PRT;
 P97 homologous protein (Fragment)
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Q8I031

RESULT

081031

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"Geno S., Kimura J., Kurohmaru M., Fukuta K., Iwashita S.;
"Gene organization of the chevrotain bcnt whose paralogue in ruminantia includes an endonuclease domain of RTE-1 in the protein.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

BERBL; AB103377; BAC57061.1; -.

NON TER.
Q867A5
AC Q867A5
AC Q867A5
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DT 1-JUN-2003 (TrEMBLrel. 24, Last update)
DT 1-JUN-2003 (TrEMBLrel. 24, Last update)
DT 1-JUN-2003 (TrEMBLrel. 24, Last update)
DT 1-JUN-2003 (TrEMBLrel. 24, Last update)
DT 1-JUN-2003 (TrEMBLrel. 24, Last update)
DT 1-JUN-2003 (TrEMBLrel. 24, Last update)
DT 1-JUN-2003 (TrEMBLrel. 24, Last update)
DT 1-JUN-2003 (TrEMBLrel. 24, Last update)
DT 1-JUN-2003 (TrEMBLrel. 24, Last update)
DT 1-JUN-2003 (TrEMBLrel. 24, Last update)
DT 1-JUN-2003 (TrEMBLrel. 24, Last up
 70.0%; Score 35; DB 6; Length 281; 54.5%; Pred. No. 29; tive 2; Mismatches 3; Indels
 281 AA; 31557 MW; 8133A9BAFF7509A6 CRC64;
 Science 294:2317-2323(2001).
 Conservative
 PRELIMINARY;
 1 EEVVPXGXDYS 11
 EDYVPSGGEYS 18
 Tragulidae; Tragulus.
NCBI_TaxID=9849;
 SEQUENCE FROM N.A.
 Local Similarity
 SEQUENCE FROM N.A.
TISSUE=Liver;
 SEQUENCE
 Query Match
 RESULT 12
Q8U7J0
 Matches
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 ;
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 Gaps
 Bos taurus (Bovine).
Bukaryota, Metazooa; Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria, Cetartiodactyla; Ruminantia; Pecora, Bovoidea;
Bovidae; Bovinae, Bos
 01-JU., 1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
P97 homologous protein.
P97 homologous protein.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 70.0%; Score 35; DB 4; Length 217; 54.5%; Pred. No. 22; ive 2; Mismatches 3; Indels
 Score 35; DB 6; Length 215;
Pred. No. 22;
2; Mismatches 3; Indels
 STRAIN=RZPD #750;
Iwashita S., Itoh T., Sezaki M., Oshima K., Hashimoto E. Kitagawawa Y., Takahashi T., Masul T., Hashimoto K.;
"A LINE-mediated gene diversity.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB081095;
BALSS, BAC1593.1;
NON_TER
 215 AA; 23822 MW; 7287C8B98E9D05C8 CRC64;
 Q81031;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
H-MAR-2003 (TrEMBLrel. 23, Last annotation update)
H-type bcnt protein (Fragment).
 215 AA
 PRT;
 70.0%;
54.5%;
 Query Match
Query Match
Best Local Similarity 54.55,
Best Local 6; Conservative
 6; Conservative
 PRELIMINARY;
 PRELIMINARY;
 1 EEVVPXGXDYS 11
 |: || | :||
16 EDYVPSGGEYS 26
 16 EDYVPSGGEYS 26
 1 EEVVPXGXDYS 11
 |: || | :||
16 EDYVPSGGEYS 26
 1 EEVVPXGXDYS 11
 Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=9913;
 Query Match
 SEQUENCE
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RESULT 10

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Matches

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RESULT 11

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Gaps

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MEDINE=21608551; PubMed=11743194; Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Goodner B., Hinkle G., Gattung S., Miller N., Halling C., Mullin L., Gurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Hounlam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flansgan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Ciel C., Slater S., Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";
 Nester B.W.;
"The genome of the natural genetic engineer Agrobacterium tumefaciens
 MEDINTE-2160850; PubMed=11743193; Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Mond G.E., Almeida N.F. Jr., Woo L., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Kutyavin T., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saemphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.NCBI _TaxID=176299;
 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
6-O-methylguanine-DNA methyltransferase.
ADA OR ATU4459 OR AGR L 218.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
290 AA.
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SEQUENCE FROM N.A.

STRAIN=MC58 / Serogroup B;

STRAIN=MC58 / Serogroup B;

STRAIN=MC58 / Serogroup B;

WEDLINR=2010755; PubMed=10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,

Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hackey E.K.,

Mason T., Ciacko A., Parksey D.S., Blair E., Cittone H., Clark B.B.,

Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,

Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., San L.,

Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.;

"Complete genome sequence of Neisseria meningitidis serogroup B strain
 SEQUENCE FROM N.A.
MEDILIPE-99267221; PubMed=9602175;
MEDILIPE-98267221; PubMed=9602175;
Takahashi I., Nobukuni T., Ohmori H., Kobayashi M., Tanaka S.,
Ohshima K., Okada N., Masui T., Hashimoto K., Iwashita S.;
"Existence of a bovine LINE repetitive insert that appears in the CDNA of bovine procein BONT in ruminant, but not in human, genomes.";
Gene 211:387-394(1998).
 SEQUENCE FROM N.A.
Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
Kalnine N., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
Phelan M., Farmer A.,
Submitted (AUG-2003) to the EWBL/GenBank/DDBJ databases.
EMBL, ABO09285; BAA1867.1; -.
EMBL, BC000991; AAH00991.1; -.
EMBL, BT009819; AARB8821.1; -.
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
NCBI_TaxID=491;
 70.0%; Score 35; DB 4; Length 299; 54.5%; Pred. No. 32; ive 2; Mismatches 3; Indels
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
 TIGR; NMB0950, -.
GO; GO:0015036, F:disulfide oxidoreductase activity, IEA.
GO; GO:0006118, P:electron transport; IEA.
InterPro; IPR003953; FAD bind2.
InterPro; IPR001327; FAD_pyr_redox.
 Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
 Genew; HGNC:1873; CFDP1.
SEQUENCE 299 AA; 33593 MW; F4A9E928B669451A CRC64;
 01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
 Succinate dehydrogenase, flavoprotein subunit
 -1. COFACTOR: FAD (BY SIMILARITY).
EMBL; AE002446; AAF41356.1; -.
PIR; F81138; F81138.
 Neisseria meningitidis (serogroup
 Science 287:1809-1815(2000)
 Best Local Similarity 54.5
Matches 6; Conservative
 PRELIMINARY;
 1 EEVVPXGXDYS 11
 16 EDYVPSGGEYS 26
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 TISSUE=Placenta;
 Query Match
 Q9JZP8
 RESULT 15
 O9JZPE
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 PIR; D98182; D98182.

PIR; D98182; D98182.

POS GO:0005622; C:intracellular; IEA.

GO; GO:0003908; F:methyltransferase activity; IEA.

GO; GO:0003168; F:renerription factor activity; IEA.

GO; GO:0006281; F:ransferase activity; IEA.

GO; GO:0006281; F:ransferase activity; IEA.

GO; GO:0006281; F:ransferase activity; IEA.

GO; GO:0006281; F:ransferase activity; IEA.

GO; GO:0006281; F:ransferase activity; IEA.

GO; GO:0006281; F:ransferase activity; IEA.

GO; GO:0006385; F:regulation of transcription, DNA-dependent; IEA.

InterPro: IPR001095; Methyltransf_1.

PEam; PP001055; HTH AraC; 2.

PEam; PP001055; Methyltransf_1; 1.
 Human-type Bont.

Bos taurus (Bovine).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Bovinae; Bos.

MCBI_TaxID=9913;
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 70.0%; Score 35; DB 16; Length 290; 50.0%; Pred. No. 31;
 70.0%; Score 35; DB 6; Length 297; 54.5%; Pred. No. 31;
 Iwashita S., Itoh T.;
"A LINE-mediated gene diversity.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, ASO81004; BAC11953.1;
SEQUENCE 297 AA; 33354 MW; D4A944BC8740373C CRC64;
 3; Indels
 SMART; SM00342; HTH_ARAC; 1.
TIGREAMS; TIGR00589; ogt; 1.
PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
Methyltransferase; Transferase; Complete proteome.
SEQUENCE 290 Aa; 31587 MW; B626592EF519977F CRC64;
 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update) BCNT protein (CRANIOFACIAL development protein 1). BCNT.
 Last sequence update)
Last annotation update)
 2; Mismatches
 2; Mismatches
 01-MAY-2000 (TrEMBLrel. 13, Created)
 Created)
 PRT;
 EMBL; AE009374; AAL45253.1; -. EMBL; AE008240; AAK88982.1; -.
 294:2323-2328(2001).
 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 1)
 Query Match
Best Local Similarity 54.5
Matches 6; Conservative
 Best Local Similarity 50.0 Matches 5, Conservative
 PRELIMINARY;
 PRELIMINARY;
 1 EEVVPXGXDYS 11
 EDYVPSGGEYS 26
 9 EDITPIGSDY 18
 1 EEVVPXGXDY 10
 SEQUENCE FROM N.A.
 TISSUE=Kidney;
 Query Match
 Science
 Q9UEE9
 COURED;
 Q8HXY9
```

RESULT 13 28HXY9

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RESULT 14 29UEE9

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Gaps

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InterPro; IPR003952; FRD/SDH_FAD_BS.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR004112; Succ DH_flav_C.
Pfam; PF00890; Prod_DH_flav_C, 1.
Pfam; PF00810; Succ_DH_flav_C, 1.
PRINTS; PR00316; PADPNR.
PRINTS; PR00411; PNDPTASEI.
PROSITE; PS00504; FRD SDH_FAD BINDING; 1.
PROSITE; PS00504; FRD SDH_FAD BINDING; 1.
PROSITE; PS010604; PR0 SDH_FAD BINDING; 1.
PROSITE; PS010604; PR0 SDH_FAD BINDING; 1.
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Query Match

70.0%; Score 35; DB 16; Length 587;

Best Local Similarity 70.0%; Pred. No. 68;

Matches 7; Conservative 0; Mismatches 3; Indels 1 EEVVPXGXDY 10 | || | || 366 EVVVPQGEDY 375 S.

0

0; Gaps

Search completed: June 3, 2004, 11:57:35 Job time: 30.8667 secs

```
Abb80525 Hepatitis
Abb80521 Hepatitis
Abb80562 Hepatitis
Abb80566 Hepatitis
Abb80567 Hepatitis
Abb80567 Hepatitis
Abb80556 Hepatitis
Abb80556 Hepatitis
Abb80556 Hepatitis
Abb80566 Hepatitis
Abb80566 Hepatitis
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 June 3, 2004, 11:31:01; Search time 45.9333 Seconds (without alignments) 67.664 Million cell updates/sec
 Description
 1586107
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1586107 segs, 282547505 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - protein search, using sw model
 ABB 0052
ABB 00521
ABB 00566
ABB 00563
ABB 00563
ABB 00564
ABB 0059
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 A_Geneseq_29Jan04:*
1: geneseqp19f67
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 Winimum DB seq length: 0
Maximum DB seq length: 200000000
 US-09-909-164-47
52
1 EEVVPXGMSYS 11
 Query
Match Length
 Copyright
 Score
 score:
 scoring table:
 M protein
 searched:
 equence:
 Database
 ino un;
 Result
```

| 56         | 44 | 84.6 | 77   | 'n | ABB80544 | Abb80544 | Hepatitis |
|------------|----|------|------|----|----------|----------|-----------|
| 27         | 44 | 84.6 | 11   | Ŋ  | ABB80553 | Abb80553 | Hepatitis |
| 28         | 44 | •    | 11   | ភា | ABB80552 | Abb80552 | Hepatitis |
| 29         | 44 | 4    | 11   | w  | ABB80545 | Abb80545 | Hepatitis |
| 30         | 42 | 80.8 | 11   | Ŋ  | ABB80530 | Abb80530 | 끍         |
| 31         | 41 | 8    | 11   | ß  | ABB80542 | Abb80542 | Hepatitis |
| 32         | 41 | 8    | 11   | ß  | ABB80543 | Abb80543 | Hepatitis |
| 33         | 41 |      | 11   | Ŋ  | ABB80538 | Abb80538 | Hepatitis |
| 34         | 40 |      | 11   | ហ  | ABB80548 | Abb80548 | Hepatitis |
| 32         | 40 | ġ    | 11   | ß  | ABB80547 | ADD80547 | ü         |
| 36         | 40 | ė    | 11   | w  | ABB80556 | Abb80556 | Hepatitis |
| 37         | 40 | 76.9 | 11   | Ŋ  | ABB80557 | Abb80557 | Hepatitis |
| 38         | 40 |      | 11   | ហ  | ABB80537 | Abb80537 | Hepatitis |
| 39         | 40 | 76.9 | 11   | Ŋ  | ABB80551 | Abb80551 | Hepatitis |
| 40         | 4  |      | 11   | 'n | ABB80541 | Abb80541 | Hepatitis |
| 41         | 40 | 76.9 | 20   | N  | AAU76810 | Aau76810 | Hepatitis |
| 42         | 40 | 76.9 | 1022 | 4  | ABG03621 | Abg03621 | Novel hum |
| 43         | 40 | 76.9 | 1022 | 4  | ABG08173 | Abg08173 | Novel hum |
| 44         | 40 | 76.9 | 1022 | 4  | ABG05826 | Abg05826 | Novel hum |
| <b>4</b> . | 39 | 75.0 | 11   | S  | ABB80546 | Abb80546 | Hepatitis |

### ALIGNMENTS

ABB80525 standard; peptide; 11 AA.

RESULT 1
ABB80525
ID ABB8

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Gaps

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Indels

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Mismatches

; 0

Conservative

11;

Matches

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have viruide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 note= "Norvalyl carbonyl forming keto-amide linkage with
invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1
 .
0
 Length 11;
 Indels
 DB 5; Leus
n. 0.002;
0;
 ch 96.2%; Score 50; DB 1 Similarity 100.0%; Pred. No. 0.0 11; Conservative 0; Mismatches
 note= "N-terminal acetyl"
 ll
/note= "C-terminal amide"
 Location/Qualifiers
 Brunck TK;
 ABB80521 standard; peptide; 11 AA.
 Claim 17; Page 64; 69pp; English.
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169
 residue 7"
 (first entry
 1 EEVVPXGMSYS 11
 11
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 EEVVPXGMSYS
 WPI; 2002-361643/39.
 Query Match
Best Local Similarity
Matches 11; Conserv
 Sequence 11 AA,
 Seguence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Novel peptide
activity usefu
 Modified-site
 Modified-site
 08-OCT-2002
 31-JAN-2002
 Synthetic
 virucide.
 protease
 ABB80521
 ABB8052
 RESULT
 88888888
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 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
 virus
 Gapa
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2.
 ..
 96.2%; Score 50; DB 5; Length 11;
100.0%; Pred. No. 0.002;
ive 0; Mismatches 0; Indels
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 note= "D-form residue"
 Location/Qualifiers
 Brunck TK;
 Š
 Claim 17; Page 64; 69pp; English.
 ABB80522 standard; peptide; 11
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169
 Query Match
Best Local Similarity 100.
Matches 11; Conservative
 1
1 EEVVPXGMSYS 11
 (CORV-) CORVAS INT INC
 1 EEVVPXGMSYS
 1 REVVPXGMSYS
 WPI; 2002-361643/39.
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Novel peptide
 Key
Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 31-JAN-2002
 08-OCT-2002
 Synthetic.
 protease.
 activity
 ABB80522
 virucide
 ABB80522
 à
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EEVVPXGMSYS

g

RESULT

Score 50; DB 5; Length 11; Pred. No. 0.002;

96.2%; S 100.0%;

Query Match Best Local Similarity

```
/note= "N-terminal acetyl"
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 Location/Qualifiers
 Location/Qualifiers
 Brunck TK;
 ABB80565 standard; peptide; 11 AA.
 Claim 17; Page 65; 69pp; English.
 19-JUL-2001; 2001WO-US023169.
 2000US-0220101P.
 (first entry)
 Query Match 96.2
Best Local Similarity 100.
Matches 11; Conservative
 11
 11
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 1 REVVPXGMSYS
 EEVVPXGMSYS
 WPI; 2002-361643/39.
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Key
Modified-site
 Modified-site
 Modified-site
 21-JUL-2000;
 08-OCT-2002
 31-JAN-2002
 Synthetic.
 Synthetic.
 protease.
 ABB80565;
 virucide.
 virucide
 RESULT
셤
 ö
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "2-aminoisobutyryl carbonyl residue forming a keto-amide linkage with residue 7"
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Gapa
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #43
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46.
 ö
 DB 5; Length 11; 0.002;
 0; Indels
 96.2%; Score 50; DB 100.0%; Pred. No. 0.0 cive 0; Mismatches
 note= "N-terminal acetyl"
 /note= "C-terminal amide"
 Location/Qualifiers
 standard; peptide; 11 AA.
 Ŕ
 Brunck TK
 Claim 17; Page 65; 69pp; English
 ABB80566 standard; peptide; 11
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 (first entry)
 (first entry)
 l Similarity 100,
11; Conservative
 금
 ដ
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 1 EEVVPXGMSYS
 EEVVPXGMSYS
 WPI; 2002-361643/39
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 08-OCT-2002
 08-OCT-2002
 31-JAN-2002
 Query Match
Best Local S
 Synthetic
 ABB80563;
 ABB80563
 ABB80566;
 protease
 Matches
 RESULT 5
 BB80566
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of the
 pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 ŏŧ
/note= "Valyl carbonyl forming keto-amide linkage with residue 7"
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCW) protease inhibitory activity. The peptides of invention are alpha-ketoamide spetide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture a medicament to treat disorders associated with HCV protease. A
 /note= "Norleucyl carbonyl forming keto-amide linkage with residue 7"
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #45
 ö
 96.2%; Score 50; DB 5; Length 11; 100.0%; Pred. No. 0.002; ive 0; Mismatches 0; Indels
```

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "Norvaly1 carbony1 forming keto-amide linkage with
residue 7"
 Hepatitis C virus, HCV, serine protease, inhibitor, alpha-ketoamide, virucide.
 btide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C ^{\circ}
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #39
 DB 5; Der.
 96.2%; Score 50; DB 100.0%; Pred. No. 0.0:ive 0; Mismatches
 note= "N-terminal acetyl"
 /note= "C-terminal amide"
 note= "D-form residue"
 'note= "Oxymethionine"
 Location/Qualifiers
 Brunck TK;
 ABB80559 standard; peptide; 11 AA.
 Brunck TK;
 Claim 17; Page 65; 69pp; English.
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 (first entry)
 11; Conservative
 1 EEVVPXGMSYS 11
 EEVVPXGMSYS 11
 (CORV-) CORVAS INT INC.
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39
 WPI; 2002-361643/39.
 Levy
 Local Similarity
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 peptide
 Modified-site
 Modified-site
 Lim-Wilby M,
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 Synthetic.
 protease.
 ABB80559;
 Query Match
 Novel
 RESULT 8
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 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 /note= "(s,s)allothreonyl carbonyl residue forming a keto-amide linkage with residue 7"
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Gapa
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #47.
 ;
0
 Score 50; DB 5; Lengtn 11, Pred. No. 0.002;
 'note= "N-terminal acetyl"
 11
/note= "C-terminal amide"
 'note= "C-terminal amide
 Location/Qualifiers
 Brunck TK;
 96.2%; Scc.
100.0%; Pred
0; F
 ABB80567 standard; peptide; 11 AA.
 Claim 17; Page 65; 69pp; English
 19-JUL-2001; 2001WO-US023169.
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 (first entry)
 Local Similarity 100
 1 EEVVPXGMSYS 11
 EEVVPXGMSYS 11
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39
 Sequence 11 AA;
 WO200208251-A2
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
Modified-site
 08-OCT-2002
 31-JAN-2002,
 31-JAN-2002
 Synthetic
```

Query Match

Best Loc Matches

protease

ABB80567;

RESULT 7

virucide.

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Gaps

ö

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RESULT 9
XEEEXXXXCCCCCCXXX
 ਨੇ
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ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
 Novel peptide
 protease
 activity
```

Claim 17; Page 65; 69pp; English

The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha \*\*Etoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus

Sequence 11 AA;

Gaps ö DB 5; Le... 96.2%; Score 50; DB 100.0%; Pred. No. 0.0; ive 0; Mismatches Query Match
Best Local Similarity 100.
Matches 11; Conservative

11 1 EEVVPXGMSYS

1 EEVVPXGMSYS 11

ABB80526 standard; peptide; 11 AA ABB80526

(first entry)

08-OCT-2002

Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #6.

Hepatitis C virus, HCV, serine protease; inhibitor; alpha-ketoamide; virucide.

Synthetic

note= "N-terminal acetyl" Location/Qualifiers Key Modified-site

note= "Norvalyl carbonyl forming keto-amide linkage with residue 7" residue Misc-difference Modified-site

/note= "C-terminal amide" note= "D-form residue" note= "D-form residue" Misc-difference Modified-site

WO200208251-A2

31-JAN-2002

19-JUL-2001; 2001WO-US023169

21-JUL-2000; 2000US-0220101P. (CORV-) CORVAS INT INC

Levy OE, Lim-Wilby M,

Ϋ́ Brunck WPI; 2002-361643/39.

ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus Novel peptide activity usefu protease

Claim 17; Page 64; 69pp; English

The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus \*88888888

Sequence 11 AA;

ô Gaps ö 96.2%; Score 50; DB 5; Length 11; 100.0%; Pred. No. 0.002; ive 0; Mismatches 0; Indels 11; Conservative Query Match Best Local Similarity Best Loc Matches

1 EEVVPXGMSYS 11 EEVVPXGMSYS 11

셤 ઠ

RESULT 10

ô

ABB80564 standard; peptide; 11

Ä

ABB80564;

08-OCT-2002

Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #44

Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.

Synthetic.

carbonyl forming keto-amide linkage with 'note= "N-terminal acetyl" Location/Qualifiers /note= "Leucyl residue 7" Key Modified-site Modified-site

/note= "C-terminal amide"

WO200208251-A2

Modified-site

31-JAN-2002

19-JUL-2001; 2001WO-US023169.

21-JUL-2000; 2000US-0220101P.

(CORV-) CORVAS INT INC

ŢK; Brunck Lim-Wilby M, Levy OE,

WPI; 2002-361643/39

Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C protease 

Claim 17; Page 65; 69pp; English.

The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus

Sequence 11 AA;

```
Hepatitis C virus, HCV, serine protease, inhibitor; alpha-ketoamide, virucide.
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C ^{\circ}
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
 'note= "N-terminal acetyl"
 /note= "C-terminal amide"
 'note= "D-form residue"
 note= "Oxymethionine"
 Location/Qualifiers
 ABB80561 standard; peptide; 11 AA.
 19-JUL-2001; 2001WO-US023169.
 21-JUL-2000; 2000US-0220101P
 residue 7"
 (first entry)
 Levy OE,
 'note=
 (CORV-) CORVAS INT INC
 WPI; 2002-361643/39.
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Modified-site
 Key
Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002.
 Synthetic.
 protease.
 ABB80561;
RESULT 12
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 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virudide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
 'note= "Alpha-propynyl-glycinyl-carbonyl residue forming i keto-amide linkage with residue 7"
 Gaps
 Gaps
 Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #48.
 ö
 ;
0
 96.2%; Score 50; DB 5; Length 11; 100.0%; Pred. No. 0.002; ive 0; Mismatches 0; Indels
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 note= "N-terminal acetyl"
 'note= "C-terminal amide"
 Location/Qualifiers
 ABB80568 standard; peptide; 11 AA.
 Claim 17; Page 65; 69pp; English.
 Brunck
 21-JUL-2000; 2000US-0220101P.
 19-JUL-2001; 2001WO-US023169
 (first entry)
 11; Conservative
 Ħ
 Ħ
 Levy OE,
 (CORV-) CORVAS INT INC
 EEVVPXGMSYS
 EEVVPXGMSYS
 WPI; 2002-361643/39.
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
 31-JAN-2002
 Synthetic.
 Query Match
Best Local S
 virucide.
 Query Match
 Best Loc
Matches
 RESULT 1.
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Brunck TK;

"Norvaly1 carbonyl forming keto-amide linkage with

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ö
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Gaps
 ö
 Length 11;
 1; Indels
 Score 46; DB 5;
Pred. No. 0.013;
); Mismatches
 ABB80524 standard; peptide; 11 AA.
Claim 17; Page 65; 69pp; English.
 88.5%;
90.9%;
 Query Match
Best Local Similarity 90.5
Matches 10; Conservative
 1 EEVVPXGMSYS 11
 Ħ
 BEVVPXGMDYS
 ABB80524
 13
 ABB80524
ID ABB
XX
AC ABB
 RESULT
```

1 EEVVPXGMSYS 11 EEVVPXGMSYS 11

ઠે

Matches

'note= "N-terminal acetyl"

Location/Qualifiers

/note= "C-terminal amide" note= "D-form residue"

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
 ABB80529 standard; peptide; 11 AA.
 Claim 17; Page 64; 69pp; English
 19-JUL-2001; 2001WO-US023169
 21-JUL-2000; 2000US-0220101P
 (first entry
(first entry)
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Best Local Similarity 90.9
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 Levy OE,
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 WPI; 2002-361643/39.
 Misc-difference
 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-Bite
 Modified-site
 Lim-Wilby M,
 08-OCT-2002
08-OCT-2002
 31-JAN-2002
 Synthetic
 Synthetic
 virucide
 ABB80529
 RESULT 14
 ABB80529
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 g
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Brunck TK,

Gaps

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Score 46; DB 5; Length 11; Pred. No. 0.013; 0; Mismatches 1; Indels

98.5%;

```
ö
 /note= "Norvaly1 carbony1 forming keto-amide linkage with
 the
 /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
 ingredient
 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have viruside activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Gaps
 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8.
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 Score 46; DB 5; Length 11;
Pred. No. 0.013;
 1; Indels
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 /note= "N-terminal acetyl"
 note= "N-terminal acetyl"
 /note= "C-terminal amide"
 note= "D-form residue"
 /note= "D-form residue"
 Location/Qualifiers
 Location/Qualifiers
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 Claim 17; Page 64; 69pp; English.
 ABB80528 standard; peptide; 11
 Brunck
 19-JUL-2001; 2001WO-US023169.
 21-JUL-2000; 2000US-0220101F.
 88.5%;
90.9%;
 10; Conservative
 덖
 1 EEVVPXGMSYS 11
 (CORV-) CORVAS INT INC
 Lim-Wilby M, Levy OE,
 EEVVPXGMDYS
 WPI; 2002-361643/39
 Query Match
Best Local Similarity
Matches 10; Conserv
 Misc-difference
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 Sequence 11 AA;
 WO200208251-A2
 Key
Modified-site
 Modified-site
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Modified-site
 Modified-site
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 08-OCT-2002
 31-JAN-2002,
 Synthetic,
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 protease
 RESULT 15
 ABB8052
 THE THE SERVE
 ઠ
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 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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\_\_\_/note= "C-terminal amide" /note= "D-form residue" 11

residue 7"

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21-JUL-2000, 2000US-0220101P.
 19-JUL-2001, 2001WO-US023169
 Lim-Wilby M, Levy OE,
 (CORV-) CORVAS INT INC.
 Misc-difference
 WO200208251-A2
 Modified-site
 31-JAN-2002.
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Brunck TK;

```
Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
 Claim 17; Page 64; 69pp; English.
WPI; 2002-361643/39.
 Sequence 11 AA;
 protease.
```

The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus

Gaps ô 88.5%; Score 46; DB 5; Length 11; 90.9%; Pred. No. 0.013; tive 0; Mismatches 1; Indels Query Match
Best Local Similarity 90.9
Matches 10; Conservative

ö

Search completed: June 3, 2004, 11:48:25 Job time: 45.9333 secs

1 EEVVPXGMDYS 11 ઠ đ

1 EEVVPXGMSYS 11

us-09-909-164-47.rai

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GENERAL INFORMATION:
APPLICANT: Lynn Doubette-Starm et al TITLE OF INVEXTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVEXTION: NUCLEIC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS FILLE REFERENCE: 032796-03.
FILLE REFERENCE: 032796-03.
CURRENT APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN VEFREND 3.1
SSOFTWARE: PATENTIN VEFREND 3.1
LENGTH: 382
 TYPE: PRT ORGANISM: Enterococcus faecalis
 Sequence 4, Appli
Sequence 73, Appl
Sequence 73, Appl
Sequence 2902, Ap
Sequence 2, Appli
Sequence 3, Appli
Sequence 236, App
Sequence 236, App
Sequence 236, App
Patent No. 5177197
Patent No. 5177197
 66, Appl
66, Appl
23, Appl
4, Appli
4, Appli
7, Appli
21, Appli
21, Appli
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 (without alignments)
48.399 Million cell updates/sec
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5,1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 US-09-228-986-73
US-09-540-236-2902
US-09-328-252-7885
US-09-760-946-3
US-08-637-759B-236
US-08-877-355A-236
US-09-201-945-236
5177197-51
 US-09-408-020-4
US-09-134-000C-3738
 13.7.17.7.9.52.66

13.09-1521-650-66

13.09-168-888-65

13.09-168-888-65

13.09-168-988-23

13.08-460-694-4

13.09-68-103-977-7

13.08-464-517-21
 US-08-246-361A-21
US-08-463-772-21
PCT-US93-05000-21
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 Total number of hits satisfying chosen parameters:
 389414 segs, 51625971 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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 BLOSUM62
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 Issued Patents AA:*
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 US-09-909-164-47
52
1 EEVVPXGMSYS 11
 Length DB
 Query
Match 1
 litle:
Perfect score:
Jequence:
 scoring table:
 Searched:
 Jatabase
 uo un
 Result
No.
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| 28<br>29                                                          | 32                                      |                | w w                     | 236<br>236  | 23         | -08<br>I-U     | 3-772-22-05000-2                         | 7        | Seq           | Sequence   | 0.0      | Appl<br>Appl |
|-------------------------------------------------------------------|-----------------------------------------|----------------|-------------------------|-------------|------------|----------------|------------------------------------------|----------|---------------|------------|----------|--------------|
| 30                                                                | 9 2                                     |                |                         | 280         |            | US-08-4        | -464-517-6<br>-463-772-6                 |          | Seq           | equence    | 0        | 44           |
| 35                                                                | 3 6                                     |                |                         | 283         |            | US-08-2        | US-08-246-361A-4                         |          | Seq           | Sequence   | 4        | 11           |
| 33                                                                | 32                                      |                |                         | 289         |            | PCT-US9        | 3-05000-4                                |          | Sed           | Sequence   | 4,       | -d -         |
| 8. c                                                              | 9 5                                     |                |                         | 291         |            | PCT-US9        | 3-05000-6                                |          | S S S         | uence      | " 'a     | - T          |
| 2 .<br>C A                                                        | 2 6                                     |                |                         | 2 6 6       |            | US-08-4        | 46-361A-6                                |          | Sec           | Sequence   | 9        | 4.4          |
| 3.7                                                               | 1 10                                    |                |                         | 292         |            | US-08-2        | 46-361A-2                                | <b>~</b> | Sed           | nence      | 23       | p]           |
| 38                                                                | 32                                      |                |                         | 292         |            | US-08-4        | 63-772-23                                |          | Sed           | nence      | 23       | ď            |
| 39                                                                | 32                                      |                |                         | 292         |            | PCI-US         | 3-02000-2                                | ~        | Sed           | Sequence   | 53       | ď,           |
| 40                                                                | 32                                      |                | •                       | 295         |            | US-07-9        | 47-120-8                                 |          | Sed           | nence      |          | 77           |
| 41                                                                | 32                                      |                |                         | 295         |            | US-08-4        | 72-893A-8                                |          | Sed           | Sequence   |          | 1 ·          |
| 24.4                                                              | en c                                    |                |                         | 0 0<br>0 0  |            | US-08-4        | US-08-460-694-2                          |          | pay.          | equence    |          | 16           |
|                                                                   | 7 0                                     |                |                         | 0 C         |            | 100-01         | 00-11-1-10-10-10-10-10-10-10-10-10-10-10 |          | 3 0           | 901010     | Ī        | Ann          |
| 4 ል<br>የ                                                          | 3 6                                     | 61             |                         | 2 2 2 2 2 2 |            | US-08-2        | 46-361A-19                               | on.      |               | ednence    | ຸ້ດ      | App1         |
|                                                                   |                                         |                |                         |             |            | ALIG           | ALIGNMENTS                               |          |               |            |          |              |
| RESULT 1                                                          |                                         |                |                         |             |            |                |                                          |          |               |            |          |              |
| US-09-408-020-4                                                   | -020                                    | 4"             |                         |             |            |                |                                          |          |               |            |          |              |
| ; Sequence 4, Applicat<br>; Patent No. 6632937                    | 0.40                                    | Appli<br>63293 | Application<br>632937   | us/         | US/0940802 | 8020           |                                          |          |               |            |          |              |
| GENERAL                                                           | INFO                                    | RMAT1          | ION:                    |             |            |                |                                          |          |               |            |          |              |
| , APPLICANT:                                                      | E.                                      | Swanson,       | son, Ro                 | Ronald      | >          |                |                                          |          |               |            |          |              |
| , APPLICANT:                                                      | Ë                                       | Felc           | ANT: Feldman, Robert A. | Rober       | יו<br>יי   |                |                                          |          |               |            |          |              |
| , APPLICANT:                                                      | i                                       | Sch            | leper,                  | Chri        | sta<br>,   | 77.6           | ON FEED COO.                             | 200      | MITARITACKNOO |            | MITOGITA | Σ            |
| ; TITLE OF INVENTION: NUCLEI                                      | 7 T T T T T T T T T T T T T T T T T T T | VENT           | 100 P                   | 000         | ₹<br>'     | TIDS AND       |                                          | PROF     | CENTRACIO     |            | 200      |              |
| TNEGGIO .                                                         | 400                                     | 1401           | APPLICATION NIMBER      | TWREE       |            | TIS/09/408     | 8.020                                    |          |               |            |          |              |
| CURRENT FILING DATE:                                              | I                                       | ING            | ATE:                    | 1999-09     | ٠,         |                |                                          |          |               |            |          |              |
|                                                                   | PPLI                                    | CATIC          | APPLICATION NUMBER:     | BER:        | 20         | 102,294        |                                          |          |               |            |          |              |
|                                                                   | ILIN                                    | G DAT          | (E: 19                  | 98-09       | -29        |                |                                          |          |               |            |          |              |
| ; NUMBER                                                          | OF S                                    | SEQ II         | ID NOS:                 | 123         |            |                |                                          |          |               |            |          |              |
| CO E                                                              | •                                       | FastSEQ        | 3Q for                  | Windows     | OWS        | Version        | 1 3.0                                    |          |               |            |          |              |
| ON OI DES!                                                        |                                         | 3472           |                         |             |            |                |                                          |          |               |            |          |              |
| GIONEL .                                                          |                                         | 4              |                         |             |            |                |                                          |          |               |            |          |              |
|                                                                   |                                         | Cenai          | Cenarchaeum symbiosum   | m SVIII     | bios       | שחנ            |                                          |          |               |            |          |              |
| US-09-408-02                                                      |                                         | 4              |                         | •           |            |                |                                          |          |               |            |          |              |
| Query Matc<br>Best Local                                          | д:                                      | Similarity     | rity                    | 73.         | 4.46       | Score<br>Pred. | 38;<br>No.                               | •-       |               | •-         |          | •            |
| Matches                                                           | φ                                       |                | Conservativ             | ative       | _          | 4; Mie         | smatches                                 | 1,       | Indels        | : <b>.</b> | Gaps     | 0            |
| È                                                                 | н                                       | EEW            | VVPXGMSYS               | S 11        |            |                |                                          |          |               |            |          |              |
| Db 2                                                              | 294                                     | EDVIPRGI       | –ເນ<br>[ਸ               | s 230       | 4          |                |                                          |          |               |            |          |              |
| RESULT 2                                                          | 6                                       |                |                         |             |            |                |                                          |          |               |            |          |              |
| . Sequence 3738, Application US/09134000C<br>. Patent No. 6617156 | 373                                     | 8, A           | pplical                 | tion        | ns/(       | 9134000        | D.                                       |          |               |            |          |              |
| GENERAL INFORMATION:                                              | INFC                                    | RMAT           | NOI:                    |             |            |                |                                          |          |               |            |          |              |

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Gaps

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Sequence 7885, Application US/09328352
Patent No. 6562958
GENERAL INPORMATION:
TITUR OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITUR OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTS-90-309A
CURRENT PILLING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7885
LENGTH: 1407
 Sequence 2, Application US/09760946

Sequence 2, Application US/09760946

Sequence 2, Application US/09760946

Sequence 2, Application US/09760946

GENERAL INFORMATION:
APPLICANT: Cameron, Dale R.
APPLICANT: Gandreau, Manhalie
APPLICANT: Ghiro, Elise
APPLICANT: Ghiro, Elise
APPLICANT: Ilinas-Brunet, Montee
TITLE OF INVENTION Macrosylic Peptides Active Against the Hepatitis C Virus
TILE PRINTEMENCE: 13/076-1-C1
CURRENT FILING DATE: 2001-08-23

FRIOR APPLICATION NUMBER: US 60/128,011

PRIOR FILING DATE: 1999-04-06

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PatentIn version 3.1

LENGTH: 12
 OTHER INFORMATION: Substrate for recombinant HCV NS3 protease radiometric assay
 Length 1407;
 Query Match 65.4%; Score 34; DB 4; Length 140
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels
 63.5%; Score 33; DB 4; Length 12; llarity 45.5%; Pred. No. 1.7; Conservative 4; Mismatches 2; Indels
) ORGANISM: Acinetobacter baumannii
US-09-328-352-7885
 Sequence 3, Application US/09760946
PREET NO. 6608027
GRNERAL INFORMATION:
APPLICANT: Teantrizos, Youla S.
APPLICANT: Cameron, Dale R.
APPLICANT: Faucher, Anne-Marie
APPLICANT: Ghico, Elise
 ORGANISM: Artificial Sequence
 1 EEVVPXGMSYS 11
 1 DDIVPCSMSYT 11
 596 EVVPEGLSF 604
 2 EVVPXGMSY 10
 Query Match
Best Local Similarity
Matches 5; Conserv
 RESULT 6
US-09-760-946-2
 US-09-760-946-3
 US-09-760-946-2
 TYPE: PRT
 RESULT 7
 qq
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 Sequence 2902, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION WIMBER: US/09/540,236
CURRENT APPLICATION WIMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
SEQ ID NOS: 3840
SEQ ID NOS: 3840
SEQ ID NOS: 3840
 Sequence 73, Application US/09228986

Patent No. 6159198

GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
ITILE OF INVENTION: Compositions Isolated from Plant Cells
ITILE OF INVENTION: Compositions in the Modification of Plant Cell Signalling
ITILE OF INVENTION: UNMBER: US/09/228,986
CURRENT APPLICATION UNMBER: US/09/228,986
CURRENT PILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 73
LENGTH: 947
) DUCATION: (327)..(328)
) OTHER INFORMATION: Amino acids 327 & 328 are Xaa wherein Xaa = any amino acid. US-09-134-000C-3738
 ö
 Gaps
 Gaps
 ö
 65.4%; Score 34; DB 4; Length 1191; 55.6%; Pred. No. 2e+02; trive 3; Mismatches 1; Indels
 Query Match 69.2%; Score 36; DB 4; Length 382; Best Local Similarity 66.7%; Pred. No. 22; Matches 6; Conservative 2; Mismatches 1; Indels
 Query Match 65.4%; Score 34; DB 4; Length 947; Best Local Similarity. 66.7%; Pred. No. 1.6e+02; Matches 6; Conservative 2; Mismatches 1; Indels
 Query Match
Best Local Similarity 55.6
Matches 5; Conservative
 332 LIPEGMSYS 340
 TYPE: PRT
ORGANISM: Pinus radiata
 686 VMPSGISYS 694
 ; ORGANISM: M.catarrhalis
US-09-540-236-2902
 3 VVPXGMSYS 11
 |::| ||:|
783 EILPVGMAY 791
 NAME/KEY: MISC FEATURE LOCATION: (327)..(328)
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 2 EVVPXGMSY 10
 RESULT 4
US-09-540-236-2902
 RESULT 5
US-09-328-352-7885
 RESULT 3
US-09-228-986-73
 US-09-228-986-73
 FEATURE:
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0; Gaps

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 1 EEVVPXGMSY 10
 1 EEISPLGWSY 10
 linear
 1 EEISPLGWSY
 TYPE: amino acid
STRANDEDNESS: si
 amino acid
 STRANDEDNESS:
 US-08-871-355A-236
 LENGIH:
 RESULT 9
 ઠે
 셤
 ò
APPLICANT: Goudreau, Nathalie
APPLICANT: Halmos, Teddy
Teddy
APPLICANT: Lilinas-Brunet, Montse
TIPLE OF INTERNICON: Macrocyclic Peptides Active Against the Hepatitis C Virus
FILE REFERENCE: 13/076-1-C1
CURRENT PELLING DATE: 10/076-1-C1
CURRENT FILING DATE: 2000-04-3
PRIOR APPLICATION NUMBER: US 60/128,011
PRIOR APPLICATION NUMBER: US 60/128,011
PRIOR APPLICATION NUMBER: US 60/128,011
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
 ö
 Gaps
 ö
 . LOCATION: (10)
, OTHER INFORMATION: Tyr at position 10 is iodinated with I-125
US-09-760-946-3
 Query Match 63.5%; Score 33; DB 4; Length 12; Best Local Similarity 45.5%; Pred. No. 1.7; Matches 5; Conservative 4; Mismatches 2; Indels
 Sequence 236, Application US/08637759B

Sequence 236, Application US/0863759B

Patent No. 5876931

Patent INFORMATION:
GENERAL INFORMATION:
APPLICANT: David William Holden

TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSE: Patrea L. Pabet
STREET: 2800 Ome Atlantic Center
STREET: 2800 Ome Atlantic Center
STREET: 2800 Ome Atlantic Center
STREET: 2800 Ome Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: 0834
ZIP 30309-3345 ORM:
MEDIUM TYPE: Floppy disk
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OFFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSIFICATION NUMBER: US/08/637,759B
FILING DATE: 11-DEC-1995
CLASSIFICATION NUMBER: 31,284
RREPRENCE/DOCKET NUMBER: RPMS 101
TELECOMMUNICATION INDERRY RPMS 101
TELECOMMUNICATION INPERMATION:
TELECOMMUNICATION INPERMATION:
 LOCATION: (1) COTHER INFORMATION: Asp at position 1 is biotinylated NAME/KEY: MOD RES LOCATION: (10) RES LOCATION: (10) COTHER INCOMPANION (10) COTHER
 FEATURE:
OTHER INFORMATION: Tracer for NS3 protease assay
NAME/KEY: MOD_RES
 TYPE: PRT ORGANISM: Artificial Sequence
 TELEPHONE: (404) 873-875
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 2
 1 EEVVPXGMSYS 11
 1 DDIVPCSMSYT 11
 US-08-637-759B-236
 SEQ ID NO 3
LENGTH: 12
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3, Mismatches

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5; Conservative
 LENGTH: 410
 SEQ ID NO:30:
 SEQ ID NO:1
 RESULT 13
5177197-30
;Patent No.
 5177197-30
 Matches
 5177197-1
 5177197-1
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 Gaps
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0
 PACIENT NO. 5177197

PAPILICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;
PRENSTEDT: CHRISTER; HELLMAN, ULF; MIXAZONO, KOHEI; CLAESSON-WELSH,
PRENSTEDT: CHRISTER; HELLMAN, ULF; MIXAZONO, KOHEI; CLAESSON-WELSH,
PRANSTEDT: CARL-HERRIK
HUMAN, HELDIN, CARL-HERRIK
HUMAN TRANSFORMING GROWTH FACTOR-BETAI-BINDING PROTEIN
NUMBER OF SEQUENCES: 53
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/487,343
FILING DATE: 27-FEB-1990
 Score 33; DB 4; Length 45; Pred. No. 7.8;
 3; Indels
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/201,945 FILING DATE: CLASSIPICATION:
 Sequence 236, Application US/09201945
Farent No. 6342215
GENERAL INFORMATION:
TITLE OF INVENTION: Genetication of Genes
FINES OF ENURS: 501
CORRESPONDENCE ADDRESS:
ADDRESSE: Partea L. Pabet
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
 1; Mismatches
 CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
 RPMS 101
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/637,759
FILING DATE:
CLASSIFICATION:
ATTOKNEY/AGRAT INFORMATION:
NAME: Pabet, Patrea L.
REGISTRATION NUMBER: 31,284
ERPERRENTO/POCKET NUMBER: RPMS 10:
TELEDONUMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
 INFORMATION: (404) 873-8794
TELEFAX: (404) 873-8794
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amin
 63.5%;
 LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS: single
 Best Local Similarity 60.0
Matches 6; Conservative
 protein
 1 EEVVPXGMSY 10
 1 EEISPLGWSY 10
 linear
 MOLECULE TYPE: HYPOTHETICAL:
 US-09-201-945-236
 JS-09-201-945-236
 Query Match
 RESULT 11
5177197-51
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Score 33; DB 6; Length 65; Pred. No. 12;

63.5%;

Query Match Best Local Similarity

SEQ ID NO:51:

5177197-51

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US-09-37-952-66

1 Sequence 66, Application US/09357952

2 Releant No. 6248904

2 RENERAL INFORMATION:

3 APPLICANT: Zhang, Han-Zhong

3 APPLICANT: Drewe, John A.

3 APPLICANT: Drewe, John A.

3 APPLICANT: Preve, John A.

4 APPLICANT: Preve, John A.

5 TITLE OF INVENTION: Pluorescence Screening Assays for Caspases, Peptidases, Protease

5 TITLE OF INVENTION: Other Enzymes and the Use Thereof

7 TITLE OF INVENTION: Other Enzymes and the Use Thereof

7 TITLE OF INVENTION: UNMERS: US/09/357,952

6 CURRENT APPLICATION NUMBER: US/093,642
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 JATALEANT: KANZAKI, TETSUTO,OLOFSSON, ANDERS;MOREN, ANITA;

PREDICANT: KANZAKI, TETSUTO,OLOFSSON, ANDERS;MOREN, ANITA;

PREDICANT: KANZAKI, TETSUTO,OLOFSSON, ANDERS;MOREN, ANITA;

JENN,HELDIN, CARL-HERRIK

TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING;

HUMAN TRANSPORMING GROWTH FACTOR-BETAL-BINDING PROTEIN

NUMBER OF SEQUENCES: 53

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/487,343

FILING DATE: 27-FEB-1990
 PACEDIC NO. 517197

PACEDIC NO. 517197

APPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;

BENSATEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH;

BENSA; HELDIN, CARL-HENRIK

TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING

HUMAN TRANSFORMING GROWTH FACTOR-BETA1-BINDING PROTEIN

NUMBER OF SEQUENCES: 53

CURRENT APPLICATION NATN:

APPLICATION NUMBER: US/07/487,343

FILING DATE: 27-PEB-1990
 Length 1394;
 63.5%; Score 33; DB 6; Length 410; 45.5%; Pred. No. 97; tive 3; Mismatches 3; Indels
 Score 33; DB 6; Length 139
Pred. No. 3.9e+02;
3; Mismatches 3; Indels
 63.5%;
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Best Local Similarity 45.5-
Conservative
5, Conservative
 Query Match
Best Local Similarity 45.5
Matches 5; Conservative
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399 KEICPGGMGYT 409
 :|: | ||:
399 KEICPGGMGYT 409
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52 KEICPGGMGYT 62
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
1 EEVVPXGMSYS 11
 LENGTH: 1394
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or Fluorescent Reporter Molecules and
 Sequence 66, Application US/09521650

Patent No. 6335429

GENERAL INFORMATION:
APPLICANT: Weber, Eckard
APPLICANT: Weber, Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Caing, Han-Zhong
ITLE OF INVENTION: Or File Applications for Whole-Cell Fluorescence
ITLE OF INVENTION: Greening Assays for Caspases and Other Enzymes and the
ITLE OF INVENTION: Use Thereof
ITLE OF INVENTION: Use Thereof
ITLE OF INVENTION: Use Thereof
CURRENT APPLICATION NUMBER: US/09/521,650
CURRENT FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 60/061,582
EARLIER APPLICATION NUMBER: US 60/061,582
EARLIER APPLICATION NUMBER: US 09/033,661
EARLIER APPLICATION NUMBER: US 09/033,661
EARLIER APPLICATION NUMBER: US 09/033,661
EARLIER PILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
SEQ ID NO 66
SEQ ID NO 66
LENGTH: 10
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 TYPE: PRT
ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
OTHER INFORMATION: Description of Artificial Sequence:Synthetic
OTHER INFORMATION: Peptide
) OTHER INFORMATION: Description of Artificial Sequence:Synthetic OTHER INFORMATION: Peptide US-09-521-650-66
 61.5%; Score 32; DB 4; Length 10;
50.0%; Pred. No. 2.3;
tive 3; Mismatches 2; Indels
 Score 32; DB 3; Length 10;
Pred. No. 2.3;
3; Mismatches 2; Indels
EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
SCFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 66
LENGTH: 10
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Best Local Similarity 50.0%;
Matches 5; Conservative 3
 TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
 Query Match
Best Local Similarity 50.0
Matches 5, Conservative
 1 DDIVPCSMSY 10
 1 DDIVPCSMSY 10
 1 EEVVPXGMSY 10
 1 EEVVPXGMSY 10
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Search completed: June 3, 2004, 12:03:09 Job time: 11.8 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Sequence 5, Al Sequence 6, Al Sequence 10, Al Sequence 10, Sequence 48, Sequence 50, Sequence 51, Sequence 8, Al Sequence 11, Al Sequence 7, Al Sequence 17, Al Sequence 11, A
 June 3, 2004, 11:57:42; Search time 33.7333 Seconds (without alignments) 91.741 Million cell updates/sec
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 Published Applications AA:*

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 1155919
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-909-164-13
US-09-909-164-13
 otal number of hits satisfying chosen parameters:
 1155919 seqs, 281338677 residues
 SUMMARIES
 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
 - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 finimum DB seq length: 0 taximum DB seq length: 2000000000
 US-09-909-164-47
52
1 EEVVPXGMSYS 11
 Query
Match Length DB
 litle:
Verfect score:
 Score
 coring table:
 M protein
 equence:
 earched:
 Jatabase
 tun on:
 Result
No.
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| Sequence 19, Appl Sequence 20, Appl Sequence 21, Appl Sequence 28, Appl Sequence 28, Appl Sequence 29, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 21, Appl Sequence 27, Appl Sequence 21, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 31, Appl Sequence 32, Appl Sequence 32, Appl Sequence 34, Appl Sequence 36, Appl Sequence 39, Appl Sequence 39, Appl Sequence 39, Appl Sequence 39, Appl | PROTEASE INHIBITORS OF HEPATITIS to example 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| US-09-909-164-19 US-09-909-164-20 US-09-909-164-23 US-09-909-164-24 US-09-909-164-24 US-09-909-164-29 US-09-909-164-29 US-09-909-164-33 US-09-909-164-31 US-09-909-164-31 US-09-909-164-31 US-09-909-164-26 US-09-909-164-26 US-09-909-164-26 US-09-909-164-26 US-09-909-164-26 US-09-909-164-31 US-09-909-164-40 US-09-909-164-40 US-09-909-164-40 US-09-909-164-46 US-09-909-164-46 US-09-909-164-31 US-09-909-164-31 US-09-909-164-31 US-09-909-164-31 US-09-909-164-31 US-09-909-164-31 US-09-909-164-31 US-09-909-164-31 US-09-909-164-31                                                                                                                                                                                                                    | C. AS NS-3-SERINE 09, 164                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 8866 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ion US/0 0206870 by, Marg dile Terence Terence NOVEL F 1192-US NUMBER: UMBER: C200-07- S: 62 version 11-mer 11-mer 11-mer 11) AMIDATI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| 0 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | RESULT 1 US-09-909-164-5 Sequence 5, Applicat Publication No. US20; GERREAL INFORMATION: APPLICANT: Lim-Wil APPLICANT: Lim-Wil APPLICANT: Lim-Wil APPLICANT: Brunck, TITLE OF INVENTION: FILE REFERENCE: INO CURRENT APPLICATION CURRENT APPLICATION FILE REFERENCE: INO CURRENT FILING DATE: NUMBER OF SEQ ID NO SOFTWARE: PATENTING DATE: PRIOR PRILING DATE: PRIOR PRILING DATE: PRIOR FILING DATE: PRIOR SEQ ID NO SOFTWARE: PATENTING CORGANISM: artificit FEATURE: NAME/KEY: MOD_RES LOCATION: (1)(1) COCATION: (6)(1) COCATION: (6)(6) CHER INFORMATION: FEATURE: NAME/KEY: MOD_RES LOCATION: (6)(1) COCATION: (6)(1) COCATION: (1)(1) 1) COCATION: (1)(1)(1) COCATION: (1)(1)(1) COCATION: (1)(1)(1) COCATION: (1)(1)(1)(1) COCATION: (1)(1)(1)(1 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |

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Length 11;

DB 12;

Score 50;

96.2%;

Query Match

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OTHER INFORMATION: 11-mer synthesized according to example 1
 OTHER INFORMATION: 11-mer synthesized according to example 1
 Query Match

96.2%; Score 50; DB 12; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.0014;

Matches 11; Conservative 0; Mismatches 0; Indels
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LOCATION: (6).7(6)
OTHER INFORMATION: norvaline-(CO)
 LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
PEATURE:
 CTHER INFORMATION: D-amino acid
US-09-909-164-9
 FEATURE:
NAME/KEY: MOD RES
LOCATION: (1) ...(1)
OTHER INFORMATION: ACETYLATION
FRATURE:
 FRATURE:
NAME/FREY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
 TYPE: PRT ORGANISM: artificial sequence
 ORGANISM: artificial sequence
 LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
 NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
FRATURE:
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 NAME/KEY; MISC_FEATURE
 NAME/KEY: MISC_FEATURE
 NAME/KEY: MOD RES
LOCATION: (11)..(
 SOFTWARE: I
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 Sequence 6, Application US/09909164

Publication No US20020068702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Wilby, Marguerita

CURRENT PLILNG DATE: 2003-03-25

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SEQ ID NO 6

LENGTH: 11
 Sequence 9, Application US/09909164
Exblication No. US20020068702A1
Exblication No. US20020068702A1
Exblication No. US20020068702A1
Explication No. US20020068702A1
APPLICANT: Corvas International, Inc.
APPLICANT: Lim Willby, Marguerita
APPLICANT: Levy, Oddle E
APPLICANT: Levy, Oddle E
APPLICANT: Levy, Oddle E
APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERBNCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
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 FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
 Query Match 96.2%; Score 50; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 11; Conservative 0; Mismatches 0; Indels
Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 11; Conservative 0; Mismatches 0; Indels
 NAME/KEY: MOD RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
FRATURE:
NAME/KEY: MISC FEATURE
LOCATION: (6) ... (6)
OTHER INFORMATION: norvaline-(CO)
 NAME/KEY: MISC FEATURE LOCATION: (9). (9) OTHER INFORMATION: D-amino acid
 TYPE: PRT
ORGANISM: artificial sequence
 NAME/KEY: MOD RES
LOCATION: (11)...(11)
COTHER INFORMATION: AMIDATION
US-09-909-164-6
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
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Sequence 49, Application US/09909164
; Sequence 49, Application US/09909164
; Publication No. US2020068702A1
; Dublication No. US2020068702A1
; GENERAL INFORMATION:
; APPLICANT: Corves International, Inc.
; APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
; APPLICANT: Lim-Wilby, Marguerita
; APPLICANT: Lim-Wilby, Marguerita
; APPLICANT: Lim-Wilby, Marguerita
; APPLICANT: Lim-Wilby, Marguerita
; APPLICANT: Lim-Wilby, Marguerita
; TER REPRENCE: NOUNBER: US/09/909,164
; CURRENT FILING DATE: 2000-07-21
; VINDER OF SEQ ID NOS: 62
; SEQ ID NOS: 62
; SEQ ID NOS 49
; LENGTH: 11
; SEQ ID NO 49
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 TYPE: PRI
ORGANISM: artificial sequence
PERATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
 TYPE: PRT
ORGANISM: artificial sequence
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 Query Match 96.2%; Score 50; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 11; Conservative 0; Mismatches 0; Indels
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 , LUCATION: (6)...(6)

, OTHER INFORMATION: norleucine-(CO)

US-09-909-164-49
 FEATURE:
NAME/KEY: MOD RES
LOCATION: (1). (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11). (11)
OTHER INFORMATION: AMIDATION
 FEATURE:
NAME/KBY: MISC_FEATURE
LOCATION: (6)...(6)
CTHER INFORMATION: leucine-(CO)
US-09-909-164-48
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 48
LENGTH: 11
 NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
PEATURE:
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 NAME/KEY: MISC FEATURE LOCATION: (6)...(6)
 US-09-909-164-49
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 Sequence 100 of
 S-09-909-164-48
S-09-909-164-48
Sequence 48, Application US/09909164
Dublication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Lim-Wilby, Depriles As Ns-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT PAPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR PILING DATE: 2000-07-21
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 FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
 Query Match
96.2%; Score 50; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels
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LOCATION: (1)_.(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
 LOCATION: (6)...(6)
OTHER INFORMATION: valine-(CO)
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IS-09-909-164-47
 JS-09-909-164-47
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Sequence 5.2, Application US/09909164

| Sequence 5.2, Application US/09009164
| Publication No. US200020068702AI
| GENERAL INFORMATION:
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
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| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| TILB OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
| TURBRIT TILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 52
| LENGTH: Limited DATE: Lim
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0
 OTHER INFORMATION: 11-mer synthesized according to example 1 FEATURE:
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96.2%; Score 50; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels
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 0; Indels
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100.0%; Pred. No. 0.0014;
tive 0; Mismatches 0
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1. LOCATION: (6)...(6)
1. OCHER INFORMATION: (8,8)-allothreonine-(CO)
US-09-909-164-51
 NAME/KEY: MISC_FEATURE
COCATION: (6)...(6)
COCHER INFORMATION: propynyl glycine-(CO)
US-09-909-164-S2
 Sequence 8, Application US/09909164
Publication No. US20020068702A1
 LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: NOD RES
COCATION: (11)
OTHER INFORMATION: AMIDATION
FEATURE:
 NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 TYPE: PRT ORGANISM: artificial sequence
 NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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Best Local Similarity 100.
Matches 11, Conservative
 1 BEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
FEATURE:
NAME/KEY: MOD_RES
 RESULT 11
US-09-909-164-8
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 DS-09-909-164-51

US-09-909-164-51

Sequence 51, Application US/09909164

Sequence 51, Application US/09909164

Publication No. US20020068702A1

Publication No. US20020068702A1

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-wilby, Marguerita

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT FILING DATE: 2003-03-25
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 CHER INFORMATION: 11-mer synthesized according to example 1 FEATURE:
NAME/FREY: MOD_RES

OTHER INFORMATION: ACETYLATION
OTHER INFORMATION: ACETYLATION
FRATURE:
NAME/KEY: MOD_RES

NAME/KEY: MOD_RES

OTHER INFORMATION: AMIDATION
OTHER INFORMATION: AMIDATION
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 ; LOCATION: (6).7(6)

organization: Depomention: 2-amino-butyric acid-(CO)
US-909-164-50
 PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 51
LENGTH: 11
 TYPE: PRT
ORGANISM: artificial sequence
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 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 1 EEVVPXGMSYS 11
 FEATURE:
NAME/KEY: MISC_FEATURE
 FEATURE:
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US-09-909-164-13

US-09-909-164-13

i Sequence 13, Application US/0909164

i Sequence 13, Application US/0909164

j Publication No. US20020068702A1

j GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

TITLE REFERENCE: IN01192-US

CURRENT APPLICATION NUMBER: 05/20,101

PRIOR PALING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQ ID NO 13

LENGTH: 11

LENGTH: 11

LENGTH: 11
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 .
 OTHER INFORMATION: 11-mer synthesized according to example 1 PERATURE:
NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
 Score 46; DB 12; Length 11;
Pred. No. 0.0091;
0; Mismatches 1; Indels
 Score 46; DB 12; Length 11;
Pred. No. 0.0091;
0; Mismatches 1; Indels
 FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
CTHER INFORMATION: norvaline-(CO)
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (8)...(8)
COCATION: (8)...(8)
COTHER INFORMATION: D-amino acid
US-09-909-164-12
 OTHER INFORMATION: norvaline-(CO) FEATURE:
 CONTROL (8) - ... (9)
OTHER INFORMATION: D-amino acids
US-09-909-164-13
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
 TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
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Best Local Similarity 90.9%;
Matches 10; Conservative
 NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
NAME/KEY: MOD RES
LOCATION: (11). (11)
OTHER INFORMATION: AMIDATION
 1 EEVVPXGMSYS 11
 1 EEVVPXGMDYS 11
 1 EEVVPXGMSYS 11
 1 EEVVPXGMDYS 11
 NAME/KEY: MISC_FEATURE LOCATION: (8)...(9)
 NAME/KEY: MISC FEATURE LOCATION: (6)...(6)
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 Sequence 12, Application US/09909164
| Sequence 12, Application US/09909164
| Sequence 12, Application US/09909164
| Publication No. US20020068702A1
| GENERAL INFORMATION:
| APPLICANT: Corvas International, Inc.
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Brunck, Terence K
| TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
| TITLE OF INVENTION NUMBER: US/09/909,164
| CURRENT PILING DATE: 2003-03-25
| CURRENT PILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| NUMBER OF SEQ ID NOS: 62
| SOOTWARE: Patentin version 3.1
 APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levo, Oddle B.
APPLICANT: Levo, Oddle B.
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROFEASE INHIBITORS OF HEPATITIS C
GURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SSOFING DATE: 2000-07-21
SSOFING DATE: Patentin version 3.1
LENGTH: 11
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 FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
 OTHER INFORMATION: 11-mer synthesized according to example 1
 Query Match 88.5%; Score 46; DB 12; Length 11; Best Local Similarity 90.9%; Pred. No. 0.0091; Matches 10; Conservative 0; Mismatches 1; Indels
 NAME/KEY: MISC_FEATURE
COCATION: (6)..(6)
COTHER INFORMATION: norvaline-(CO)
FEATURE:
 NAME/KEY: MISC FEATURE LOCATION: (9). . . (9) OTHER INFORMATION: D-amino acid
 NAME/KEY: MOD RES
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OTHER INFORMATION: ACETYLATION
 LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
 TYPE: PRT
ORGANISM: artificial sequence
 ORGANISM: artificial sequence
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JS-09-909-164-8
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 FEATURE:
NAME/KEY: MOD_RES
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LOCATION: (11)..(:
 SEQ ID NO 12
LENGTH: 11
 TYPE: PRT
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Score 45; DB 12; Length 11;
Pred. No. 0.015;
0; Mismatches 1; Indels
 Search completed: June 3, 2004, 12:57:17 Job time : 33,7333 secs
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NAME/KEY: MOD RES
LOCATION: (11) ... (11)
OTHER INFORMATION: AMIDATION
FRATURE:
NAME/KEY: MISC FRATURE
LOCATION: (6) ... (6)
OTHER INFORMATION: NOTVALINE-(CO)
 FEATURE:
NAME/KEY: NISC FEATURE
LOCATION: (8)..(8)
OTHER INFORMATION: D-amino acid
US-09-909-164-11
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
 1 EEVVPXGMSYS 11
 1 EEVVPXGMHYS 11
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 Sequence 11. Application US/09909164

Sequence 11. Application VS20020068702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lin-Wilby, Marguerita

APPLICANT: Lin-Wilby, Marguerita

APPLICANT: Lin-Wilby, Marguerita

APPLICANT: Brunck, Terence K

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

TILE REPREBUCE: IN01192-US

CURRENT FILING DATE: 2000-03-25

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SEQ ID NO: 11

LENTH: 11
Sequence 7, Application US/0990164
Sequence 7, Application US/0990164
Sequence 7, Application US/0990164
Sequence 7, Application No. US20020068702A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim.Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Novel PETTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2003-03-25
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
SEQ ID NO 7
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 TYPE: PRT
PERGRANSM: artificial sequence
PERTURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
 THER INFORMATION: 11-mer synthesized according to example 1 PRATURE:
 Query Match

86.5%; Score 45; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 1; Indels
 TANAME/KEY: MOD_RES
LOCATION: (1) ... (1)
COTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6) ... (6)
FEATURE:
COTHER INFORMATION: norvaline-(CO)
FEATURE:
COTHER INFORMATION: 09 ... (9)
OTHER INFORMATION: D-amino acid
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (9) ... (9)
OTHER INFORMATION: AMIDATION
US-09-909-164-7
 TYPE: PRT ORGANISM: artificial sequence
 1 EEVVPXGMSYS 11
 1 EEVVPXGMHYS 11
 LENGTH: 11
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

June 3, 2004, 11:35:47; Search time 9 Seconds (without alignments) 117.567 Million cell updates/sec

US-09-909-164-47 52 1 EEVVPXGMSYS 11 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PiR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description | •      | probable sulfate p | fate perme | V1 protein - tobac | DNA segregation AT | hypothetical prote | hypothetical prote | zinc finger protei |        | DNA-binding protei | hypothetical prote | cell division inhi |       | hypothetical prote | -      | _      |        | _      | ٦,     | _      | hypothetical prote | 3-phosphoshikimate | cdc37 protein - fi | iron(III) ABC tran | bacteriocin BCN5 - | ATP-dependent DNA | C2     | gro | DNA-directed RNA p |
|-----------|-------------|--------|--------------------|------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|-------|--------------------|--------|--------|--------|--------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------|-----|--------------------|
| SUMMARIES | CI          | T31308 | T39116             | T40413     | A42452             | B97355             | S57810             | T24111             | S22293             | H82691 | A34203             | 854619             | H69491             | 290   | 140758             | E90544 | D69493 | C81374 | T34536 | 875817 | T47670 | F72281             | D82163             | T43653             | 8235               | A30481             | 14                | D87046 | m   | G82336             |
|           | gth         | !      |                    |            |                    | 1498 2             |                    |                    |                    | σ.     | _                  |                    | ٥,                 | 544 2 | _                  |        |        | 23     | 59     | 84     | 86     | 80                 | 26                 | 99                 | m                  | 90                 | 028               | 25     | 394 | 01                 |
| ave E     | Match       | 73.1   | 71.2               | •          | 69.2               | 69.2               | 7.                 | 67.3               | 67.3               | 67.3   | 67.3               | S                  | 65.4               | 65.4  | m,                 | 63.5   | w.     | m.     | •      | m.     | ų.     | ٠                  | •                  | 63.5               | 63.5               | m,                 | ω.                | •      | ω.  | •                  |
|           | Score       | 38     | 37                 | 37         | 36                 | . 36               | 35                 | 35                 | 35                 | 35     | 35                 | 34                 | 34                 | 34    | 33                 | 33     | 33     | 33     | 33     | 33     | 33     | 33                 | 33                 | 33                 | 33                 | 33                 | 33                | 33     | 33  | 33                 |
|           | . oN        |        | 7                  | m          | 44                 | 5                  | 9<br>  <u>}</u>    | ر<br>ح             | )                  | σ      | 10                 | 11                 | 12                 | 13    | 14                 | 15     | 16     | 17     | 18     | 19     | 20     | 21                 | 22                 | 23                 | 24                 | 25                 | 26                | 27     | 28  | 29                 |

| hypothetical prote<br>masking protein pr<br>hypothetical prote | transport protein<br>rho protein GDP-di<br>hypothetical prote<br>cyclin D2 ; rat | cyclin D2 - rat cyclin D2 - mouse cyclin D2 - human cyclin D1 - Africa                           | cyclin D2 - chicke<br>cyclin D2 - chicke<br>cyclin D1 - zebra<br>cyclin D3 - human<br>cyclin D1 - human |
|----------------------------------------------------------------|----------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------|
| T04456<br>A38261<br>E97333                                     |                                                                                  | IS8372<br>A41984<br>A42822<br>S57922                                                             | S57925<br>JC4579<br>S62730<br>B42822<br>A38977                                                          |
| 1548 2<br>1712 2<br>84 2                                       | 175<br>223<br>279<br>288<br>2                                                    | 22888                                                                                            | 00000<br>0000<br>00000<br>00000                                                                         |
| 63.5<br>63.5                                                   | 61:5<br>61:5<br>61:5<br>61:5                                                     | 6<br>6<br>6<br>7<br>6<br>7<br>7<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8 | 61.5<br>61.5<br>61.5<br>61.5                                                                            |
| ო ო ი<br>ო ო ო                                                 | 2222                                                                             | 8888                                                                                             | 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8                                                                   |
| 0 H 8                                                          | ነ ፈ ଘ ଘ ଘ<br>ነ ፌ ፌ ፒ ሴ                                                           |                                                                                                  | 4 4 4 4 4<br>11 62 64 62                                                                                |

## ALIGNMENTS

hypothetical 367K protein - Cenarchaeum symbiosum C;Species: Cenarchaeum symbiosum C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 18-Feb-2000 C;Species: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 18-Feb-2000 C;Accession: T31308 R;Schleper, C:; DeLong, E.F.; Freston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V. J. Bacteriol. 180, 5003-5009, 1998 chromosomal variation in natural populations of the UA;Title: Genomic analysis reveals chromosomal variation in natural populations of the UA;Title: Genomic analysis reveals chromosomal variation in natural populations of the UA;Generon number: 220994; MUID:98422450; PMID:9748430 A;Generon: T31308 A;Accession: T31308 A;Generon: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Generon: 1-3772 GCH>A;Generon: 1-3772 G

ö Gaps ö Score 38; DB 2; Length 3472; Pred. No. 60; 4; Mismatches 1; Indels Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative

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T39116
probable sulfate permease - fission yeast (Schizosaccharomyces pombe)
probable sulfate permease - fission yeast (Schizosaccharomyces pombe
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C;Species: O3-Dec-1999 #sequence\_revision O3-Dec-1999 #text\_change O3-Dec-1999
C;Accession: T39116
K;Hunt, C; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, November 1999
A;Reference number: Z21829
A;Accession: T39116

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A;Experimental source: strain 972h-; cosmid c869

A; Gene: SPDB: SPAC869.05c A; Map position: 1

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135 VVPQGMSYA 143 3 VVPXGMSYS 11 ઠે g ò

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1276 EQKIPMGMSY 1285
 1 EEVVPXGMSYS 11
 32 DEVVPNGKTYA 42
 335 EQIVEGGLQY 344
 1 EEVVPXGMSY 10
 1 EEVVPXGMSY 10
 A,Gene: CESP:R10D12.10
 RESULT 8
 RESULT 7
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 VI protein - tobacco yellow dwarf virus (strain Australia)
C;Species: tobacco yellow dwarf virus
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Accession: A42452
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
Virology 187, 633-642, 1992
Virile: The nucleotide sequence of the infectious cloned DNA component of tobacco yelld
A;Reference number: A42452; MUID:92188538; PMID:1546458
 C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: B97355
R;Nolling, J.; Brecon, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A;Reference number: A96900; MUID:21359325; PMID:21359325
 DNA segregation ATPase, FtsK/SpollIE family, YUKA B. subtilis ortholog [imported] - Clos
 "Cross-references: EMBL:AL031261; PIDN:CAA20298.1; GSPDB:GN00067; SPDB:SPBC3H7.02. Bxperimental source: strain 972h-; cosmid c3H7
 ô
 A.Status: preliminary
A.Molecule type: DNA
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A.Cross-references: GB.ME001437; PIDN:AAKB1629.1; PID:g15026814; GSFDB:GN00168
A.Experimental source: Clostridium acetobutylicum ATCC824
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;Species: Schizosaccharomyces pombe
;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 0; Gaps
 0; Gaps
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A;Residues: 1-102 <MOR>
A;Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
 ;Accession: T40413
;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
Ubmitted to the EMBL Data Library, August 1998
;Reference number: 221926
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Best Local Similarity 77.8%; Pred No. 22;
Matches 7; Conservative 1; Mismatches 1; Indels
 ;Status: preliminary; translated from GB/EMBL/DDBJ
 2 EVVPXGMSYS 11
 7 OVVPSGINYS 16
 148 VVPQGMSYA 156
 3 VVPXGMSYS 11
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 Gene: SPDB:SPBC3H7.02
 Accession: T40413
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 A:Gene: CAC3709
 Genetics:
ESULT 3
 RESULT 5
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A, Cross-references: EMBL: Z81109; PIDN: CAB03241.1; GSPDB: GN00023; CESP:R10D12.10 A, Experimental source: clone R10D12
 hypothetical protein precursor (clone TPP11) - tomato
C,Species Lycoperaticon esculentum (tomato)
C,Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
C,Accession: 857810
 hypothetical protein R10D12.10 - Caenorhabditis elegans
C;Spscies Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24111
 zinc finger protein AT-BP2 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Sep-1999
C;Accession: 822293; I786ap.
R;Mitchimore, C.; Traboni, C.; Cortese, R.
Nucleic Acids Res. 19, 141-147, 1991
 A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-225 kMID:
A;Cross-references: EMBL:U20592; NID:9924625; PIDN:AAA80497.1; PID:g924626
C;Superfamily: plant Kunitz-type proteinase inhibitor
 0; Gaps
 Gaps
 RiMiligan, S.B.; Gasser, C.S.
Plant Mol. Biol. 28, 691-711, 1995
Affilte: Nature and regulation of pistil-expressed genes in tomato.
A;Reference number: S57808; MUID:95375233; PMID:7647301
A;Accession: S57810
Query Match
69.2%; Score 36; DB 2; Length 1498;
Best Local Similarity 60.0%; Pred. No. 63;
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 A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 1-425 <WIL>
 Nirelly, C. A. B. B. B. Data Library, October 1996
A;Reference number: 219842
A;Accession: T24111
 A;Map position: 5
A:Introns: 23/3; 56/3; 113/3; 257/2
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APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Lim.wilby, Marguerita
APPLICANT: Lim.wilby, Marguerita
APPLICANT: Lim.vilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 00/220,101
PRIOR APPLICATION NUMBER: 00/220,101
NUMBER OF SEQ ID NOS: 62
SEQ ID NOS: 62
SEQ ID NO 7
LENGTH: 11
 APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Gaile E
APPLICANT: Levy, Gaile E
APPLICANT: Levy, Gaile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINB PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOFTARRE: Patentin version 3.1
LENGTH: 11
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 0; Gaps
 FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
 PEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
 86.5%; Score 45; DB 12; Length 11; 90.9%; Pred. No. 0.015; tive 0; Mismatches 1; Indels
 (ESULT 15
13-09-164-11
13-09-909-164-11
Septence 11, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
SSULT 14
3.09-909-164-7
Sequence 7, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
 NAME/KEY: MISC FEATURE
LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
 NAME/KEY: MISC FEATURE LOCATION: (9)...(9)
OTHER INFORMATION: D-amino acid
 LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FRATURE:
 ORGANISM: artificial sequence
 TYPE: PRT ORGANISM: artificial sequence
 NAWE/KEY: MOD_RES
LOCATION: (11)...(11)
CTHER INFORMATION: AMIDATION
IS-09-909-164-7
 Query Match
Best Local Similarity 90.9°
Matches 10; Conservative
 1 EEVVPXGMSYS 11
 1 EEVVPXGMHYS 11
 FEATURE:
NAME/KEY: MOD_RES
 TYPE: PRT
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Sequence 13, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION

APPLICANT: Corvas International, Inc.

APPLICANT: Lewy, Odile B.

APPLICANT: Lewy, Odile B.

APPLICANT: Brunck, Terence K.

ITILE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C.

FILE REPERENCE: IN 1001192-US

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT FILING DATE: 2003-03-25

PRIOR PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Batentin version 3.1

LENGTH: 11

LENGTH: 11
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 Gaps
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 88.5%; Score 46; DB 12; Length 11; 90.9%; Pred. No. 0.0091; tive 0; Mismatches 1; Indels
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Pred. No. 0.0091;
0; Mismatches 1; Indels
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OTHER INFORMATION: AMIDATION
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MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
 ; LOCATION: (8)..(9)
; OTHER INFORMATION: D-amino acids
US-09-909-164-13
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OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
 PEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (8)..(8)
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US-09-909-164-12
 ORGANISM: artificial sequence
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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Matches 10; Conservative
 1 BEVVPXGMSYS 11
 1 EEVVPXGMDYS 11
 EEVVPXGMDYS 11
 1 EEVVPXGMSYS 11
 NAME/KEY: MISC FEATURE
 NAME/KEY: MOD_RES
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US-09-9164-12
US-09-164-12
Sequence 12, Application US/09909164
Sequence 12, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Low, Odile E
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT PILING DATE: 2003-03-25
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 11
LENGTH: 11
 ö
 Gaps
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 FEMTURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEMTURE:
 FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
 Query Match

88.5%; Score 46; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 1; Indels
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LOCATION: (6) ... (6)
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OTHER INFORMATION: ACETYLATION
 TYPE: PRT
ORGANISM: artificial sequence
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ORGANISM: artificial sequence
 NAME/KEY: MOD RES
LOCATION: (11)...(11)
CTHER INFORMATION: AMIDATION
US-09-909-164-8
 1 EEVVPXGMSYS 11
 1 EEVVPXGMDYS 11
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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M protein - protein search, using sw model

June 3, 2004, 11:35:47; Search time 9 Seconds (without alignments) 117.567 Million cell updates/sec un on:

US-09-909-164-47 52 1 BEVVPXGMSYS 11 fitle: Perfect score: Requence: BLOSUM62 Gapop 10.0 , Gapext 0.5 scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Ainimum DB seg length: 0 (aximum DB seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Jatabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description |        | probable sulfate p | sulfate permease - | V1 protein - tobac | DNA segregation AT | hypothetical prote | hypothetical prote | zinc finger protei |        | DNA-binding protei | hypothetical prote | cell division inhi | probable ABC subst | -      | _      |        |        |        | hypothetical prote | _      | hypothetical prote | 3-phosphoshikimate | cdc37 protein - fi | iron(III) ABC tran | bacteriocin BCN5 - | ATP-dependent DNA | conserved hypothet | ğ      | DNA-directed RNA p |
|-------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|--------|--------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------|--------------------|
| Ω           | T31308 | T39116             | T40413             | A42452             | B97355             | S57810             | T24111             | S22293             | H82691 | A34203             | 854619             | H69491             | C82900             | I40758 | E90544 | D69493 | C81374 | T34536 | S75817             | T47670 | F72281             |                    | 4                  | D82352             | A30481             | AF3286            | D87046             | A35626 | 33                 |
| DB          | 2      | N                  | N                  | 7                  | N                  | N                  | 7                  | ~                  |        |                    |                    |                    |                    |        |        |        |        |        |                    |        |                    |                    |                    |                    |                    |                   |                    |        |                    |
| Lengt       | 3472   | 840                | 877                | 102                | 1498               | 225                | 425                | 670                | 749    | 2717               | 156                | 252                | 544                | 94     | 116    | 165    | 253    | 259    | 284                | 298    | 368                | 426                | 466                | 653                | 890                | 1028              | 1152               | 1394   | 1401               |
| 당성          | 73.1   |                    | 71.2               |                    |                    |                    | ۲.                 | 67.3               | 7      | ۲.                 | 65.4               | ď.                 | 65.4               | ω.     | ω,     | e,     | ë,     | w.     | ω.                 | 63.5   | e,                 | m.                 | 'n                 | m.                 | 63.5               | w.                | 63.5               | w.     | 63.5               |
| Score       | 38     | 37                 |                    |                    | 36                 |                    | 35                 | 35                 | 35     | 35                 | 34                 | 34                 | 34                 | 33     | 33     | 33     | 33     | 33     | 33                 | 33     | 33                 | 33                 | 33                 | 33                 | 33                 | 33                | 33                 | 33     | 33                 |
| Result No.  |        | 7                  | ო                  | 4                  | 7                  | 9                  | -                  | <b>&amp;</b>       | თ      | 10                 | 11                 | 12                 | 13                 | 14     | 15     | 16     | 17     | 18     | 19                 | 20     | 21                 | 22                 | 23                 | 24                 | 25                 | 26                | 27                 | 28     | 29                 |

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| hypothetical prote<br>masking protein pr<br>hypothetical prote | transport protein rho protein GDP-di hypothetical prote | cyclin D2 - rat<br>cyclin D2 - rat<br>cyclin D2 - mouse | cyclin D2 - human<br>cyclin D1 - Africa<br>cyclin D2 - Africa | cyclin D2 - chicke<br>cyclin D1 - zebra<br>cyclin D3 - human | cyclin D1 - human |
|----------------------------------------------------------------|---------------------------------------------------------|---------------------------------------------------------|---------------------------------------------------------------|--------------------------------------------------------------|-------------------|
| T04456<br>A38261<br>E97333                                     | PQ0616<br>T01457<br>B72481                              | JC4011<br>I58372<br>A41984                              | A42822<br>S57922<br>S57925                                    | JC4579<br>S62730<br>B42822                                   | A38977            |
| 000                                                            | 0000                                                    | 200                                                     | 0 0 0                                                         | 000                                                          | 0                 |
| 1548<br>1712<br>84                                             | 175<br>223<br>279                                       | 7 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3                 | 289<br>291<br>291                                             | 291<br>291<br>292                                            | 295               |
| 63.5<br>63.5<br>61.5                                           | 611.5                                                   | 61.5<br>61.5<br>61.5                                    | 61.5<br>61.5<br>61.5                                          | 61.5                                                         | 61.5              |
| # # # #<br># # #                                               | 2222                                                    | 3 5 5                                                   | 0 0 0<br>0 0 0                                                | 01 01 01<br>m m m                                            | 35                |
| 310<br>310                                                     | დ დ დ ი<br>დ <b>4 მ</b> ი                               | 3 3 4 8<br>3 8 4 8                                      | 6 4 4<br>6 0 1                                                | 4 4 4<br>2 8 4                                               | 5.4               |

## ALIGNMENTS

| PRESTUT. 1  191308  Prochetical 367K protein - Cenarchaeum symbiosum  C)Species: Cenarchaeum symbiosum;  C)Species: Cenarchaeum symbiosum;  C)Species: Cenarchaeum symbiosum;  C)Aste: 11-2a1-2000  C)Accession: 131308  A)Statesfario: 131308  A)Statesfario: 131308  A)Statesfario: 131308  A)States produce: 220994; MUID: 98423450; PMID: 9748430  A)States produce: 131308  A)States produce: 131309  A)States and B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)States B)Stat | Score 37; DB 2; Length 840;<br>Pred. No. 21;<br>1; Mismatches 1; Indels 0; Gaps 0; |
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A,Accession: T40413 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-877 <LYN>

Best Local Similarity 77.8 Matches 7; Conservative

Query Match

C;Genetics: A;Gene: SPDB:SPBC3H7.02 A;Map position: 2

148 VVPQGMSYA 156

3 VVPXGMSYS 11

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A;Accession: T24111
A;Status: preliminary; translated from GB/BMBL/DDBJ
A;Status: preliminary; translated from GB/BMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-425 < WIL>
A;Cross-references: ZMBL:281109; PIDN:CAB03241.1; GSPDB:GN00023; CESP:R10D12.10
A;Experimental source: clone R10D12
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0
 Mypothetical protein precursor (clone TPP11) - tomato
Cippecies: Lycopersicon esculentum
Cipate: 28-Oct.1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
Cipate: 28-Oct.1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
Cipacession: S57810
Rivilliagan, S.B.; Gasser, C.S.
Plant Mol. Biol. 28, 691-711, 1995
A;Title: Nature and regulation of pistil-expressed genes in tomato.
A;Reference number: S57808; MUID: 95375233; PMID: 7647301
A;Accession: S57810
A;Accession: S57810
A;Accession: S57810
 hyporhetical protein R10D12.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24111
R;Percy, C.
 zinc finger protein AT-BP2 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Sep-1999
C;Jaccession: S22293; 178656
R;Mitchelmore, C; Trabon1, C; Cortese, R.
Nucleic Acids Res. 19, 141-147, 1991
 A,Cross-references: EMBL:U20592, NID:g924625, PIDN:AAA80497.1, PID:g924626
C,Superfamily: plant Kunitz-type proteinase inhibitor
 Gaps
 Gaps
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DB 2; Length 1498;
 DB 2; Length 225;
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67.3%; Score 35; DB 2; Length 425;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 5; Conservative 3; Mismatches 2; Indels
 2; Indels
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Pred. No. 63;
2; Mismatches
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54.5%; Pred. No. 13;
live 3; Mismatches
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69.2%;
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 Best Local Similarity 54.5
Matches 6; Conservative
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 DEVVPNGKTYA 42
 1 BEVVPXGMSYS 11
 335 EQIVEGGLQY 344
 1 EEVVPXGMSY 10
 1 EEVVPXCMSY 10
 A;Molecule type: mRNA
A;Residues: 1-225 <MIL>
 A; Gene: CESP:R10D12.10
 Query Match
 RESULT 8
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 DIN Segregation ATPase, FtsK/SpoiliE family, YUKA B. subtilis ortholog [imported] - Clost Species: Clostridium acetobutylicum () Species: Clostridium acetobutylicum () Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 () Accession: B97355 () Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 () Accession: B97355 () Date: 14-Sep-2001 () Date: 14-Sep-2001 () Date: 15-Sep-2001 () Date: 15-Sep-
 "I protein - tobacco yellow dwarf virus (strain Australia)
C;Species: tobacco yellow dwarf virus
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Accession: A42452
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
A;Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yello
 Cross-references: EMBL:AL031261, PIDN:CAA20298.1; GSPDB:GN00067; SPDB:SPEC3H7.02; Experimental source: strain 972h-; cosmid c3H7
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 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1498 «KUR»
A;Residues: 1-1498 «KUR»
A;Cresines references: GB:AE001437; PIDN:AAK81629.1; PID:g15026814; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
 C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40413
C;Accession: T40413
R;Lyne, M; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
submitted to the EMBL Data Library, August 1998
A;Reference number: 221926
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A;Residues: 1-102 <MOR>
A;Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
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77.8%; Pred. No. 22;
tive 1; Mismatches 1; Indels
 Length 102;
 1; Indels
 sulfate permease - fission yeast (Schizosaccharomyces pombe)
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Score 36; DB 2; Pred. No. 3.5; 3; Mismatches

69.2%;

Query Match Best Local Similarity 60.0 Matches 6; Conservative

OVVPSGINYS 16

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A; Gene: CAC3709

2 EVVPXGMSYS 11

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Query Match
Best Local Similarity 66./*,
Best Local 6; Conservative
 Best Local Similarity 66.7
Matches 6; Conservative
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2405 VVPAGLTYS 2413
 3 VVPXGMSYS 11
 2 EVVPXGMSY 10
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50 EVMPLGMDY 58
 Query Match
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 "Residues: 1-749 c5TM>
"Tross-references: GB:AB003967; GB:AE003849; NID:g9106347; PIDN:AAF84162.1; GSPDB:GN001
"Experimental source: strain 9a5c.
"Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Arlones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, I.E.A.; Carraro, D.M.; Carrer, H.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, I.E.A.; Carraro, D.M.; Carrer, Docenan, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
"Dubmitted to GenBank, June 2000
"Authors: Ferreira, W.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
"D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr.
hado, M.A.; Madeira, A.M.B.N.; Matsukuma, A.Y.; Marino, C.L.; Marques, M.V.; Martins, E.M.F.; Matsukuma, A.Y.; Marino, C.L.; Marques, M.V.; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P.
odrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak, Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvair, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z., Contents annotation
Fitle: Isolation of two cDNAs encoding zinc finger proteins which bind to the alpha 1-;Reference number: 158280; MVID:91187610; PMID:1901405
;Accession: 822293
;Accession: 822293
;Molecule type: mRNA
;Molecule type: mRNA
;Residues: 1-670 cMTJ>
;Cross-references: BMEL:X54250; NID:957519; PIDN:CAA38151.1; PID:957520
;Note: the authors did not translate the codon for residue 1
;Superfamily: HIV-EP2 enhancer-binding protein
;Keywords: DNA binding; transcription regulation; zinc finger
 Accession: H82691
Janonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequentanonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequency 406, 151-157, 2000
Title: The genome sequence of the plant pathogen Xylella fastidiosa.
Reference number: A82515; MUID:20365717; PMID:10910347
Note: for a complete list of authors see reference number A59328 below
Accession: H82691
Status: preliminary
Molecule type: DNA
 Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomerase
 134203

NA-binding protein PRDII-BF1 - human
NA-binding protein PRDII-BF1 - human
1.5Decies: Homo sapiens (man)
1.5Decies: Homo sapiens (man)
1.5Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Sep-1999
1.5Accession: A34709
1.5Accession: A34709
1.5Accession: A24203, 334779
1.5Ean, C.M.; Maniatis, T.
1.5enes Dev. 4, 29-42, 1990
 opoisomerase IV subunit XF1353 [imported] - Xylella fastidiosa (strain 9a5c);Species: Xylella fastidiosa;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
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Best Local 77.0
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 376 VVPAGLTYS 384
 2 EVVPXGMSY 10
 3 VVPXGMSYS 11
 ,;Gene: XF1353
 ESULT 10
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NASOLATION SAGES ACCORDANCE CEREVISIAE)

NATIONALE INTEGRAL PROTECT TO THE SAGES ACCORDANCE CEREVISIAE)

NATIONALE DATE TO THE SAGES ACCORDANCE CERVISIAE

C) Species Saccharomyces CERVISIAE

C) Species Saccharomyces CERVISIAE

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C) Species Saccharomyces CERVISIAE

C) Species Saccharomyces CERVISIAE

C) Species Saccharomyces CERVISIAE

C) Accession: S54619

NA Reference number: S54617

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A) RACCESSION: S54617

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A) Residues: 1-156 ADEN-

A) Residues: 1-156 ADEN-

A) Residues: 1-156 CEM-

A) RESIDUE RESIDUE RESIDUE RESIDUE RESIDUE RESIDUE RESIDUE RESIDUE RE
A; Title: A DNA-binding protein containing two widely separated zinc finger motifs that z A;Reference number: A34203; MUID:90169514; PMID:2106471
A;Reference number: A34203; MUID:90169514; PMID:2106471
A;Retaus: preliminary
A;Rolecule type: mRNA
A;Retaus: preliminary
A;Retaus: preliminary
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A;Reference: EMBL:X5141, 1990
A;Title: A large protein containing zinc finger domains binds to related sequence elemen A;Reference number: A34779; MUID:90205817; PMID:2108316
A;Retaus: preliminary; nucleic acid sequence not shown
A;Retaus: preliminary; nucleic acid sequence not shown
A;Retaus: greliminary; nucleic acid sequence not shown
A;Retaus: 801-1072, N', 1074-1168, 'K', 1170-1225, 'V', 1227-1434,'N', 1436-1607,'I', 1609-16
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C;Superfamily: HIV-EP2 enhancer-binding protein
C;Keywords: DNA binding; transcription regulation; zinc finger
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H69491
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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 26-Aug-1999
C;Accession: H69491
C;Accession: H69491
S;Klerk, H.B.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
C;Fileischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
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 Length 156
 2; Indels
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Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: H69491

A;Accession: H69491

A;Accession: H69491

A;Residues: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-252 < KLE>

A;Cross-references: GB:AE000970; GB:AE000782; NID:g2689293; PIDN:AAB89318.1; PID:g264860

C;Superfamily: cell division inhibitor minD
 .Species: Ureaplasma urealyticum
.Space: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
.Accession: C82900
.Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
.bmitted to GanBank, February 2000
.Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
.Reference number: A82870
 ypochetical protein 1 - Campylobacter jejuni (fragment)
,Species: Campylobacter jejuni
,Species: Campylobacter jejuni
,Date: 16-Aug-1996 #text_change 08-Oct-1999
,Accession: 140758; S47317
,Hani, B.K.; Chan, V.L.
. Bacteriol: 177, 2396-2402, 1995
. Title: Expression and characterization of Campylobacter jejuni benzoylglycine amidohyd; Recession: 140758; MUID:9247673; PMID:7730270
 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-544 <GLAS
A;Residues: 1-544 <GLASD02133; GB:AF222894; NID:g6899339; PIDN:AAF30768.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
 obable ABC substrate-binding protein, iron UU359 [imported] - Ureaplasma urealyticum
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 A, Cross-references: EMBL: 236940; NID: 9535805; PIDN: CAA85392.1; PID: 9535806
 Gaps
 Gaps
 Gaps
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0
 ..
0
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 DB 2; Length 544;
 Score 34; DB 2; Length 252;
Pred. No. 24;
1; Mismatches 1; Indels
 Score 33; DB 2; Length 94;
Pred. No. 14;
2; Mismatches 2; Indels
 Indels
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-94 <RES>
 Query Match 65.4%; Score 34; DB Best Local Similarity 70.0%; Pred. No. 55; Matches 7; Conservative 1; Mismatches
 63.54;
55.64;
 Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
 Query Match
Best Local Similarity 55.0
Thes 5; Conservative
 135 EEVVPHYLSY 144
 1 EEVVPXGMSY 10
 2 EVVPXGMSY 10
 ||:| |||
81 EVIPAGMS 88
 2 EVVPXGMS 9
 A;Gene: ABCsbp-5; UU359
A;Genetic code: SGC3
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:: | |||| 26 DIFPSGMSY 34

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SOS ribosomal protein L20 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: E90544
R;Chanbaud, I:; Heilid; R; Ferris, S:; Barbe, V; Samson, D.; Galisson, F.; Moszer, I.
R;Chanbaud, I:; Heilid; R; Ferris, S0: Barbe, V; Samson, D.; Galisson, F.; Moszer, I.
R;Chanbaud, I:; Heilid; R; Ferris, S0: Barbe, V; Samson, D.; Galisson, F.; Moszer, I.
R;Chanbaud, I.; Moszer, S0: Barbe, V; Samson, D.; Galisson, F.; Moszer, I.
R;Chanbaud, I.; Moszer, S0: MulD:21267165; PMID:11353084
A;Reference number: A95512; MulD:21267165; PMID:11353084
A;Reference number: A95512; MulD:21267165; PMID:11353084
A;Reference number: A95512; MulD:21267165; PMID:11353084
A;Residues: 1-116 «KURA
A;Residues: 1-116 «KURA
A;Residues: 1-116 «KURA
A;Residues: 1-116 «KURA
A;Gene: Gode: GS: Goore 33; DB 2; Length 116;
C;Genetics: A;Genetic code: SGC3
C;Superfamily: Escherichia coli ribosomal protein L20
Cuery Match
Guery Match
Best Local Similarity 77.8%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Cy 3 vvpxGMSYS 11
Db 68 VRPLGMSYS 76
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 STRAIN-ATCC 25586;

WEDLIKE=21886394; PubMed=11889109;

Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Rapatral V., Anderson I., Ivanova N., Grechkin G., Zhu L., Rapatral Y., Chaga O., Goltsman E., Bernal A., Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Iarsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Iarsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Tonstein M., Kyrpides M., Overbeek R.; Genome sequence and analypsis of the oral bacterium Fusobacterium Turoleatum strain ATCC 25586."; J. Bacteriol. 184:2005-2018(2002).

T. GARALYTC ACTIVITY: 2 AFP + L-glutamine + CO(2) + H(2)O = 2 ADP + Dosphate + L-glutamate + carbamoyl phosphate.

T. CARALYTC ACTIVITY: 2 AFP + L-glutamine + CO(2) + H(2)O = 2 ADP + Dosphate + L-glutamate + carbamoyl phosphate.

T. PATHWAY: Arginine biosynthesis.

T. PATHWAY: Arginine biosynthesis.

T. SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).
 075355 homo sapien
099616 homo sapien
p90818 crithidia f
P52384 human herpe
P52544 human herpe
P52544 human herpe
P52541 toman oxpe
P528931 tomato aspe
P16916 escherichia
P16918 escherichia
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (BC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB OR FW0422.
 Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
Fusobacterium.
 -!- SIMILARITY: Belongs to the carB family.
 PRT; 1058 AA
 AL I GNMENTS
TOLB HABIN
BENP3 HUMAN
S216 HUMAN
GSP CRIFA
PRTP HSV6U
PRTP HSV6Z
SCTI_XTEAT
EDD_KAT
V1A_TAV
RHSA_ECOLI
RHSC_ECOLI
 EMBL; AE010554; AAL94625.1; ALT_INIT.
HAMAP; MF_01210; -; 1.
 HAMBL, ARULOZZI,
HAMBA, MF DIZIO, -1 1.
HAMBA, MF DIZIO, -1 1.
INTERPRO, IPRO05483, CPASE L.
INTERPRO, IPRO05483, CPASE L. D2.
INTERPRO, IPRO05480, CPASE L. D2.
INTERPRO, IPRO05481, CPASE L. D3.
INTERPRO, IPRO05481, CPASE L. N.
INTERPRO, IPRO05482, MGS LIKE.
INTERPRO, IPRO04362, MGS LIKE.
 PF00289; CPSase L Chain;
PF02786; CPSase L D2; 2.
PF02787; CPSase L D3; 1.
 427
529
719
726
726
920
920
13377
 STANDARD;
 SEQUENCE FROM N.A.
 NCBI_TaxID=76856;
 FUSIN
 CARB FU
QBRG86;
 Pfam;
Pfam;
 CARB_FUSNN
 gallus gall
homo sapien
homo sapien
mus musculu
rattus norv
 homo sapien
mycoplasma
archaeoglob
campylobact
 gallūs gall
xenopus lae
 homo sapien
clostridium
 homo sapien
mus musculu
 tobacco yel
clostridium
 mus musculu
vibrio chol
 homo sapien
vibrio chol
 homo sapien
 rattus norv
 mus musculu
 brachydanio
 homo sapien
 schizosacch
 mus musculu
 rattus norv
 xenopus lae
 28rg86 fusobacteri
 schizosacch
 neurospora
 June 3, 2004, 11:32:06 ; Search time 4.86667 Seconds (without alignments) 117.693 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 004351
P15822
P23622
P23622
P23622
C060312
C08330
C08330
C09krbo
C09krbo
C09krbo
C09krbo
C09krbo
C09krbo
C09krbo
C09krbo
 0000018
0000018
0000018
0000018
00004827
0004827
 P50755
P49706
P53782
P55169
P55169
P24385
P25322
P39948
 290459
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
 hits satisfying chosen parameters:
 141681 segs, 52070155 residues
 SUMMARIES
 SULH_SCHPO
YINK_TROYA
YINK_TROYA
YINAGE
ZEPI_HUMAN
ALOA_HUMAN
RL20 WYCPU
YJ490_CARJE
CTX3 WOUSE
CTX3 MOUSE
AROA_VIECH
 CAMJE
MOUSE
VIBCH
 HUMAN
RAT
MOUSE
RAT
 CHICK
XENLA
 CARB_FUSNN
SULH_SCHPO
 SCHPO
HUMAN
CLOPE
MOUSE
 MOUSE
 ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 HUMAN
 protein - protein search, using sw model
 Gapop 10.0 , Gapext 0.5
 991
 finimum DB seq length: 0 faximum DB seq length: 2000000000
 US-09-909-164-47
52
 1 EEVVPXGMSYS 11
 DB
DB
 SwissProt_42:*
 1058
877
102
1499
27117
788
1499
1165
165
280
426
 Length
 BLOSUM62
 Query
Match
 otal number of
 'itle:
'erfect score:
 coring table:
 Score
 latabase :
 equence:
 earched:
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 Result
No.
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N

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TRANSMEM
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 TRANSMEM
 FRANSMEM
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 PRANSMEN
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 Matches
 SOLUTION SOL
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 ID ACT DE SERVICE SERV
 STRAIN=972.

STRAIN=972.

STRAIN=972.

MEDLINE=21840191 PubMed=11859360,

WEDLINE=21840191 PubMed=11859360,

WEDLINE=2184019101 PubMed=11859360,

WEDLINE=21840191 PubMed=11859360,

WEDLINE=21840191 PubMed=11859360,

WEDLINE=2184011 PubMed=11850.

Bacoks K., Brown D., Harris D., Hidalgo J., Hodgson G., Honlow B., Honneby T., Howarth S., Horlby D., Hodgson G., Honlow B., Jones M., Lather S., McDonald S., McDean J., Andlovg S., Horneby T., Howarth S., McDonald S., McLean J., McDonald S., Sawares S., Stevens K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Malb S., Welton S., McDonald S., McDonald J., Willeard J., Willeard J., McDonald S., McDonald J., Willeard S., McDonald S., McDon
 ô
DR PEAM; PF02142; MGS; 1.

DR PRINTS; PR00098; CPSASE.

DR PROSTIE; PS00866; CPSASE.1.

DR PROSITE; PS00866; CPSASE.1; 2.

DR PROSITE; PS00867; CPSASE.2; 2.

KM Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

KM Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

KM Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

KM Arginine biosynthesis; Ligase; Complete protecome.

ARE-binding; Manganese; Complete protecome.

CARBOXYPHOSPHATE SYNTHETIC DOMAIN.

CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

***ARFERIC DOMAIN.
 Gaps
 ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
 ö
 DB 1; Length 1058;
 1; Indels
 ED7037AF77C1E39F CRC64;
 Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2003 (Rel. 42, Last annotation update)
Probable sulfate permease C3H7.02.
 Score 38; DB 1
Pred. No. 7;
3; Mismatches
 73.1%;
60.0%;
 117451
 6; Conservative
 STANDARD;
 190 EIVPNGLNYS 199
 2 EVVPXGMSYS 11
 Schizosaccharomyces.
NCBI_TaxID=4896;
 1058 AA;
 Query Match
Best Local Similarity
Matches 6; Conserv
 SULH SCHPO
074377;
 SPBC3H7.02
 METAL
SEQUENCE
 REPEAT
NP_BIND
NP_BIND
METAL
 RESULT 2
SULH SCHPO
 METAL
 SPITTTTTTTTTTTTTS
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 Gaps
 당
 -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential). -!- SIMILARITY: Belongs to the SLC26A/Sulp transporter (TC 2.A.53)
 MEDLINE=92188558; PubMed=1546458; Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.; Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.; "The nucleotide sequence of the infectious cloned DNA component tobacco yellow dwarf virus reveals features of geminiviruses infecting monocotyledonous plants."; virology 187:633-642(1992).
 Nature 415:871-880(2002).
-i- FUNCTION: HIGH AFPINITY UPTAKE OF SULFATE INTO THE CELL (BY
 ;
0
 71.2%; Score 37; DB 1; Length 877; 77.8%; Pred. No. 9.4; ive 1; Mismatches 1; Indels
 56995A8493371E43 CRC64;
 Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses, ssDNA viruses; Geminiviridae; Mastrevirus.
NCBI_TaxID=31599;
genome sequence of Schizosaccharomyces pombe.";
 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
 102 AA
 POTENTIAL. POTENTIAL.
 POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
 POTENTIAL. POTENTIAL.
 POTENTIAL. POTENTIAL.

 -!- SIMILARITY: Contains 1 STAS domain.

 POTENTIAL
 PIR; T40413; T40413.
GeneDB SPombe; SPBC3H7.02; -.
InterPro; IPR001264; STAS.
InterPro; IPR001902; Sulph transpt.
Pfam; PF01740; STAS; 1.
Pfam; PF00116; Sulfate transp; 1.
TIGRFAMS; TIGR00815; SULP; 1.
PROSITE; PS01130; SLC26A; 1.
PROSITE; PS010130; STAS; 1.
 96373 MW;
 EMBL; AL031261; CAA20298.1; -.
 Local Similarity 77.8 es 7; Conservative
 ransmembrane
 STANDARD;
 148 VVPOGMSYA 156
 3 VVPXGMSYS 11
 [1]
SEQUENCE FROM N.A.
 Transport; T
 RESULT 3
Y11K_TYDVA
ID Y11K_TYDVA
AC P31619;
 DOMAIN
SEQUENCE
 Query Match
```

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 Sauer U., Duerre P.;
"Sequence and molecular characterization of a DNA region encoding a
"Sequence and molecular characterization of a DNA region encoding a
small hear shock protein of Clostridium acetobutylicum.";
J. Bacteriol. 175:3394-3400(1993).
-!- SIMILARITY: Conteains 2 FtsK domains.
-!- CAUTION: Ref.2 sequence differs from that shown due to frameshifts
in positions 76 and 106.
 STRAIN=ATC. 824 / DSM 792 / VKM B-1787;
MEDLINE=2135925; PubMed=11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Xoonin B.V., Sahth D.R.;
Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
 Gaps
 Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 ..
0
 Score 36; DB 1; Length 102;
Pred. No. 1.6;
 1; Indels
 11178 MW; A40ECF1E0AF55B67 CRC64;
 01-FEB-1994 (Rel. 28, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypothetical protein CAC3709.
 PRT; 1498 AA.
 3; Mismatches
 SEQUENCE OF 1-108 FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=93273706; Pubmed=8501044;

 Bacteriol. 183:4823-4838(2001)

 PIR; A42452; A42452.
InterPro; IPR002621; Gemini mov.
Jemi, PP01708; Gemini mov; I.
Hypothetical protein.
SEQUENCE 102 AA; 11178 MW; A4
 69.2%;
 EMBL; M81103; AAA47947.1; -.
 6; Conservative
 STANDARD;
 2 EVVPXGMSYS 11
 ||| |::|| |::|
7 QVVPSGINYS 16
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=1488;
 Y1A9 CLOAB
 TA9_CLOAB
 Best Loca
Matches
⋩
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EMBL); AE007866; AAK81629.1; -. EMBL, X65276; CAA46379.1; ALT\_FRAME. PIR; B97355; B97355. PIR, B97355, B97355. InterPro, IPR002543, Ft8K\_SpolIIE

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 01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
2inc finger protein 40 (Human immunodeficiency virus type I enhancer-binding protein 1) (HIV-EPI) (Major histocompatibility complex binding protein 1) (MIV-EPI) (Major histocompatibility complex binding protein 1) (MSP-1) (Positive regulatory domain II binding factor 1)
 "High-resolution solution structure of the double Cys2His2 zinc finger from the human enhancer binding protein MBP-1.";
Biochemistry 31:3907-2917(1992).
Biochemistry 31:3907-2917(1992).
FUNCTION: THIS PROTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE S'-GGGACTTTCC-3' WHICH IS FOUND IN THE ENHANCER ELEMENTS OF NUMBROUS VIRAL PROMOTERS SUCH AS THOSE OF SY40, CWT, OR HIV1.
IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I MHC. INTERLEUKIN-2 RECEPTOR, AND INTERPERON-BETA GENES: IT MAY ACT
 Gaps
 "High-resolution three-dimensional structure of a single zinc finger from a human enhancer binding protein in solution."; Biochemistry 29:9324-9334(1990).
 -i- INDUCTION: By mitogens and phorbol ester.
-i- DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH ZINC-FINGER IN-BETWEEN.
-i- SIMILARITY: STRONG, TO HIVEP2.
 MEDIINE=90169514; PubMed=2106471; MEDIINE=90169514; Maniatis T.; Man C.M., Maniatis T.; Man C.M., Maniatis T.; Man DNA-binding protein containing two widely separated zinc finger motifs that recognize the same DNA sequence.";
 MEDLINE-92232684; PubMed=1567844;
Omichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E.,
Gronenborn A.M.;
 ö
 Complete proteome; Repeat.
 Score 36; DB 1; Length 1498;
Pred. No. 27;
2; Mismatches 2; Indels
 675 682 ATP (POTENTIAL).
1498 AA; 168968 MW; FF42037A335A9649 CRC64;
 STRUCTURE BY NNR OF 2113-2142.
MEDLINE=91064333, PubMed=2248949;
MEDLINE=10.05. Clore G.M., Appella E., Sakaguchi K.,
Gronemborn A.M.;
 2717 AA.
Pfam, PF01580, FtsK_Spoilis, 2.
PROSTIE; PS05901, FTSK, 2.
DOMAIN 655 857 FTSK 1.
DOMAIN 1001 1188 FTSK 1.
DOM BIND 675 682 ATP (PO)
SEQUENCE 1498 AA, 168968 NW; FF94.
 IN T-CELL ACTIVATION.
 STRUCTURE BY NMR OF 2087-2142
 69.2%;
 Conservative
 STANDARD;
 1276 EQKIPMGMSY 1285
 Genes Dev. 4:29-42(1990)
 1 EEVVPXGMSY 10
 (Human)
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 HIVEP1 OR ZNF40.
 Homo sapiens
 9
 HUMAN
 P15822
 IT 5
HUMAN
 Matches
 RANTITIOS
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788 AA;
 Query Match
Best Local Similarity
 [2]
SEQUENCE FROM N.A.
 9
 family.
 Transport;
TRANSMEM
TRANSMEM
TRANSMEM
 TRANSMEM
TRANSMEM
TRANSMEM
 TRANSMEM
 CARBOHYD
SEQUENCE
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 A10A_HUMAN
SOLUTION TO THE STATE OF THE ST
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 Gaps
 PROBABLE REVISIONS.
MEDIINE-9418925. Pubmed-8140616;
Sandal N. N., Marcker K.A.;
"Similarities between a soybean nodulin, Neurospora crassa sulphate
 SEQUENCE FROM N.A.
MEDLINE=91129256; PubMed=1825178;
Ketter J.S., Jarai G., Fu Y.-H., Marzluf G.A.;
Ketter J.S., Jarai G., Fu Y.-H., Marzluf G.A.;
"Nucleotide sequence, messenger RNA stability, and DNA recognition elements of cys-14, the structural gene for sulfate permease II in
 MIM; 194540; ...

MIM; 194540; ...

GO; GO:0005634; C:nucleus; TAS.

GO; GO:000367; F:DNA binding; TAS.

InterPro; IPR007087; Znf CZH2;

Enm; PR0096; Zf CZH2; 5.

PROSITE; PS00028; ZINC_FINGER_CZH2 1; 4.

PROSITE; PS017; ZINC_FINGER_CZH2 2; 4.

Transcription regulation; Zinc-finger; Metal-binding; DNA-binding;

Nuclear protein; Repeat; 3D-structure.
 ;
 Neurospora crassa.
Sukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
 Score 35; DB 1; Length 2717;
Pred. No. 80;
2; Mismatches 1; Indels
 2124
2135
A: 297217 MW; D45D3CA951FEAS61 CRC64;
 C2H2-TYPE.
C2H2-TYPE (POTENTIAL).
C2H2-TYPE.
C2H2-TYPE.
 01-NOV-1991 (Rel. 20, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Sulfate permease II.
 Biochemistry 30:1780-1787(1991)
 67.3%;
 EMBL; X51435; CAA35798.1; -
 PDB; 3ZNF; 15-JAN-92.
PDB; 4ZNF; 15-JAN-92.
PDB; 1BSO; 31-OCT-93.
TRANSPAC; TO0497; -.
Genew; HGNC:4920; HIVEP1.
 6; Conservative
 STANDARD;
 ||| |::||
2405 VVPAGLTYS 2413
 2092
2095
2108
2109
 3 VVPXGMSYS 11
 PIR; A34203; A34203
 Best_Local Similarity
Matches 6; Conserv
 CY14_NEUCR
 STRAND
HELIX
SEQUENCE
 Query Match
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 7714_NEUCR
11D CY144_N
12D CY1
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 ö
permease II and a putative human tumour suppressor.";
Trends Biochem. Sci. 19:19-19(1994).
-!- PUNCTION: UPTAKE OF SULFAIE INTO THE CELL.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- INDUCTION: Highly expressed, but only in cells subject to sulfur limitation, and it is turned on by the positive-acting Cys-3 sulfur regulatory protein.
-!- MISCELLANEOUS: SULPAIE PERMEASE II IS MAINLY FOUND IN MYCELIA.
-!- SIMILARITY: Belongs to the SLC26A/SulP transporter (TC 2.A.53)
 Gaps
 Aloa HUMAN STANDARD; PRT; 1499 AA.

060312; 096914;
060312; 0000 (Rel. 39, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
40-benerial phospholipid-transporting ArPase VA (EC 3.6.3.1) (ATPVA)
AMPIDA OR ATPLC OR ATPVC OR KIAA0566.
 POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mamalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 ö
 Score 34; DB 1; Length 788; Pred. No. 36;
 2; Mismatches
 InterPro, IPR001902; Sulph_transpt.
Plan, PR00916; Sulfate_transp; 1.
IIGRFAMB; IIGR00815; aulp; 1.
PROSITE; PS01130; SLC26A; 1.
 EMBL; M59167; AAA33615.1; ALT_SEQ.
 87864 MW;
 65.4%;
 Conservative
 3 VVPXGMSYS 11
 A37956; A37956.
 Homo sapiens (Human)
```

SEQUENCE FROM N.A.

```
RA Nagase T. Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
RT "Prediction of the coding sequences of unidentified human genes. IX.
RT The complete sequences of 100 new cDNA clones from brain which can
red for large proteins in vitro.";
DNA Res. 5:31-39(1998)
C. -- CATALTYIC ACTIVITY: ATP + H(2) 0 = ADP + phosphate.
C. -- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
C. -- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
C. -- TISSUE SPECIFICITY: Widely expressed, with highest levels in
Kidney, followed by lung, brain, prostate, testis, ovary and
SMAIL intestine.
C. -- DISEASE: Defects in ATP10A are a cause of Angelman syndrome (AS)
(MIN:105830]; also known as 'happy puppet syndrome'. AS is
C. -- DISEASE: Defects in ATP10A are a cause of Angelman syndrome (AS)
C. -- Characterized by features of severe motor and intellectual
C. -- Characterized by macrostomia, hypotomia, hyperactivity,
C. -- Angension, a great propensity for protruding the tongue ('tongue
C. -- SIMILARITY: Belongs to the cation transport ATPases family (P-type
C. -- SIMILARITY: Belongs to the cation transport ATPases family (P-type
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 AY029487; AAK33100.1; JOINED.
AY029488; AAK33100.1; JOINED.
AY029489; AAK33100.1; JOINED.
AY029480; AAK33100.1; JOINED.
AY029491; AAK33100.1; JOINED.
AY029492; AAK33100.1; JOINED.
 EMBL; AB051358; BAB47392.1; -.
EMBL; AY029504; AAX33100.1; -.
 SEQUENCE OF 337-1499 FROM N.A.
 rissum=Brain;
 EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
 EMBL;
```

```
MIN; 105830; ...

R GO; GO:0016021; C:integral to membrane; NAS.

GO; GO:00046021; C:integral to membrane; NAS.

GO; GO:00046021; P:plospholipid-translocating Arpase activity; NAS.

GO; GO:0008360; P:regulation of cell shape; NAS.

InterPro; IPR001757; Arpase E1-E2.

InterPro; IPR005839; Flippase.

R InterPro; IPR005839; Flippase.

R PRINTS; PR00119; CATAIPASE.

R TIGRFAMS; TIGR01494; ArPase-Pitpid; 1.

TIGRFAMS; TIGR01494; ArPase P-type; 6.

R PROSITE; PS00118; ArPasE E1-E2; 1.

Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;

M Multigene family.

T TRANSMEM 87 106

POTENTIAL.

T TRANSMEM 87 106

POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY)
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
 Score 34; DB 1; Length 1499;
Pred. No. 70;
0; Mismatches 3; Indels
 167687 MW; D4996A4D0635A68D CRC64;
 EXTRACELLULAR (POTENTIAL)
POTENTIAL.
 POTENTIAL.
EXTRACELLULAR (POTENTIAL)
 EXTRACELLULAR (POTENTIAL)
 EXTRACELLULAR (POTENTIAL)
 EXTRACELLULAR (POTENTIAL)
 POTENTIAL.
CYTOPLASMIC (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).

 Created)
 Last sequence update)
 Last annotation update)

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 POLY-GLU
 AAK33100.1; JOINED.
AAK33100.1; JOINED.
AAK33100.1; JOINED.
AAK33100.1; JOINED.
AAK33100.1; JOINED.
AAK33100.1; JOINED.
AAK33100.1; JOINED.
AAK33100.1; JOINED.
 AAH52251.1; -.
BAA25492.1; -.
 65.4%;
 EMBL, AY029494, AAK33100.11
EMBL, AY029495, AAK33100.11
EMBL, AY029496, AAK33100.11
EMBL, AY029496, AAK33100.11
EMBL, AY029498, AAK33100.11
EMBL, AY029498, AAK33100.11
EMBL, AY029501, AAK33100.11
EMBL, AY029501, AAK33100.11
EMBL, AY029501, AAK33100.11
EMBL, AY029503, AAK33100.11
EMBL, AY029503, AAK33100.11
EMBL, AY029503, AAK33100.11
EMBL, BAD11138, BAAS2492.1,
GGDGW, HGNC.13542, ATP10A.
 Query Match
Best Local Similarity 72...,
Best Local Similarity 72...,
 STANDARD;
 EEVVPRGGSVS 479
 1 EEVVPXGMSYS 11
 264
264
295
499
 1499 AA;
 (Rel.
(Rel.
 Genew; HGNC:13542
MIM; 605855; -.
MIM; 105830; -.
 _RL20 MYCPU
Q98QV0;
28-FEB-2003 (
28-FEB-2003 (
28-FEB-2003 (
 469
 TRANSMEM
DOMAIN
TRANSMEM
DOMAIN
 DOMAIN
CONFLICT
SEQUENCE
 DOMAIN
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 MOD RES
 RESULT 8
RL20 MYCPU
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Herzing L.B.K., Kim S.-J., Cook E.H. Jr., Ledbetter D.H.; "The human aminophospholipid-transporting ATPase gene ATP10C maps adjacent to UB83A and exhibits similar imprinted expression."; Am. J. Hum. Genet. 68:1501-1505(2001).
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Gaps

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Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Badow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 MEDINE-20150912; PubMed=10688204;

Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies N.M., Feltwell T., Holroyd S.,
Dagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.";
Nature 403:665-668(2000).
 Gaps
 Campylobacter jejuni.
Badcteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Campylobacteraceae; Campylobacter.
NCBI_TaxID=197;
 "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
 /[2]
SEQUENCE OF 160-253 FROM N.A.
STRAIN-AFTCC 43431 / TGH 9011;
MEDLINE-95247673; PubMed=7730270;
Hanl E.K., Chan V.L.;
Expression and characterization of Campylobacter jejuni
"Expression and characterization of Escherichia benzoylglycine amidohydrolase (Hippuricase) gene in Escherichia
 .;
0
 63.5%; Score 33; DB 1; Length 165; 60.0%; Pred. No. 12; ive 1; Mismatches 3; Indels
 Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 7 27 27
 165 AA; 17588 MW; BBC17054810ADBF8 CRC64;
 137. CHUND SIMMARU)
157. CHUND 1958; OPRNO; Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
17-OCT-2001 (Rel. 40, Last annotation update)
CJ0990C.
 253 AA.
 J. Bacteriol. 177:2396-2402(1995).
 EMBL; AE000968; AAB89307.1; -.
PIR; D69493; D69493.
 6; Conservative
 STANDARD;
 1 REVVPXGMSY 10
 60 RESIPDGASY 69
 Local Similarity
 SEQUENCE FROM N.A.
STRAIN=NCTC 11168;
 TIGR; AF1949; -.
 CAMUE
 SEQUENCE
 TRANSMEM
 Query Match
 Matches
 RESULT 10
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 ö
 Galisson F.,
 SEQUENCE FROM N.A.
STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MIDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Kterk H.-P., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 ö
 Mycoplasna pulmonis.
Bacteria, Firmicutes, Mollicutes, Mycoplasmataceae, Mycoplasma.
 PIR; ESUGHA; ESCOTT.

Mypulist; MYPU 2610; -.

HAMAP, MF 00382; -; 1.

InterPro; IPR005813; Ribosomal L20.

R InterPro; IPR006813; Ribosomal L20b/o.

PEam; PF00453; Ribosomal L20; 1.

R Probom; PP004239; Ribosomal L20; 1.

R Probom; PF004319; L20; 1.

R TIGREAMS; TIGR01032; rplT bact; 1.

R PROSTIES; P8009373; RIBOSOWAL L20; 1.

R Ribosomal protein; rRNA-binding; Complete proteome.
 STRAIN-UAB CTIP:
MDDLINE-1267165; PubMed=11353084; Barbe V., Samson D., Gal
Chambaud I., Heallig R., Ferris S., Barbe V., Samson D., Gal
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.
 Length 116;
 2; Indels
 Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
 DB 1;
 028330;
28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
AF1949.
 Score 33; DB 1
Pred. No. 8.1;
0; Mismatches
 165 AA
 EMBL; AL445563; CAC13434.1; ~.
PIR; E90544; E90544.
 63.5%;
 Query Match
Best Local Similarity 77.8%,
Rocal 7; Conservative
 50S ribosomal protein L20. RPLT OR MYPU 2610.
 STANDARD;
 VRPLGMSYS 76
 3 VVPXGMSYS 11
 SEQUENCE FROM N.A.
 NCBI_TaxID=2107;
 Moszer I., Dyf
Blanchard A.,
 YJ49 ARCFU
ID YJ49 ARCFU
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SCHAUBDER R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klauener R.D., Collins F.S., Wagner L.L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McZwan P.J., McKernan K.J., Malek J., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 "Functional annotation of a full-length mouse cDNA collection.";
 ö
 h Similarity 55.6%; Pred. No. 18; 5; Conservative 2; Mismatches 2; Indels
 EMBL; AL139076; CAB73246.1; -.
EMBL; Z36940; CAA85392.1; -.
PIR; C81374; C81374.
PIR; 1,40758; 140758.
Hypothetical protein; Complete proteome.
SEQUENCE 253 AA; 29783 MW; F96D3FF3265F8A6A CRC64;
 CTX3_MOUSE STANDARD; PRT; 280 AA. 091387; 09CXQ4; 1, Created) 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 110-0CT-2003 (Rel. 42, Last annotation update) Protein C20orf103 homolog precursor.
 Nature 409:685-690(2001).
 185 DIFPSGMSY 193
 2 EVVPXGMSY 10
 Mus musculus (Mouse)
 Query Match
Best Local Similarity
 NCBI_TaxID=10090;
 TX3 MOUSE
 Best Loc
Matches
 RESULT 11
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 ISOId=09D387-2; Sequence=VSP 003820; CAUTION: Ref.1 sequence differs from that shown due to frameshifts in positions 174 and 239.
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.M., Kzrywinski M.I., Skalska U., Smailus D.E., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 Gaps
 28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
29-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, La
 POTENTIAL.

CYTODIASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

MISSING (in isoform 2).

/FIId=VSP_003820.
 ;
0
 Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBI_TaxID=666;
 Score 33; DB 1; Length 280;
Pred. No. 20;
 E -> V (IN REF. 1; BAB31124)
Q -> P (IN REF. 1; BAB31124)
P -> A (IN REF. 1; BAB31124)
 2; Indels
 PROTEIN C200RF103 HOMOLOG. EXTRACELLULAR (POTENTIAL).
 Svent=Alternative splicing; Named isoforms=2;
 31721 MW; FALID7BF9FD5CCEF
 Transmembrane; Signal; Alternative splicing.
SIGNAL 1 29 POTENTIAL.
CHAIN 30 280 PROTEIN C20ORFI
 426 AA
 0; Mismatches
 IsoId=Q9D387-1; Sequence=Displayed;
 EMBL; AKO14127; BAB29169.1; -.
EMBL; AKO18222; BAB31124.1; ALT_FRAME.
EMBL; BC004791; AAH04791.1; -.
 PRT;
 MGD; MGI:1920368; 3110035N03Rik.
MGD; MGI:1923411; 6330527006Rik.
 AROA_VIECH
ID AROA_VIECH
STANDARD;
ID AROA_VIECH
SCHEBO;
DT 28-FEB-2003 (Rel. 41, Created)
 63.5%;
 Query Match
Best Local Similarity 75.v.
6; Conservative
 173 VTPAGMSY 180
 3 VVPXGMSY 10
 238 2
280 AA;
 Vibrio cholerae.
 Name=1
 CONFLICT
CONFLICT
CONFLICT
SEQUENCE
 TRANSMEM
DOMAIN
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: : | | | | | | 98 DSAIPGGMSY 107
 1 EEVVPXGMSY 10
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 ö
 SEQUENCE FROM N.A.
STRAINEE TOR NIGHT Serotype O1;
STRAINEE TOR NIGHE SEROTYPE O1;
MEDINIE-20406833; PubMed-10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Doddon R.C., Haft D.H., Hickey B.K., Peterson J.D., Umayam L.A.,
Ermolaeva M.D., Vamathevan J., Pettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., Milte O.,
Salzberg S.L., Smith H.O., Colwell R.R., Meskalnos J.J., Venter J.C.,
Fraser C.M.;
 Gaps
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hsp90 co-chaperone Cdc37 (Hsp90 chaperone protein kinase-targeting subunit) (Cell division control protein 37).
 Nature 466:477-483 (2000)

-!- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyviny1)-3-phosphoshikimate.
-!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
 "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 ö
 63.5%; Score 33; DB 1; Length 426; 60.0%; Pred. No. 31; ive 1; Mismatches 3; Indels
 Westwood P.K., Preston N.C., Fantes P.A.;
"Schizosaccharomyces pombe cdc37 gene.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
 Schizosaccharomyces pombe (Fission yeast).
Brkaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomyces.
 sixth step.
--- SUBUNIT: Monomer (By similarity).
--- SUBGELLUTAR LOCATION: Cytoplasmic (Probable).
--- SIMILARITY: Belongs to the EPSP synthase family.
 EMBL; AE004251; AAF94882.1; -. PIR; D82163; D82163.
 6; Conservative
 STANDARD;
 223 EFVIPAGOSY 232
 1 EEVVPXGMSY 10
 Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=4896;
 CC37 SCHPO
094740;
 cholerae."
 Query Match
 RESULT 13
CC37_SCHPO
 Matches
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 MEDLINE=2298825); PubMed=12477932;
A Klausner R.D., Collins F.S., Magner L., Schemen C.M., Schuler G.D.,
A Klausner R.D., Collins F.S., Magner L., Schemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Maruslina K., Farmer A.A., Rubin G.M., Hong L.,
Bolatchenko L., Maruslina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
A Raha S.S., McEwan P.J., McKernen K.J., Malek J.A., Gunarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodriques S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I. Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length
 SEQUENCE OF 9-478 FROM N.A., AND SUBCELLULAR LOCATION.
MEDLINE=929131319, PubMed=10196275,

"A novel cellular protein, p60, interacting with both herpes simplex virus 1 regulatory proteins 100, interacting with both nerges simplex virus 1 regulatory proteins ICP22 and ICP0 is modified in a cell-type-specific manner and is recruited to the nucleus after infection."
 SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=20175430; PubMed=10708517;
Smith J.S., Tachibana I., Pohl U., Lee H.K., Thanarajasingam U.,
Portier B.P., Ucki K., Billings S., Ramaswamy S., Mohrenweiser H.W.,
Schatthauer B.W., Louis D.N., Jenkins R.B.;
"A transcript map of the chromosome 19q-Arm glioma tumor suppressor
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 GSR2_HUMAN STANDARD;
Q9NZM5; Q9BTC6; Q9HAX6; Q9NPP1; Q9NPR4; Q9UF12;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glioma tumor suppressor candidate region gene 2 protein (p60).
 Andreu N., Estivill X., Escarceller M., Sumoy L.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
 human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 Virol, 73:3810-3817(1999).
 [5]
SEQUENCE OF 218-477 FROM N.A.
 SEQUENCE OF 12-478 FROM N.A.
 Genomics 64:44-50(2000)
 Homo sapiens (Human)
 [2]
SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 TISSUE=Testis;
 PQEEEBBQQQXAAX444FHARAQX44456666444444446EEHBBBX4EEBBBBBBBBBBBBCCQQQQQ
```

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 R -> Q.

GGS -> HEG (IN REF. 2; AAH04229).

G -> R (IN REF. 3).

RRKEQLWEKLAKQGELPREYRRAGARLLNPSATRAKPGPQD

RYERP -> SGRSSYGRSWPSRASSPGGAQGPSPVAQPFCN

KGPNPAPGHRIAA (IN REF. 3).

SONPLDRPLVGQDBFFLE -> LNNPDKPVVWPGCLFPG
 PEGNIILDRFKSFQRRNMIEPRERAKFKRKYKVKLVEKRAF
REIQ -> VLTVSCRGAPCPVMTPSILLPVPPRGYGRHHGCP
 WAGPVGPMPRG (IN REF. 5).
EGNILRDRFKSFQRRNMIEPRERAKFKRKYKVKLVEKRAFR
 Gaps
 MEDILINE-88336297; PubMed=2901768;
Garnier T., Cole S.T.;
Complete nucleotide sequence and genetic organization of the
bacteriocinogenic plasmid, plP404, from Clostridium perfringens.";
Plasmid 19:134-150(1988).
 MEDLINE=8705/020; PubMed=2877971;
Garnier T., Cole S.T.;
"Characterization of a bacteriocinogenic plasmid from Clostridium
 Plasmid pIP404.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
 EIQL -> RGQHSFETGSRAFRGGI (IN REF. 7F18923E348CB52B CRC64;
 Ö,
 63.5%; Score 33; DB 1; Length 478; 60.0%; Pred. No. 35; ive 1; Mismatches 3; Indels
 A -> S (IN REF. 2; AAH04229)
D -> H (IN REF. 3).
 01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
Bacteriocin BCN5.
 (IN REF. 3)
 MIM, 605691, -.
GO, 60016622; C:intracellular; NAS.
Nuclear protein; Polymorphism.
VARLANT 389 389 R -> Q.
 EMBL, AF182076, AAF62873.1; --
EMBL, BC004229; AAH04229.1; --
EMBL, BC006311, AAH06311.1; --
EMBL, BC010095, AAH10095.1; --
EMBL, AF286124; AAG30413.1; --
EMBL, AL359336; CAB94787.1; --
EMBL, AL122063; CABS9242.1; --
 478 AA; 54417 MW;
 SWISS-2DPAGE; Q9NZM5; HUMAN.
Genew; HGNC:4333; GLTSCR2.
 STANDARD;
 Clostridium perfringens.
 239 EVAPAGASYN 248
 235
417
477
 478
 9 6 191
 2 EVVPXGMSYS 11
 FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=1502;
 4
9
146
 434
 STRAIN=CPN50;
 SEQUENCE FROM
STRAIN=CPN50;
 BCN5 CLOPE
 CONFLICT
 CONFLICT
 CONFLICT
 SEQUENCE
 CONFLICT
 CONFLICT
 CONFLICT
 P08696;
 RESULT 15
BCN5_CLOPE
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 SEQUENCE OF 1-14 FROM N.A.
STRAIN=CRN50;
MEDLINE=S8039249; PubMed=2460717;
Garnier T., Cole S.T.;
"Studies of UV-inducible promoters from Clostridium perfringens in vivo and in vitro.";
Mol. Microbiol. 2:607-614(1988).
-1- FUNCTION: MAY FUNCTION AS AN IONOPHORE.
-1- INDUCTION: By UV irradiation.
 63.5%; Score 33; DB 1; Length 890; 66.7%; Pred. No. 67; tive 1; Mismatches 2; Indels
 DOMAIN 815 869 HYDROPHOBIC.
SEQUENCE 890 AA, 96699 MW; P4E5E8971C31C6C6 CRC64;
perfringens and molecular genetic analysis of the bacteriocin-encoding gene. ", J. Bacteriol. 168:1189-1196 (1986).
 EMBL; M14481; AAA982481;
EMBL; M32882; AAA982491;
PIR; A30481; A30481;
InterPro; IPR000834; Peptidase M14.
InterPro; IPR003646; SH3 bac.
Pfam; PF00246; Zn carbopept; 1.
SWART; SW00287; SH3b; 3.
Antibiotic; Bacteriocin; Plasmid.
DOMAIN
 Query Match
Best Local Similarity 66.79
Matches 6; Conservative
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0; Gaps

Search completed: June 3, 2004, 11:49:56 Job time: 4.86667 Becs

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Q8dihO synechococc Q8disa bacillus ce Q98fx1 rhizobium 1 O74056 cenarchaeum Q9ury8 schizosacch Q8ew4 mycoplasma Q8r126 mus musculu Q8bx35 mus musculu Q8bx35 mus musculu Q8bx35 mus musculu Q895y7 pseudomonas Q40129 lycopersico Q9xxk4 cenorlabdi Q8cud7 mus musculu Q8cud7 mus musculu Q8gyzy copersico Q9xxk4 cenorlabdi Q8cud7 mus musculu Q8cud7 mus musculu
 June 3, 2004, 11:35:06 ; Search time 29.8667 Seconds (without alignments) 116.206 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1017041 seqs, 315518202 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 SPTREMBL 25:*
1: Sp_archea!*
2: Sp_bacteria:*
3: Sp_human:*
5: Sp_human:*
5: Sp_human:*
6: Sp_human:*
6: Sp_numan:*
 Q8DIHO
Q8L5A7
Q8L5A7
Q9UXY8
Q9UXY8
Q8UXD8
Q8R126
Q8BTX1
Q8BTX1
Q8BTX1
Q8BTX1
Q8BTX1
Q8BTX1
Q8BY1
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 sp_rvirus:*
sp_bacteriap:*
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 sp_archeap:*
 US-09-909-164-47
52
1 EEVVPXGMSYS 11
 Query
Match Length DB
 Title:
Perfect score:
Sequence:
 Scoring table:
 Score
 Database :
 Searched:
 Run on:
 Result
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| Q726FO homo sapien Q9bh83 plasmodium Q8bh83 plasmodium Q81587 plasmodium Q81587 plasmodium Q81587 plasmodium Q81487 rattus ratt Q8pm16 xxlthomonas Q8pdm6 xylella fas Q14122 homo sapien Q12479 saccharomyC Q97182 sulfolobus Q87422 sulfolobus Q86m1 homo sapien Q92md6 rhizobium m Q81ym3 homo sapien Q92md6 rhizobium m Q81ym3 homo sapien Q92md6 rhizobium m Q81ym3 homo sapien Q92md6 rhizobium m Q81ym3 homo sapien Q92md6 rhizobium m Q81ym3 homo sapien Q92md6 rhizobium g Q81ym3 homo sapien Q92md6 rhizobium g Q91ym3 principlium Q9ury4 penicillium | Q8ktq4 candidatus<br>Q8ktq4 candidatus<br>Q8r55 fusobacteri<br>Q7sy67 xenopus lae<br>Q7u552 synechococc |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------|
| 88 88 88 88 88 88 88 88 88 88 88 88 88                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 224<br>856<br>552                                                                                       |
| Q7Z6R0<br>Q9BH83<br>Q0BH83<br>Q0BH84<br>Q0BH16<br>Q0BH16<br>Q0BH16<br>Q0PDM6<br>Q14122<br>Q14122<br>Q141479<br>Q97152<br>Q96H91<br>Q92MD6<br>Q98BP5<br>Q98BP5<br>Q98BP5<br>Q98BP5<br>Q98BP5<br>Q98BP5<br>Q98BP5<br>Q98BP5<br>Q98BP5<br>Q98BP5<br>Q98BP5<br>Q98BP5<br>Q98BP5<br>Q97XG2<br>Q87XG2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Q8KTQ4<br>Q8RE56<br>Q7SY67<br>Q7U552                                                                    |
| 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 133                                                                                                     |
| 555<br>583<br>583<br>583<br>583<br>583<br>100<br>100<br>100<br>100<br>100<br>100<br>100<br>100<br>100<br>10                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 208<br>209<br>209<br>209<br>209<br>209                                                                  |
| 00000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | <b>നെന്ന</b>                                                                                            |
| ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | , e, e, e, e,                                                                                           |
| 11110000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 14444<br>18848                                                                                          |

## ALIGNMENTS

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```
Pfam; PF01546; Peptidase_M20; 1.
Hydrolase; Complete proteome.
SEQUENCE 387 AA; 41180 MW; 131BFF8E64306829 CRC64;
 / Match 73.1%;
Local Similarity 54.5%;
les 6; Conservative 4
 |:|:| |:|:|
2294 EDVIPRGISFS 2304
 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
 PRELIMINARY;
 PRELIMINARY;
 1 EEVVPXGMSYS 11
 367 DEALPHGMSY 376
 1 EEVVPXGMSY 10
 Schizosaccharomyces
NCBI_TaxID=4896;
 SEQUENCE FROM N.A. STRAIN=972h-;
 SEQUENCE FROM N.A.
 SPAC869.05C
 STRAIN=B;
 Query Match
Best Local S
 Q9URY8
 074056
 RESULT 5
Q9URY8
 RESULT 4
074056
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 STRAIN=MAPP303099;
X MEDLINE=21082930; PibMed=11214968;
A REDLINE=21082930; PibMed=11214968;
A Ratarabe A., IdeBawa K., Ishikawa A., Kawashima K., Kimura T.,
A Rishida Y., Kiyokawa C., Kohara M., Marsumoto M., Marsuno A.,
A Kishida Y., Kiyokawa C., Kohara M., Marsumoto M., Marsuno A.,
A Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
A Takeuchi C., Yamada M., Tabara S.,
I "Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
DNA Res. 7:331-338(200).
R EMBL; APRO3002; BABS0445.1;
R GO, GO:0006708; F:hydrolase activity; IEA.
R GO, GO:0006303; F:metallopeptidase activity; IEA.
R GO; GO:0006308; P:proteclysis and peptidolysis; IEA.
 MEDLINE-22668415; PubMed=12721630; Rableron N., Candelon B., Raplare N., Sorokin A., Anderson I., Galleron N., Candelon B., Kapatral V., Bhattecharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Mauur M., Goltsman E., Larsen N., D'Souza M., Malunas T., Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D., Overbeek R., Xyrpides N., Genome sequence of Bacilus cereus and comparative analysis with Bacillus anthracis.
 Gaps
 ô
 Bacteria; Protecbacteria; Alphaprotecbacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
 Score 38; DB 16; Length 344;
Pred. No. 13;
 2; Indels
 Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
 344 AA; 38539 MW; C55268ACB7225995 CRC64;
 Created)
Last sequence update)
Last annotation update)
 Last sequence update)
Last annotation update)
 387 AA.
 2; Mismatches
 01-07N-2003 (TrEMBLrel. 24, Created)
01-07N-2003 (TrEMBLrel. 24, Last sequence of colory (TrEMBLrel. 25, Last annotation ABC transporter substrate-binding protein.
 EMBL, AE017015; AAP12123.1; -.
INTERPLO; IPR000437; Prok lipoprot S.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
 Rhizobium loti (Mesorhizobium loti).
 PRT;
 GO; GO:0008237; F:metallopeptidase
GO; GO:0006508; P:proteolysis and J
InterPro; IPR002933; Peptidase_M20
 73.1%;
 098FX1;
01-0CT-2001 (TrEMBLrel. 18,
01-0CT-2001 (TrEMBLrel. 18,
01-JUN-2003 (TrEMBLrel. 24,
 Conservative
 |||:||:||
843 EEVLPNGIGYS 853
 PRELIMINARY;
 PRELIMINARY;
 1 EEVVPXGMSYS 11
 152 ÉÉIAPLGLSÝ 161
 1 EEVVPXGMSY 10
 Nature 423:87-91(2003)
 Query Match
Best Local Similarity
 Hippurate hydrolase.
MLR3583.
 SEQUENCE FROM N.A.
 MCBI_TaxID=226900;
 SEQUENCE FROM N.A.
 Q815A7
Q815A7;
 098FX1
 RESULT 3
 RESULT 2
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 Gaps
 01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 25, Last sequence update)
Hypothetical protein.
Cenarchaeum symbiosum.
Archaea; Crenarchaeota; Thermoprotei; Cenarchaeum.
NCBL_TaxID=46770;
 Gaps
 Hunt C., Aves S., McDougall R.C., Rajandream M.A., Barrell B.G.,
 .
0
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 MEDLINE-98422450; PubMed-9748430;
Schleper C., DeLong B.F., Preston C.M., Feldman R.A., Wu K.Y.,
Swanson R.V.;
 Length 3472;
73.1%; Score 38; DB 16; Length 387; 60.0%; Pred. No. 15; tive 2; Mismatches 2; Indels
 1; Indels
 Schizosaccharomyces pombe (Fission yeast).
Bukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2003 (TrEMBLrel. 24, Last annotation update) Probable sulfate permease.
 Score 38; DB 1; I
Pred. No. 1.7e+02;
4; Mismatches 1;
 PRT; 3472 AA.
```

Gaps

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SEQUENCE FROM N.A.
STRAIN=NOD; TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
 Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 69.2%; Score 36; DB 11; Length 484; 60.0%; Pred. No. 53; Live 2; Mismatches 2; Indels
 69.2%; Score 36; DB 11; Length 471; 60.0%; Pred. No. 51; tive 2; Mismatches 2; Indel8
 01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
51milar to glioma tumor suppressor candidate region gene
GLTSCR2 OR AW536411.
 Strausberg R.;
Submitted (MR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025810; AAH25810.1; -.
MGD; MGT:2154441; Gltscr2.
Hypothetical protein.
NGN TER 1
SEQÜENCE 471 AA; 54506 MW; E0DA685C374A9760 CPC61.
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MIN-2003 (TrEMBLrel. 24, Last annotation update)
01-UIN-2004 (TrEMBLrel. 24, Last annotation update)
Similar to glioma tumor suppressor CANDIDATE region gene
 Straubberg R.; straubberg R.; submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC01637; ARH17637.1; -. MDD; MGI:2154441; Gltscr2.
RMD; MGI:2154441; Gltscr2.
RMD; MGI:2154441; Gltscr2.
 484 AA
 484 AA.
 PRT;
 PRT;
 Query Match
Best Local Similarity 60.v
 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
 PRELIMINARY;
 PRELIMINARY;
 239 EVIPAGASYN 248
 226 EVIPAGASÝN 235
 SEQUENCE FROM N.A.
TISSUE=Salivary gland;
 2 EVVPXGMSYS 11
 2 EVVPXGMSYS 11
 Mus musculus (Mouse).
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 NCBI_TaxID=10090;
 protein.
 Q8VD18;
 Q8BTX4;
 Q8VD18
 Q8BTX4
 RESULT 9
 RESULT 8
 287018
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 Saski Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K., Yasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K., Yoshiho C., Horino A., Shiba T., Sasaki T., Hattori M.;
Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
"The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans.";
Nucleic Acids Res. 30:5293-5300(2002).
EMBL, AP004171; BAC4405.1; -
EMBL, AP004171; BAC4405.1; -
InterPro; IPR007826; Lipoprotein.7.
Ffam, FF04000; Lipoprotein.7.
Complete proteome.
Complete proteome.
SEQUENCE 1123 AA; 123636 MW, A4D707330E3DB4AC CRC64;
 Gaps
 Gaps
 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 Mycoplasma penetrans.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=28227;
 ö
 ö
 71.2%; Score 37; DB 16; Length 1123; 70.0%; Pred. No. 81; 2; Indels Live 1; Mismatches 2; Indels
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

REMEL; AL132779; CAB60015.1; -.

PIR; T39116; T39116; T39116;
GenebB Spombe; SPAC869.05c; -.

GO; GO:0008271; F:sulfate porter activity; IEA.

GO; GO:0008271; F:sulfate transport; IEA.

RICEPPO; IPRO02645; STAS.

RICEPPO; IPRO01995; Sulfate transpt.

PEAM; PF001914; STAS.

REAM; PF001916; Sulfate transpt.

REQUENCE 840 AA; 93517 MW; ED4833B162B69077 CRC64;
 Query Match
71.2%; Score 37; DB 3; Length 840;
Best Local Similarity 77.8%; Pred. No. 59;
Matches 7; Conservative 1; Mismatches 1; Indels
 QBR126 PRELIMINARY; PRT; 471 AA. QBR126; 01-JUN-2002 (TrEMBLrel. 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JON-2003 (TrEMBLrel. 25, Last annotation update) Hypothetical protein (Fragment)
 Last sequence update)
Last annotation update)
 PRT; 1123 AA
 Created)
 Q8EWD4 PRELIMINARY;
Q8EWD4;
01-WAR-2003 (TrEMBLrel. 23, C3)
01-MAR-2003 (TrEMBLrel. 23, L6)
01-OCT-2003 (TrEMBLrel. 25, L6)
MYPE 2560 paralog, 57%.
 Query Match
Best Local Similarity 70...
7; Conservative
 658 EYVPMGLSYS 667
 2 EVVPXGMSYS 11
 135 VVPQGMSYA 143
 3 VVPXGMSYS 11
 SEQUENCE FROM N.A. STRAIN=HF-2;
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RESULT 6

⋧ ત્ RESULT 7 Q8R126

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Gaps

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mobile DNA in the evolution of vancomycin-resistant
 NCBI_TaxID=323;
 Query Match
 Role of
 Q889X7
 Best Loca
Matches
 RESULT 12
0889X7
AC 0889X AC 0889X AC 0889X AC 0889X AC 0889X AC 01-UC DT 0
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 8
 (I) SEQUENCE FROM N.A.

STRIN=C57BL/6J; TISSUE-Fituitary;

RX The FANTOW Consortium,

RA The FANTOW Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of 60.70 full-length cDNAs.";

RI Nature 420:563-573(2002)

RE MED; MGI:2154441; Gltscr2.

PR MGD; MGI:2154441; Gltscr2.

SEQUENCE 484 AA; 55792 MW; EB67949BCBE92D44 CRC64;
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 SEQUENCE FROM N.A.
STRAIN=V883 / ATCC 700802;
MEDLINE=2250857; PubMed=12663927;
MEDLINE=2250857; PubMed=12663927;
Paulsen I.T., Banerriei L., Myers G.S.A., Nelson K.E., Seshadri R., Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F., Tettelin H., Dodson R.J., Unrkin S., Kolomay J., Madupu R., Nelson W., Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H., Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
 Gaps
 Enterococcus faecalis (Streptococcus faecalis).
Bacteria, Firmicutes, Lactobacillales, Enterococcaceae, Enterococcus.
NCBI_TaxID=1351;
 Gaps
 Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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 Query Match 69.2%; Score 36; DB 11; Length 484; Best Local Similarity 60.0%; Pred. No. 53; Matches 6; Conservative 2; Mismatches 2; Indels
 QBEX35;
QBEX35;
01-MAR-2003 (TERBLrel. 23, Last sequence update)
01-MAR-2003 (TERBLrel. 24, Last annotation update)
01-JUN-2003 (TERBLrel. 24, Last annotation update)
Similar to glioma tumor suppressor CANDIDATE region gene 2
 2; Indels
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL AKO88461; BAC40357.1; -.
MGD; MGI:2154441; G1tscr2.
SEQUENCE 484 AA; 55806 MW; B3056425B5EECAD8 CRC64;
 Q839T9;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pheromone binding protein, putative.
EF0063.
 484 AA.
 559 AA
 2; Mismatches
 PRT;
 PRT;
 Match 69.2%;
Local Similarity 60.0%;
Les 6; Conservative 5
 PRELIMINARY;
 PRELIMINARY;
 239 EVIPAGASYN 248
 2 EVVPXGMSYS 11
 2 EVVPXGMSYS 11
 Q839T9
 Q8BK35
 RESULT 10
08BK35
AC 08BK3
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 RESULT 11
 Q839T9
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STRAIN=DC3000;

A Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,

Buell R., Joardar Y., Wan Aken S., Feldblyum T., Gwinn M.,

Berry K., Uterback T., Van Aken S., Feldblyum T., Gwinn M.,

A Brinkac L., Beanan M., Haft D., Selengut J., Nalson W., Davidsen T.,

Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,

Riche O., Fraser C., Collner A.,

Riche O., Fraser C., Collner A.,

Rubmitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

BMBL; AE016858; AA054162.1; -..

BREL; AE016858; RAM-Doll-Rpbl. A.

GO; GO:000550; P:transcription; IRA.

GO; GO:000550; P:transcription; IRA.

BO; GO:000550; P:transcription; IRA.

BREL; BREL; BRENGYOSS; RNA DOLRPbl. A.

BREL; BREL; BRENGYOSS; RNA DOLRPbl. A.

BREL; BREL; BRENGYOSS; RNA DOLRPbl. A.

BRENGY PEAN; PE04999; RNA DOLRPbl. A.

BREM; PEO490; RNA DOLRPbl. A.

BREM; PEO499; RNA DOLRPbl. A.

BREM; PEO499; RNA DOLRPbl. A.

BREM; PEGNS PEO499; RNA DOLRPbl. A.

BREM; PEGNS PEO499; RNA DOLRPbl. A.

BREM; PEGNS PEO499; RNA DOLRPbl. A.

BREM; PEGNS PEO499; RNA DOLRPbl. A.

BREM; PEGNS PEO499; RNA DOLRPbl. A.

BREM; PEGNS PEO499; RNA DOLRPbl. A.

BREM; PEGNS PEGNS PEO499; RNA DOLRPBL. A.

BREM; PEGNS PEO499; RNA DOLRPBL. A.

BREM; PEGNS PEGNS PEO499; RNA DOLRPBL. A.

BREM; PEGNS PEGNS PEO499; RNA DOLRPBL. A.

BREM; PEGNS PEGNS PEO499; RNA DOLRPBL. A.

BREM; PEGNS PEGNS PEO499; RNA DOLRPBL. A.

BREM; PEGNS PEGNS PEO499; RNA DOLRPBL. A.

BREM; PEGNS PEGNS PEO499; RNA DOLRPBL. A.

BREM; PEGNS PEGN
 Gaps
 Gaps
 01-07N-2003 (TrEMBLrel. 24, Created)
01-07N-2003 (TrEMBLrel. 24, Last sequence update)
01-07TN-2003 (TrEMBLrel. 24, Last annotation update)
01-07TREMBLrel. 25, Last annotation update)
DNA-directed RNA polymerase, beta' subunit.
RPOC OR PSPTO0620.
Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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 69.2%; Score 36; DB 16; Length 1399; 66.7%; Pred. No. 1.7e+02; tive 2; Mismatches 1; Indels (
 69.2%; Score 36; DB 16; Length 559; 66.7%; Pred. No. 62; ive 2; Mismatches 1; Indels
Enteroccus faecalis.";
Science 299:2071-2074(2003).
EMBL; ABCO16947; AAO79943.1; -.
TIGR; ERFO16947; AAO79943.1; -.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IRR00047; Prok lipoprot_S.
InterPro; IRR000914; SBP bac_5.
Fram; PF00466; SBP bac_5.
Prom; PF00466; SBP bac_5.
Refam; PR001696; SBP b
 PRT; 1399 AA
 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
 Local Similarity 66.7
 PRELIMINARY;
 351 LIPEGMSYS 359
 :||| |:||
581 QVVPAGLSY 589
 2 EVVPXGMSY 10
 3 VVPXGMSYS 11
 SEQUENCE FROM N.A. STRAIN=DC3000;
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Indels

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Pred. No. 41; 2; Mismatches

60.08;

Best Local Similarity 60.0 Matches 6; Conservative

:||| |: || 179 QVVPVGLGYS 188

2 EVVPXGMSYS 11

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 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein precursor.
Lycopersicon esculentum (Tomato).
Eukaryotas, Viridiplantae, Strepticphyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, repticotyledons; core eudicots; asterids, lamiids, Solanales, Solanaceae, Solanum.
NCBI_TaxID=4081;
 Gaps
 "Genome divergence in two Prochlorococcus ecotypes reflects oceanic niche differentiation.";
 SEQUENCE FROM N.A.

STAIN=V736; TISSUE=Pistil;

X MEDLINE=95375233; PubMed=7647301;

X MILLIGAN S.B., Gasser C.S.;

MILLIGAN S.B., Gasser C.S.;

T "Nature and regulation of pistil-expressed genes in tomato.";

ID Plant Mol. Biol. 28:691-711(1995).

R EMBL, U20592; AAA80497.1; -.

R GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.

R GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.

R PRO197; Kunitz_legume.

R PRINTS; PRO0291; Kunitz_legume.

R PRINTS; PRO0291; Kunitz_legume; 1.

R SMART; SM00452; STI; 1.

R PROSITE; PS00283; SOYBEAN_KUNITZ; 1.
 MEDIINE=22825699; PubMed=12917642;
Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Johnson Z.I., Land M., Lidlin D., Post A.F., Regala W., Shah M.
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb E.A., Zinser E.R., Chisholm S.W.;
 01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Phospholipid and glycerol acyltransferase (From 'motifs_6.msf').
 ö
 Prochlorococcus marinus (strain MIT 9313).
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 DB 16; Length 245;
 67.3%; Score 35; DB 10; Length 225; 54.5%; Pred. No. 37;
 2; Indels
 nature 424:1042-1047(2003).
EMBL, BX572098; CAE21267.1; -.
Acyltransferase, Transferase, Complete proteome.
SEQUENCE 245 AA; 26907 MW; 106F7C4CBE2C6427 CRC64;
 25188 MW; 1074C261D20CFDAD CRC64;
 245 AA
 3; Mismatches
 67.3%; Score 35;
 POTENTIAL.
UNKNOWN.
 PRT;
 Hypothetical protein; Signal SIGNAL 1
 6; Conservative
 PRELIMINARY;
 1 EEVVPXGMSYS 11
 32 DEVVPNGKTYA 42
 21 2
225 AA;
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=74547;
 SEQUENCE
 Query Match
 Q7V6Q4
Q7V6Q4;
 ESULT 14
77V6Q4
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 Gaps
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
 .;
0
 "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 282:2012-2018(1998). BMEL; Z81109; CAB03241.1; -. BMEL; Z811109; CAB1241.1; -- WormPep; R10D12.10; CE12690.
 67.3%; Score 35; DB 5; Length 425; 50.0%; Pred. No. 75; 2; Indels iive 3; Mismatches 2; Indels
 GO; GO:0005524; F.ATP binding; IEA.
GO; GO:0004672; F:protein Kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Prot_kinase.
 Percy C.M.; Submitted (OCT-1996) to the BMBL/GenBank/DDBJ databases
 ATP-binding; Transferase. SEQUENCE 425 AA; 49410 MW; 5D96E29B08C8E9D6 CRC64;
 Last sequence update)
Last annotation update)
 Premi PP00069; pkinase; 1.
Prodom; PD000001; Prot kinase; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 3, 2004, 11:57:35
 Created)
 SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
 01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-OCT-2003 (TrEMBLrel. 25,
 Query Match
Best Local Similarity 50.0
Matches 5; Conservative
 PRELIMINARY;
 335 EQIVEGELQY 344
 1 EEVVPXGMSY 10
 R10D12.10.
Caenorhabditis elegans
 Search completed: June Job time: 29.8667 secs
 SEQUENCE FROM N.A.
 R10D12.10 protein.
 NCBI_TaxID=6239;
 Q9XVK4
RESULT 15
Q9XVK4
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